

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 09:34:25 ; Search time 884.571 Seconds  
(without alignments)  
1314.676 Million cell updates/sec

Title: US-10-688-489-75  
Perfect score: 24  
Sequence: 1 tcgagacggtctctgagggttac 24  
Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database :

- GenEmbl:\*
- 1: gb\_ba:\*
  - 2: gb\_htg:\*
  - 3: gb\_in:\*
  - 4: gb\_om:\*
  - 5: gb\_ov:\*
  - 6: gb\_pac:\*
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  - 8: gb\_pr:\*
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  - 11: gb\_scs:\*
  - 12: gb\_sy:\*
  - 13: gb\_un:\*
  - 14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| C 1        | 24    | 100.0       | 395    | 14    | AF458358    |
| C 2        | 24    | 100.0       | 451    | 14    | AF458353    |
| C 3        | 24    | 100.0       | 462    | 14    | AF458350    |
| C 4        | 24    | 100.0       | 463    | 14    | AF458344    |
| C 5        | 24    | 100.0       | 463    | 14    | AF458347    |
| C 6        | 24    | 100.0       | 463    | 14    | AF458348    |
| C 7        | 24    | 100.0       | 463    | 14    | AF458355    |
| C 8        | 24    | 100.0       | 463    | 14    | AF458360    |
| C 9        | 24    | 100.0       | 463    | 14    | AF458361    |
| C 10       | 24    | 100.0       | 464    | 14    | AF458361    |
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| C 14       | 24    | 100.0       | 464    | 14    | AF458361    |
| C 15       | 24    | 100.0       | 464    | 14    | AF458361    |
| C 16       | 24    | 100.0       | 464    | 14    | AF458361    |
| C 17       | 24    | 100.0       | 464    | 14    | AF458361    |
| C 18       | 24    | 100.0       | 464    | 14    | AF458361    |
| C 19       | 24    | 100.0       | 464    | 14    | AF458361    |

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| C 93  | 24   | 100.0 | 11029 | 14 | AF404756   | AF404756 West Nile     | C 166 | 22.4 | 93.3 | 10977  | 14 | AF069076   | AF069076 Japanese    |
| C 94  | 24   | 100.0 | 11029 | 14 | AF404757   | AF404757 West Nile     | C 167 | 22.4 | 93.3 | 10977  | 14 | AF486638   | AF486638 Japanese    |
| C 95  | 24   | 100.0 | 11029 | 14 | AF481864   | AF481864 West Nile     | C 168 | 22.4 | 93.3 | 10978  | 14 | AY184212   | AY184212 Japanese    |
| C 96  | 24   | 100.0 | 11029 | 14 | AF533540   | AF533540 West Nile     | C 169 | 22.4 | 93.3 | 10989  | 14 | AY268132   | AY268132 West Nile   |
| C 97  | 24   | 100.0 | 11029 | 14 | AY289214   | AY289214 West Nile     | C 170 | 21.4 | 89.2 | 524    | 14 | AF297851   | AF297851 Kunjin vi   |
| C 98  | 24   | 100.0 | 11057 | 14 | AY688948   | AY688948 West Nile     | C 171 | 20.8 | 86.7 | 459    | 14 | AF297851   | AF297851 Kunjin vi   |
| C 99  | 23   | 95.8  | 456   | 14 | AF458351   | AF458351 Kunjin vi     | C 172 | 20.8 | 86.7 | 576    | 14 | AF308515   | AF308515 Japanese en |
| C 100 | 22.4 | 93.3  | 346   | 14 | AF148902   | AF148902 Japanese      | C 173 | 20.8 | 86.7 | 576    | 14 | AF308515   | AF308515 Japanese en |
| C 101 | 22.4 | 93.3  | 424   | 14 | AF092550   | AF092550 Japanese      | C 174 | 20.8 | 86.7 | 10963  | 14 | AF308516   | AF308516 Japanese    |
| C 102 | 22.4 | 93.3  | 424   | 14 | AF092552   | AF092552 Japanese      | C 175 | 20.8 | 86.7 | 10976  | 14 | AF315119   | AF315119 Japanese    |
| C 103 | 22.4 | 93.3  | 424   | 14 | AF092553   | AF092553 Japanese      | C 176 | 20.8 | 86.7 | 10977  | 14 | AF080251   | AF080251 Japanese    |
| C 104 | 22.4 | 93.3  | 424   | 14 | JEVNSSGAC  | JEVNSSGAC Japanese en  | C 177 | 19.4 | 80.8 | 129841 | 2  | AC140102   | AC140102 Felis cat   |
| C 105 | 22.4 | 93.3  | 424   | 14 | JEVNSSGAD  | JEVNSSGAD Japanese en  | C 178 | 19.2 | 80.0 | 585    | 14 | AF308517   | AF308517 Japanese    |
| C 106 | 22.4 | 93.3  | 424   | 14 | JEVNSSGAE  | JEVNSSGAE Japanese en  | C 179 | 19.2 | 80.0 | 10741  | 14 | AF277751   | AF277751 West Nile   |
| C 107 | 22.4 | 93.3  | 424   | 14 | JEVNSSGAF  | JEVNSSGAF Japanese en  | C 180 | 18.8 | 78.3 | 3000   | 8  | AF430213   | AF430213 Cryptococ   |
| C 108 | 22.4 | 93.3  | 424   | 14 | JEVNSSGAG  | JEVNSSGAG Japanese en  | C 181 | 18.8 | 78.3 | 165714 | 10 | AC103376   | AC103376 Mus muscu   |
| C 109 | 22.4 | 93.3  | 424   | 14 | JEVNSSGAH  | JEVNSSGAH Japanese en  | C 182 | 18.8 | 78.3 | 182831 | 2  | AC131037   | AC131037 Mus muscu   |
| C 110 | 22.4 | 93.3  | 424   | 14 | JEVNSSGAI  | JEVNSSGAI Japanese en  | C 183 | 18.8 | 78.3 | 240626 | 2  | AC105660   | AC105660 Rattus no   |
| C 111 | 22.4 | 93.3  | 424   | 14 | JEVNSSGAJ  | JEVNSSGAJ Japanese en  | C 184 | 18.2 | 75.8 | 6851   | 9  | AC027343   | AC027343 Homo sapi   |
| C 112 | 22.4 | 93.3  | 451   | 14 | AF458352   | AF458352 West Nile     | C 185 | 18.2 | 75.8 | 103428 | 9  | AC024577   | AC024577 Homo sapi   |
| C 113 | 22.4 | 93.3  | 458   | 14 | AF458356   | AF458356 Kunjin vi     | C 186 | 18.2 | 75.8 | 193105 | 10 | AC107236   | AC107236 Mus muscu   |
| C 114 | 22.4 | 93.3  | 463   | 14 | AF458343   | AF458343 West Nile     | C 187 | 17.8 | 74.2 | 1588   | 8  | GMA563382  | AY563382 Glycine m   |
| C 115 | 22.4 | 93.3  | 463   | 14 | AY278556   | AY278556 Japanese en   | C 188 | 17.8 | 74.2 | 1628   | 8  | GMA563382  | AY563382 Glycine m   |
| C 116 | 22.4 | 93.3  | 533   | 14 | JEVNSSGAA  | JEVNSSGAA Japanese en  | C 189 | 17.8 | 74.2 | 147908 | 5  | AC091293   | AC091293 Takifugu    |
| C 117 | 22.4 | 93.3  | 536   | 14 | AF148900   | AF148900 Japanese      | C 190 | 17.8 | 74.2 | 159100 | 2  | AC073224   | AC073224 Homo sapi   |
| C 118 | 22.4 | 93.3  | 542   | 14 | AF297850   | AF297850 Kunjin vi     | C 191 | 17.8 | 74.2 | 169954 | 10 | AL672269   | AL672269 Mouse DNA   |
| C 119 | 22.4 | 93.3  | 545   | 14 | FVNSSGAH   | FVNSSGAH Japanese      | C 192 | 17.8 | 74.2 | 174458 | 9  | AC091189   | AC091189 Homo sapi   |
| C 120 | 22.4 | 93.3  | 566   | 14 | VPNG6544P2 | VPNG6544P2 Japanese    | C 193 | 17.8 | 74.2 | 178804 | 9  | AC113134   | AC113134 Homo sapi   |
| C 121 | 22.4 | 93.3  | 572   | 14 | AF306514   | AF306514 Japanese      | C 194 | 17.8 | 74.2 | 188111 | 2  | AC113118   | AC113118 Mus muscu   |
| C 122 | 22.4 | 93.3  | 582   | 14 | AF218068   | AF218068 Japanese      | C 195 | 17.8 | 74.2 | 211998 | 10 | AL732530   | AL732530 Mouse DNA   |
| C 123 | 22.4 | 93.3  | 583   | 14 | AF297857   | AF297857 Kunjin vi     | C 196 | 17.8 | 74.2 | 217089 | 2  | AC109899   | AC109899 Rattus no   |
| C 124 | 22.4 | 93.3  | 583   | 14 | AF251616   | AF251616 Japanese      | C 197 | 17.8 | 74.2 | 227370 | 2  | AC116888   | AC116888 Mus muscu   |
| C 125 | 22.4 | 93.3  | 583   | 14 | AF297840   | AF297840 Kunjin vi     | C 198 | 17.8 | 74.2 | 246669 | 2  | AC096099   | AC096099 Rattus no   |
| C 126 | 22.4 | 93.3  | 583   | 14 | AF297847   | AF297847 Kunjin vi     | C 199 | 17.8 | 74.2 | 299050 | 1  | BX251411   | BX251411 Tropherym   |
| C 127 | 22.4 | 93.3  | 583   | 14 | AF297852   | AF297852 Kunjin vi     | C 200 | 17.8 | 74.2 | 302529 | 1  | AE016851   | AE016851 Tropherym   |
| C 128 | 22.4 | 93.3  | 594   | 14 | AF297853   | AF297853 Kunjin vi     | C 201 | 17.6 | 73.3 | 1150   | 14 | D86537     | D86537 Hepatitis C   |
| C 129 | 22.4 | 93.3  | 598   | 14 | AF289816   | AF289816 Japanese      | C 202 | 17.6 | 73.3 | 1776   | 8  | ATH419854  | ATH419854 Arabidops  |
| C 130 | 22.4 | 93.3  | 600   | 14 | AF297846   | AF297846 Kunjin vi     | C 203 | 17.6 | 73.3 | 1823   | 8  | AY085706   | AY085706 Arabidops   |
| C 131 | 22.4 | 93.3  | 625   | 14 | AF3118291  | AF3118291 Japanese     | C 204 | 17.6 | 73.3 | 74316  | 8  | T21E18     | AC024174 Sequence    |
| C 132 | 22.4 | 93.3  | 972   | 14 | AF311748   | AF311748 Japanese      | C 205 | 17.6 | 73.3 | 95600  | 2  | AC024227   | AC024227 Arabidops   |
| C 133 | 22.4 | 93.3  | 10951 | 14 | JEVNLINGCG | JEVNLINGCG Japanese en | C 206 | 17.6 | 73.3 | 127200 | 10 | AC132580   | AC132580 Mus muscu   |
| C 134 | 22.4 | 93.3  | 10963 | 14 | AF045551   | AF045551 Japanese      | C 207 | 17.6 | 73.3 | 169769 | 10 | AC147631   | AC147631 Mus muscu   |
| C 135 | 22.4 | 93.3  | 10964 | 14 | AF217620   | AF217620 Japanese      | C 208 | 17.6 | 73.3 | 188095 | 4  | AC091505   | AC091505 Sus scrof   |
| C 136 | 22.4 | 93.3  | 10965 | 14 | AB051292   | AB051292 Japanese      | C 209 | 17.6 | 73.3 | 192971 | 10 | AC118012   | AC118012 Mus muscu   |
| C 137 | 22.4 | 93.3  | 10968 | 14 | AY585242   | AY585242 Japanese      | C 210 | 17.6 | 73.3 | 195773 | 2  | AC145532   | AC145532 Ootolemur   |
| C 138 | 22.4 | 93.3  | 10968 | 14 | AY585243   | AY585243 Japanese      | C 211 | 17.6 | 73.3 | 195773 | 2  | AC145532   | AC145532 Ootolemur   |
| C 139 | 22.4 | 93.3  | 10969 | 14 | JEU15763   | JEU15763 Japanese en   | C 212 | 17.6 | 73.3 | 215508 | 10 | AC118704   | AC118704 Mus muscu   |
| C 140 | 22.4 | 93.3  | 10969 | 14 | JEVCMNAA   | JEVCMNAA Japanese en   | C 213 | 17.6 | 73.3 | 229872 | 10 | AL591514   | AL591514 Mouse DNA   |
| C 141 | 22.4 | 93.3  | 10970 | 14 | AF254452   | AF254452 Japanese      | C 214 | 17.6 | 73.3 | 236158 | 10 | AL808112   | AL808112 Mouse DNA   |
| C 142 | 22.4 | 93.3  | 10970 | 14 | AF254453   | AF254453 Japanese      | C 215 | 17.4 | 72.5 | 11066  | 14 | AY453412   | AY453412 Usutu vir   |
| C 143 | 22.4 | 93.3  | 10970 | 14 | AY303791   | AY303791 Japanese      | C 216 | 17.4 | 72.5 | 11066  | 14 | AY453411   | AY453411 Usutu vir   |
| C 144 | 22.4 | 93.3  | 10970 | 14 | AY303792   | AY303792 Japanese      | C 217 | 17.4 | 72.5 | 139273 | 9  | AL596275   | AL596275 Human DNA   |
| C 145 | 22.4 | 93.3  | 10970 | 14 | AY303793   | AY303793 Japanese      | C 218 | 17.4 | 72.5 | 187999 | 2  | AC026928   | AC026928 Homo sapi   |
| C 146 | 22.4 | 93.3  | 10970 | 14 | AY303794   | AY303794 Japanese      | C 219 | 17.4 | 72.5 | 194630 | 10 | AL833780   | AL833780 Mouse DNA   |
| C 147 | 22.4 | 93.3  | 10970 | 14 | AY303795   | AY303795 Japanese      | C 220 | 17.4 | 72.5 | 214395 | 2  | AC130993   | AC130993 Rattus no   |
| C 148 | 22.4 | 93.3  | 10970 | 14 | AY303796   | AY303796 Japanese      | C 221 | 17.4 | 72.5 | 215217 | 2  | AC127984   | AC127984 Rattus no   |
| C 149 | 22.4 | 93.3  | 10970 | 14 | AY303797   | AY303797 Japanese      | C 222 | 17.2 | 71.7 | 511    | 10 | AB076985   | AB076985 Rattus no   |
| C 150 | 22.4 | 93.3  | 10970 | 14 | AY303798   | AY303798 Japanese      | C 223 | 17.2 | 71.7 | 752    | 9  | HSAC324661 | AC244661 Homo sapi   |
| C 151 | 22.4 | 93.3  | 10976 | 14 | AF014160   | AF014160 Japanese      | C 224 | 17.2 | 71.7 | 55399  | 2  | AC068179   | AC068179 Homo sapi   |
| C 152 | 22.4 | 93.3  | 10976 | 14 | AF014161   | AF014161 Japanese      | C 225 | 17.2 | 71.7 | 110000 | 8  | CR382123   | Continuation (4 of   |
| C 153 | 22.4 | 93.3  | 10976 | 14 | AF017523   | AF017523 Japanese      | C 226 | 17.2 | 71.7 | 138663 | 10 | AL713874   | AL713874 Mouse DNA   |
| C 154 | 22.4 | 93.3  | 10976 | 14 | AF098735   | AF098735 Japanese      | C 227 | 17.2 | 71.7 | 139226 | 2  | AC148378   | AC148378 Sorex ara   |
| C 155 | 22.4 | 93.3  | 10976 | 14 | AF098736   | AF098736 Japanese      | C 228 | 17.2 | 71.7 | 157771 | 2  | AC148432   | AC148432 Sorex ara   |
| C 156 | 22.4 | 93.3  | 10976 | 14 | AF098737   | AF098737 Japanese      | C 229 | 17.2 | 71.7 | 166731 | 4  | AC129065   | AC129065 Didelphis   |
| C 157 | 22.4 | 93.3  | 10976 | 14 | AF221499   | AF221499 Japanese      | C 230 | 17.2 | 71.7 | 173910 | 2  | AC147398   | AC147398 Sus scrof   |
| C 158 | 22.4 | 93.3  | 10976 | 14 | AF221500   | AF221500 Japanese      | C 231 | 17.2 | 71.7 | 178169 | 2  | AC144169   | AC144169 Macaca mu   |
| C 159 | 22.4 | 93.3  | 10976 | 14 | AF416457   | AF416457 Japanese      | C 232 | 17.2 | 71.7 | 179871 | 2  | AC109185   | AC109185 Mus muscu   |
| C 160 | 22.4 | 93.3  | 10976 | 14 | JEU14163   | JEU14163 Japanese en   | C 233 | 17.2 | 71.7 | 204306 | 2  | AC141521   | AC141521 Rattus no   |
| C 161 | 22.4 | 93.3  | 10976 | 14 | JEU47032   | JEU47032 Japanese en   | C 234 | 17.2 | 71.7 | 212753 | 9  | HS212A2    | Z95114 Human DNA s   |
| C 162 | 22.4 | 93.3  | 10976 | 14 | JEVBTICG   | JEVBTICG Japanese en   | C 235 | 17.2 | 71.7 | 212884 | 2  | AC139964   | AC139964 Rattus no   |
| C 163 | 22.4 | 93.3  | 10976 | 14 | JEVBCG     | JEVBCG Japanese en     | C 236 | 17.2 | 71.7 | 223397 | 2  | EX001052   | EX001052 Mus muscu   |
| C 164 | 22.4 | 93.3  | 10976 | 14 | JEVSA      | JEVSA Japanese en      | C 237 | 17.2 | 71.7 | 250391 | 2  | AC128962   | AC128962 Rattus no   |
| C 165 | 22.4 | 93.3  | 10976 | 14 | JEVSAV     | JEVSAV Japanese en     | C 238 | 17.2 | 71.7 | 298008 | 2  | AC123723   | AC123723 Mus muscu   |



|       |      |      |        |    |             |                      |       |      |      |        |    |             |
|-------|------|------|--------|----|-------------|----------------------|-------|------|------|--------|----|-------------|
| C 239 | 17.2 | 71.7 | 302921 | 2  | AC090998    | AC090998 Homo sapi   | 312   | 16.6 | 69.2 | 81020  | 8  | AB026645    |
| 240   | 17.2 | 71.7 | 347786 | 1  | BX640438    | Bordetelli           | C 313 | 16.6 | 69.2 | 83178  | 2  | AC117537    |
| 241   | 17.2 | 71.7 | 349146 | 1  | BX640424    | Bordetelli           | C 314 | 16.6 | 69.2 | 90180  | 2  | AC008176    |
| C 242 | 16.8 | 70.0 | 438    | 3  | MMDH6       | X07299 M.musculus    | C 315 | 16.6 | 69.2 | 105199 | 9  | AP001576    |
| 243   | 16.8 | 70.0 | 2418   | 3  | PELCP8K     | L40818 Periplaneta   | C 316 | 16.6 | 69.2 | 105999 | 9  | HS73M5      |
| 244   | 16.8 | 70.0 | 2799   | 6  | AR207538    | L40818 Periplaneta   | C 317 | 16.6 | 69.2 | 110000 | 1  | AE000516_23 |
| 245   | 16.8 | 70.0 | 2799   | 6  | BD003326    | BD003326 Phospholi   | C 318 | 16.6 | 69.2 | 110000 | 1  | AE017225_50 |
| 246   | 16.8 | 70.0 | 3440   | 10 | BC047268    | BC047268 Mus muscu   | C 319 | 16.6 | 69.2 | 110000 | 1  | AE017283_12 |
| 247   | 16.8 | 70.0 | 3490   | 6  | BD003327    | BD003327 Phospholi   | C 320 | 16.6 | 69.2 | 110000 | 1  | AE017283_13 |
| 248   | 16.8 | 70.0 | 3494   | 10 | MMU87557    | U87557 Mus musculu   | C 321 | 16.6 | 69.2 | 110000 | 1  | AE017334_50 |
| 249   | 16.8 | 70.0 | 3671   | 10 | BC068317    | BC068317 Mus muscu   | C 322 | 16.6 | 69.2 | 110000 | 2  | AP006490_4  |
| 250   | 16.8 | 70.0 | 3852   | 10 | MMFLD2G1    | AF052291 Mus muscu   | C 323 | 16.6 | 69.2 | 113250 | 9  | AC004900    |
| 251   | 16.8 | 70.0 | 13512  | 1  | AE001045    | AE001045 Archaeogl   | C 324 | 16.6 | 69.2 | 115916 | 9  | AL590618    |
| 252   | 16.8 | 70.0 | 66886  | 8  | AE016817_14 | Continuation (15 o   | C 325 | 16.6 | 69.2 | 115916 | 9  | AL590618    |
| 253   | 16.8 | 70.0 | 98760  | 8  | AC133749    | AC133749 Homo sapi   | C 326 | 16.6 | 69.2 | 132403 | 2  | AL590618    |
| C 254 | 16.8 | 70.0 | 110000 | 8  | AE016815_1  | Continuation (2 of   | C 327 | 16.6 | 69.2 | 135855 | 9  | HS135814    |
| 255   | 16.8 | 70.0 | 116932 | 8  | AC074232    | AC074232 Oryza sat   | C 328 | 16.6 | 69.2 | 141529 | 9  | AC011369    |
| C 256 | 16.8 | 70.0 | 122214 | 8  | AP004033    | AP004033 Oryza sat   | C 329 | 16.6 | 69.2 | 142233 | 10 | AC125129    |
| C 257 | 16.8 | 70.0 | 123943 | 10 | AL592547    | AL592547 Mouse DNA   | C 330 | 16.6 | 69.2 | 145729 | 9  | AC117489    |
| 258   | 16.8 | 70.0 | 132444 | 9  | AC091878    | AC091878 Homo sapi   | C 331 | 16.6 | 69.2 | 150735 | 9  | AC090687    |
| C 259 | 16.8 | 70.0 | 141852 | 8  | AP004863    | AP004863 Oryza sat   | C 332 | 16.6 | 69.2 | 151009 | 2  | AC135784    |
| C 260 | 16.8 | 70.0 | 144339 | 2  | AF290942    | AF290942 Homo sapi   | C 333 | 16.6 | 69.2 | 152605 | 2  | AC136886    |
| 261   | 16.8 | 70.0 | 144383 | 9  | AC102944    | AC102944 Homo sapi   | C 334 | 16.6 | 69.2 | 154195 | 2  | AC142242    |
| C 262 | 16.8 | 70.0 | 147710 | 2  | AC090070    | AC090070 Homo sapi   | C 335 | 16.6 | 69.2 | 154653 | 9  | AC146050    |
| 263   | 16.8 | 70.0 | 155014 | 2  | AC140065    | AC140065 Homo sapi   | C 336 | 16.6 | 69.2 | 159681 | 10 | AC132088    |
| C 264 | 16.8 | 70.0 | 155161 | 9  | AC083900    | AC083900 Homo sapi   | C 337 | 16.6 | 69.2 | 159709 | 9  | AC008705    |
| C 265 | 16.8 | 70.0 | 160481 | 2  | AC021784    | AC021784 Homo sapi   | C 338 | 16.6 | 69.2 | 161589 | 2  | AC136881    |
| C 266 | 16.8 | 70.0 | 162593 | 2  | AC022576    | AC022576 Homo sapi   | C 339 | 16.6 | 69.2 | 162258 | 9  | AC105748    |
| C 267 | 16.8 | 70.0 | 163965 | 10 | AC132919    | AC132919 Mus muscu   | C 340 | 16.6 | 69.2 | 164331 | 2  | AC118869    |
| C 268 | 16.8 | 70.0 | 165072 | 2  | AC120286    | AC120286 Rattus no   | C 341 | 16.6 | 69.2 | 166234 | 9  | HS273P12    |
| 269   | 16.8 | 70.0 | 170591 | 2  | AC022936    | AC022936 Homo sapi   | C 342 | 16.6 | 69.2 | 166355 | 9  | AP000888    |
| 270   | 16.8 | 70.0 | 175202 | 9  | AC022733    | AC022733 Homo sapi   | C 343 | 16.6 | 69.2 | 166763 | 2  | AC112941    |
| 271   | 16.8 | 70.0 | 175491 | 2  | AC129683    | AC129683 Rattus no   | C 344 | 16.6 | 69.2 | 170465 | 3  | AC091128    |
| 272   | 16.8 | 70.0 | 175784 | 9  | AP003789    | AP003789 Homo sapi   | C 345 | 16.6 | 69.2 | 170928 | 2  | AC148803    |
| C 273 | 16.8 | 70.0 | 192938 | 10 | AC125067    | AC125067 Mus muscu   | C 346 | 16.6 | 69.2 | 177727 | 2  | AC022178    |
| C 274 | 16.8 | 70.0 | 193170 | 2  | AC068652    | AC068652 Mus muscu   | C 347 | 16.6 | 69.2 | 178804 | 9  | AC113134    |
| 275   | 16.8 | 70.0 | 194609 | 2  | AC013775    | AC013775 Mus muscu   | C 348 | 16.6 | 69.2 | 178965 | 9  | AC098850    |
| 276   | 16.8 | 70.0 | 195529 | 2  | AC025714    | AC025714 Homo sapi   | C 349 | 16.6 | 69.2 | 180783 | 2  | AC128244    |
| 277   | 16.8 | 70.0 | 201403 | 9  | AC145921    | AC145921 Pan trogl   | C 350 | 16.6 | 69.2 | 182003 | 9  | AL355987    |
| C 278 | 16.8 | 70.0 | 214125 | 10 | AC083948    | AC083948 Mus muscu   | C 351 | 16.6 | 69.2 | 185902 | 10 | AC122428    |
| C 279 | 16.8 | 70.0 | 241775 | 2  | AC131140    | AC131140 Rattus no   | C 352 | 16.6 | 69.2 | 187438 | 3  | AC010711    |
| C 280 | 16.8 | 70.0 | 246006 | 2  | AC102141    | AC102141 Mus muscu   | C 353 | 16.6 | 69.2 | 191174 | 10 | AC116586    |
| C 281 | 16.8 | 70.0 | 251571 | 2  | AC114093    | AC114093 Rattus no   | C 354 | 16.6 | 69.2 | 191727 | 10 | AC150744    |
| 282   | 16.8 | 70.0 | 259978 | 2  | AC073819    | AC073819 Mus muscu   | C 355 | 16.6 | 69.2 | 195007 | 9  | CNS06C81    |
| C 283 | 16.8 | 70.0 | 270738 | 2  | AC095854    | AC095854 Rattus no   | C 356 | 16.6 | 69.2 | 195202 | 2  | AC132669    |
| C 284 | 16.8 | 70.0 | 274766 | 2  | AC135283    | AC135283 Rattus no   | C 357 | 16.6 | 69.2 | 196086 | 10 | AC104889    |
| C 285 | 16.8 | 70.0 | 286178 | 2  | AC091290    | AC091290 Mus muscu   | C 358 | 16.6 | 69.2 | 198552 | 2  | AC025638    |
| C 286 | 16.8 | 70.0 | 300029 | 8  | AE017114    | AE017114 Oryza sat   | C 359 | 16.6 | 69.2 | 198965 | 2  | AC148961    |
| 287   | 16.6 | 69.2 | 183    | 11 | BV171141    | BV171141 sqmm40750   | C 360 | 16.6 | 69.2 | 200151 | 2  | AC151872    |
| C 288 | 16.6 | 69.2 | 345    | 14 | AY089756    | AY089756 Hepatitis   | C 361 | 16.6 | 69.2 | 201512 | 9  | AL391833    |
| C 289 | 16.6 | 69.2 | 345    | 14 | AY089758    | AY089758 Hepatitis   | C 362 | 16.6 | 69.2 | 202083 | 2  | AC023833    |
| C 290 | 16.6 | 69.2 | 597    | 6  | CX524047    | CX524047 Sequence    | C 363 | 16.6 | 69.2 | 202383 | 2  | AC139291    |
| 291   | 16.6 | 69.2 | 723    | 3  | TVCP1       | TVCP1 Sequence       | C 364 | 16.6 | 69.2 | 203226 | 2  | AC105479    |
| C 292 | 16.6 | 69.2 | 1021   | 3  | GDHXA2      | GDHXA2 Sequence      | C 365 | 16.6 | 69.2 | 207086 | 10 | AL596117    |
| C 293 | 16.6 | 69.2 | 1261   | 5  | GDHXA2      | GDHXA2 Sequence      | C 366 | 16.6 | 69.2 | 209111 | 9  | CNS00YVG    |
| 294   | 16.6 | 69.2 | 1283   | 9  | AK098639    | AK098639 Homo sapi   | C 367 | 16.6 | 69.2 | 212111 | 2  | AC094482    |
| C 295 | 16.6 | 69.2 | 1381   | 8  | AY096674    | AY096674 Arabidops   | C 368 | 16.6 | 69.2 | 213244 | 10 | AC113016    |
| C 296 | 16.6 | 69.2 | 1758   | 8  | AY050889    | AY050889 Arabidops   | C 369 | 16.6 | 69.2 | 227877 | 2  | AC109725    |
| C 297 | 16.6 | 69.2 | 1832   | 8  | AY084738    | AY084738 Arabidops   | C 370 | 16.6 | 69.2 | 228232 | 2  | AC090293    |
| C 298 | 16.6 | 69.2 | 1837   | 1  | STWMP1A     | STWMP1A Sequence     | C 371 | 16.6 | 69.2 | 228742 | 2  | AC134190    |
| 299   | 16.6 | 69.2 | 2238   | 3  | AB006454    | AB006454 Streptomyce | C 372 | 16.6 | 69.2 | 228940 | 2  | AC126890    |
| C 300 | 16.6 | 69.2 | 2922   | 3  | TTT276471   | TTT276471 Tetrahyme  | C 373 | 16.6 | 69.2 | 229710 | 2  | AC130229    |
| C 301 | 16.6 | 69.2 | 3000   | 9  | AK095805    | AK095805 Homo sapi   | C 374 | 16.6 | 69.2 | 231736 | 2  | AC117323    |
| C 302 | 16.6 | 69.2 | 5870   | 6  | CQ363854    | CQ363854 Sequence    | C 375 | 16.6 | 69.2 | 231750 | 2  | AC095594    |
| C 303 | 16.6 | 69.2 | 11199  | 1  | AE001061    | AE001061 Archaeogl   | C 376 | 16.6 | 69.2 | 232649 | 2  | AC108267    |
| C 304 | 16.6 | 69.2 | 12439  | 1  | AE009153    | AE009153 Agrobacte   | C 377 | 16.6 | 69.2 | 233784 | 2  | AC130877    |
| C 305 | 16.6 | 69.2 | 12606  | 1  | AE008118    | AE008118 Agrobacte   | C 378 | 16.6 | 69.2 | 238653 | 2  | AC099453    |
| C 306 | 16.6 | 69.2 | 37586  | 6  | AX191745    | AX191745 Sequence    | C 379 | 16.6 | 69.2 | 239875 | 2  | AC126827    |
| C 307 | 16.6 | 69.2 | 37959  | 9  | BX537333    | BX537333 Human DNA   | C 380 | 16.6 | 69.2 | 240091 | 2  | AC137350    |
| C 308 | 16.6 | 69.2 | 43489  | 2  | AC019833    | AC019833 Drosophil   | C 381 | 16.6 | 69.2 | 241859 | 2  | AC136406    |
| 309   | 16.6 | 69.2 | 61880  | 2  | AC021135    | AC021135 Homo sapi   | C 382 | 16.6 | 69.2 | 243329 | 5  | AC145979    |
| C 310 | 16.6 | 69.2 | 61880  | 2  | AC021135    | AC021135 Homo sapi   | C 383 | 16.6 | 69.2 | 244978 | 9  | AF241726    |
| 311   | 16.6 | 69.2 | 69776  | 9  | AL953870    | AL953870 Human DNA   | C 384 | 16.6 | 69.2 | 250023 | 2  | AC111499    |

|                    |           |
|--------------------|-----------|
| AB026645           | Arabidops |
| AC117537           | Magnapor  |
| AC008176           | Homo sapi |
| AP001576           | Homo sapi |
| AJ010597           | Homo sapi |
| Continuation (24 o |           |
| Continuation (51 o |           |
| Continuation (13 o |           |
| Continuation (14 o |           |
| Continuation (51 o |           |
| Continuation (5 of |           |
| AC004900           | Homo sapi |
| AL590618           | Human DNA |
| AL590618           | Human DNA |
| AC148792           | Ocolemur  |
| AJ010598           | Homo sapi |
| AC011369           | Homo sapi |
| AC125129           | Mus muscu |
| AC117489           | Homo sapi |
| AC090687           | Homo sapi |
| AC135784           | Homo sapi |
| AC136886           | Sus scrof |
| AC142242           | Acelexix  |
| AC146050           | Pan trogl |
| AC132088           | Mus muscu |
| AC008705           | Homo sapi |
| AC136881           | Sus scrof |
| AC105748           | Homo sapi |
| AC118869           | Rattus no |
| AL034372           | Human DNA |
| AP000888           | Homo sapi |
| AC112941           | Mus muscu |
| AC091128           | Drosophil |
| AC148803           | Ocolemur  |
| AC022178           | Homo sapi |
| AC113134           | Homo sapi |
| AC098850           | Homo sapi |
| AC128244           | Rattus no |
| AL355987           | Human DNA |
| AC122428           | Mus muscu |
| AC010711           | Drosophil |
| AC116586           | Mus muscu |
| AC150744           | Mus muscu |
| AL391749           | Human chr |
| AC132669           | Rattus no |
| AC104889           | Mus muscu |
| AC025638           | Homo sapi |
| AC148961           | Callithri |
| AC151872           | Lemur cat |
| AL391833           | Human DNA |
| AC023833           | Mus muscu |
| AC139291           | Mus muscu |
| AC105479           | Rattus no |
| AL596117           | Mouse DNA |
| AC094482           | Human chr |
| AC13016            | Mus muscu |
| AC109725           | Rattus no |
| AC090293           | Mus muscu |
| AC134190           | Rattus no |
| AC126890           | Rattus no |
| AC130229           | Rattus no |
| AC117323           | Rattus no |
| AC095594           | Rattus no |
| AC108267           | Rattus no |
| AC130877           | Rattus no |
| AC099453           | Rattus no |
| AC126827           | Rattus no |
| AC137350           | Rattus no |
| AC136406           | Rattus no |
| AC145979           | Gallus ga |
| AF241726           | Homo sapi |
| AC111499           | Rattus no |

|     |      |      |        |    |           |                     |       |      |      |       |    |            |                     |
|-----|------|------|--------|----|-----------|---------------------|-------|------|------|-------|----|------------|---------------------|
| 385 | 16.6 | 69.2 | 253176 | 2  | AC094477  | AC094477 Rattus no  | C 458 | 16.2 | 67.5 | 2459  | 6  | CQ842165   | CQ842165 Sequence   |
| 386 | 16.6 | 69.2 | 254778 | 2  | AC1136532 | AC126532 Rattus no  | C 459 | 16.2 | 67.5 | 2459  | 9  | AKI25202   | AKI25202 Homo sapi  |
| 387 | 16.6 | 69.2 | 258207 | 2  | AC115279  | AC115279 Rattus no  | 460   | 16.2 | 67.5 | 2666  | 10 | MUSEPO     | L77979 Mus musculus |
| 388 | 16.6 | 69.2 | 260860 | 2  | AC115982  | AC125982 Rattus no  | 461   | 16.2 | 67.5 | 2666  | 10 | BC052881   | BC052881 Mus muscu  |
| 389 | 16.6 | 69.2 | 263088 | 2  | AC130872  | AC130872 Rattus no  | 462   | 16.2 | 67.5 | 2694  | 10 | MUSEPP     | D78353 Mus musculus |
| 390 | 16.6 | 69.2 | 264504 | 1  | AE017041  | AE017041 Bacillus   | 463   | 16.2 | 67.5 | 3831  | 6  | CQ581577   | CQ581577 Sequence   |
| 391 | 16.6 | 69.2 | 268718 | 2  | AC106377  | AC106377 Rattus no  | 464   | 16.2 | 67.5 | 4004  | 3  | AY119106   | AY119106 Drosophila |
| 392 | 16.6 | 69.2 | 279912 | 2  | AC136572  | AC126572 Rattus no  | 465   | 16.2 | 67.5 | 4369  | 1  | AF057021   | AF057021 Salmonella |
| 393 | 16.6 | 69.2 | 286205 | 2  | CR739869  | CR739869 Danio rer  | 466   | 16.2 | 67.5 | 5561  | 9  | HUMIL28    | AF057021 Salmonella |
| 394 | 16.6 | 69.2 | 296500 | 1  | SC0939128 | AL939128 Streptomy  | C 467 | 16.2 | 67.5 | 5737  | 6  | A37269     | A37269 Sequence 9   |
| 395 | 16.6 | 69.2 | 304282 | 1  | AE016910  | AE016910 Chromobac  | C 468 | 16.2 | 67.5 | 5737  | 6  | HUMIL2     | J00264 Homo sapien  |
| 396 | 16.6 | 69.2 | 306050 | 1  | EX248341  | EX248341 Mycobacte  | 469   | 16.2 | 67.5 | 6566  | 6  | CQ581576   | CQ581576 Sequence   |
| 397 | 16.6 | 69.2 | 318699 | 3  | AE003470  | AE003470 Drosophila | C 470 | 16.2 | 67.5 | 6566  | 6  | HSIL05     | X06935 Human inter  |
| 398 | 16.6 | 69.2 | 340000 | 9  | HS21C010  | AL113210 Homo sapi  | C 471 | 16.2 | 67.5 | 6752  | 9  | AF359939   | AF359939 Homo sapi  |
| 399 | 16.6 | 69.2 | 346186 | 1  | EX842578  | EX842578 Mycobacte  | C 472 | 16.2 | 67.5 | 7978  | 14 | AE093615   | AE093615 Turnip mo  |
| 400 | 16.4 | 68.3 | 1839   | 6  | CQ804202  | CQ804202 Sequence   | C 473 | 16.2 | 67.5 | 12232 | 1  | AE013121   | AE013121 Thermoana  |
| 401 | 16.4 | 68.3 | 1870   | 8  | BT001966  | BT001966 Arabidops  | 474   | 16.2 | 67.5 | 14659 | 1  | HTH243655  | AJ743655 Methanoba  |
| 402 | 16.4 | 68.3 | 1929   | 6  | AX112678  | AX112678 Sequence   | C 475 | 16.2 | 67.5 | 18573 | 9  | HSOXP3     | Y09980 H. sapiens H |
| 403 | 16.4 | 68.3 | 1929   | 6  | AX506546  | AX506546 Sequence   | C 476 | 16.2 | 67.5 | 21721 | 6  | AR410075   | AR410075 Sequence   |
| 404 | 16.4 | 68.3 | 1929   | 6  | AX652042  | AX652042 Sequence   | C 477 | 16.2 | 67.5 | 21721 | 6  | AX000057   | AX000057 Sequence   |
| 405 | 16.4 | 68.3 | 2039   | 8  | AF360282  | AF360282 Arabidops  | C 478 | 16.2 | 67.5 | 21721 | 6  | AX969164   | AX969164 Sequence   |
| 406 | 16.4 | 68.3 | 2161   | 8  | AY062544  | AY062544 Arabidops  | C 479 | 16.2 | 67.5 | 21721 | 6  | BD062437   | BD062437 LSR recep  |
| 407 | 16.4 | 68.3 | 2193   | 8  | BT000695  | BT000695 Arabidops  | C 480 | 16.2 | 67.5 | 22976 | 6  | AR410057   | AR410057 Sequence   |
| 408 | 16.4 | 68.3 | 2872   | 8  | AK118741  | AK118741 Arabidops  | C 481 | 16.2 | 67.5 | 22976 | 6  | AX000035   | AX000035 Sequence   |
| 409 | 16.4 | 68.3 | 11039  | 1  | AE005828  | AE005828 Caulobact  | C 482 | 16.2 | 67.5 | 22976 | 6  | AX969142   | AX969142 Sequence   |
| 410 | 16.4 | 68.3 | 12347  | 1  | AE005387  | AE005387 Escherich  | C 483 | 16.2 | 67.5 | 22976 | 6  | BD062419   | BD062419 LSR recep  |
| 411 | 16.4 | 68.3 | 17829  | 9  | AP001438  | AP001438 Homo sapi  | C 484 | 16.2 | 67.5 | 23187 | 6  | AR253031   | AR253031 Sequence   |
| 412 | 16.4 | 68.3 | 35296  | 3  | U61944    | U61944 Caenorhabdi  | C 485 | 16.2 | 67.5 | 23187 | 6  | AX100598   | AX100598 Sequence   |
| 413 | 16.4 | 68.3 | 48091  | 2  | AC115963  | AC115963 Mus muscu  | C 486 | 16.2 | 67.5 | 24057 | 1  | AE008725   | AE008725 Salmonell  |
| 414 | 16.4 | 68.3 | 64470  | 2  | AC100171  | AC100171 Mus muscu  | C 487 | 16.2 | 67.5 | 41936 | 6  | AX335752   | AX335752 Sequence   |
| 415 | 16.4 | 68.3 | 79569  | 9  | AC092449  | AC092449 Homo sapi  | C 488 | 16.2 | 67.5 | 41936 | 9  | CH19R30879 | AD000684 Homo sapi  |
| 416 | 16.4 | 68.3 | 8452   | 2  | AC138690  | AC138690 Homo sapi  | C 489 | 16.2 | 67.5 | 45328 | 9  | AC002128   | AC002128 Human DNA  |
| 417 | 16.4 | 68.3 | 91938  | 8  | ATF20M13  | AL035540 Arabidops  | C 490 | 16.2 | 67.5 | 47098 | 6  | AX695416   | AX695416 Sequence   |
| 418 | 16.4 | 68.3 | 100000 | 9  | AP000020  | AP000020 Homo sapi  | C 491 | 16.2 | 67.5 | 51463 | 2  | AC095742   | Continuation (5 of  |
| 419 | 16.4 | 68.3 | 100000 | 9  | AP000020  | AP000020 Homo sapi  | C 492 | 16.2 | 67.5 | 51463 | 2  | AC117148   | Continuation (4 of  |
| 420 | 16.4 | 68.3 | 107740 | 8  | AP000162  | AP000162 Homo sapi  | C 493 | 16.2 | 67.5 | 71894 | 2  | AC027754   | AC027754 Homo sapi  |
| 421 | 16.4 | 68.3 | 126083 | 9  | AC069558  | AC069558 Genomic S  | C 494 | 16.2 | 67.5 | 71894 | 2  | AC027754   | AC027754 Homo sapi  |
| 422 | 16.4 | 68.3 | 130058 | 8  | AC105337  | AC105337 Homo sapi  | C 495 | 16.2 | 67.5 | 73198 | 9  | HSJ127L3   | AL096793 Human DNA  |
| 423 | 16.4 | 68.3 | 148841 | 9  | AC078840  | AC078840 Oryza sat  | C 496 | 16.2 | 67.5 | 73198 | 9  | HSJ127L3   | AL096793 Human DNA  |
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| 425 | 16.4 | 68.3 | 158896 | 2  | AC144354  | AC144354 Homo sapi  | C 498 | 16.2 | 67.5 | 86026 | 8  | AC144727   | AC144727 Medicago   |
| 426 | 16.4 | 68.3 | 159598 | 9  | AP004386  | AP004386 Homo sapi  | C 499 | 16.2 | 67.5 | 94779 | 9  | AP000664   | AP000664 Homo sapi  |
| 427 | 16.4 | 68.3 | 176952 | 8  | AC084023  | AC084023 Oryza sat  | C 500 | 16.2 | 67.5 | 95720 | 2  | AC149154   | AC149154 Xenopus t  |
| 428 | 16.4 | 68.3 | 177341 | 2  | AC079764  | AC079764 Homo sapi  |       |      |      |       |    |            | AC020220 Drosophila |
| 429 | 16.4 | 68.3 | 177737 | 2  | AC146859  | AC146859 Homo sapi  |       |      |      |       |    |            |                     |
| 430 | 16.4 | 68.3 | 179071 | 2  | AC146655  | AC146655 Homo sapi  |       |      |      |       |    |            |                     |
| 431 | 16.4 | 68.3 | 191424 | 9  | BS000127  | BS000127 Pan trogl  |       |      |      |       |    |            |                     |
| 432 | 16.4 | 68.3 | 197877 | 9  | AC090142  | AC090142 Homo sapi  |       |      |      |       |    |            |                     |
| 433 | 16.4 | 68.3 | 198176 | 2  | AC069127  | AC069127 Homo sapi  |       |      |      |       |    |            |                     |
| 434 | 16.4 | 68.3 | 199476 | 2  | AC143053  | AC143053 Macaca mu  |       |      |      |       |    |            |                     |
| 435 | 16.4 | 68.3 | 199789 | 8  | ATCHR1V89 | AL115193 Arabidops  |       |      |      |       |    |            |                     |
| 436 | 16.4 | 68.3 | 200946 | 2  | AC148421  | AC148421 Meleagris  |       |      |      |       |    |            |                     |
| 437 | 16.4 | 68.3 | 213584 | 2  | AC135700  | AC135700 Rattus no  |       |      |      |       |    |            |                     |
| 438 | 16.4 | 68.3 | 229583 | 10 | AL844566  | AL844566 Mouse DNA  |       |      |      |       |    |            |                     |
| 439 | 16.4 | 68.3 | 257071 | 1  | AP002558  | AP002558 Escherich  |       |      |      |       |    |            |                     |
| 440 | 16.4 | 68.3 | 257918 | 2  | AC130780  | AC130780 Rattus no  |       |      |      |       |    |            |                     |
| 441 | 16.4 | 68.3 | 261278 | 2  | AC107586  | AC107586 Rattus no  |       |      |      |       |    |            |                     |
| 442 | 16.4 | 68.3 | 262632 | 2  | AC119780  | AC119780 Rattus no  |       |      |      |       |    |            |                     |
| 443 | 16.4 | 68.3 | 301934 | 8  | AE017110  | AE017110 Oryza sat  |       |      |      |       |    |            |                     |
| 444 | 16.4 | 68.3 | 340000 | 9  | AP0001731 | AP0001731 Homo sapi |       |      |      |       |    |            |                     |
| 445 | 16.2 | 67.5 | 571    | 10 | CLUPS     | X75640 C. longicaud |       |      |      |       |    |            |                     |
| 446 | 16.2 | 67.5 | 636    | 6  | CNS01A6C  | AL112540 Botrytis   |       |      |      |       |    |            |                     |
| 447 | 16.2 | 67.5 | 921    | 8  | AR347653  | AR347653 Sequence   |       |      |      |       |    |            |                     |
| 448 | 16.2 | 67.5 | 1350   | 8  | BT002231  | BT002231 Arabidops  |       |      |      |       |    |            |                     |
| 449 | 16.2 | 67.5 | 1391   | 8  | AF372951  | AF372951 Arabidops  |       |      |      |       |    |            |                     |
| 450 | 16.2 | 67.5 | 1815   | 6  | AR271274  | AR271274 Sequence   |       |      |      |       |    |            |                     |
| 451 | 16.2 | 67.5 | 1815   | 6  | AR274520  | AR274520 Sequence   |       |      |      |       |    |            |                     |
| 452 | 16.2 | 67.5 | 1815   | 6  | AX283089  | AX283089 Sequence   |       |      |      |       |    |            |                     |
| 453 | 16.2 | 67.5 | 1815   | 6  | AX283091  | AX283091 Sequence   |       |      |      |       |    |            |                     |
| 454 | 16.2 | 67.5 | 1836   | 10 | RNO245648 | AJ745648 Rattus no  |       |      |      |       |    |            |                     |
| 455 | 16.2 | 67.5 | 1966   | 8  | AY645664  | AY645664 Fusarium   |       |      |      |       |    |            |                     |
| 456 | 16.2 | 67.5 | 2180   | 8  | AY645666  | AY645666 Fusarium   |       |      |      |       |    |            |                     |
| 457 | 16.2 | 67.5 | 2345   | 10 | MM087620  | U87620 Mus musculus |       |      |      |       |    |            |                     |

## ALIGNMENTS

| RESULT 1   | LOCUS      | DEFINITION  | ACCESSION  | KEYWORDS    | SOURCE                | ORGANISM        |
|------------|------------|---|------------|-------------|-----------------------|-----------------|
| AF458358/c | AF458358   | West Nile virus strain AnMg798 nonstructural protein 5 gene, partial cds.   | AF458358   | GENE        | West Nile virus (WNV) | West Nile virus |
| AF458358.1 | AF458358.1 | West Nile virus (WNV)   | AF458358.1 | GI:21636495 | West Nile virus (WNV) | West Nile virus |
|            |            | Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.  |            |             |                       |                 |
|            |            | 1 (bases 1 to 395)  |            |             |                       |                 |
|            |            | Beasley, D.W., Li, L., Suderman, M.T. and Barrett, A.D.   |            |             |                       |                 |
|            |            | Mouse neuroinvasive phenotype of West Nile virus strains varies depending upon virus genotype   |            |             |                       |                 |
|            |            | Virology 296 (1), 17-23 (2002)  |            |             |                       |                 |
|            |            | 12036314  |            |             |                       |                 |
|            |            | 2 (bases 1 to 395)  |            |             |                       |                 |
|            |            | Beasley, D.W.C., Li, L., Suderman, M.T. and Barrett, A.D.   |            |             |                       |                 |
|            |            | Direct Submission   |            |             |                       |                 |
|            |            | Submitted (14-DEC-2001) Department of Pathology and WHO Collaborating Center for Tropical Diseases, The University of Texas Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA |            |             |                       |                 |

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RESULT 2
AF458353/c
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DEFINITION partial cds.
ACCESSION AF458353
VERSION   AF458353.1 GI:21636485
KEYWORDS
SOURCE    West Nile virus (WNV)
ORGANISM  West Nile virus
           Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
           Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 451)
AUTHORS   Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE     Mouse neuroinvasive phenotype of West Nile virus strains varies
           depending upon virus genotype
JOURNAL   Virology 296 (1), 17-23 (2002)
MEDLINE   22033887
PUBMED    12036314
REFERENCE 2 (bases 1 to 451)
AUTHORS   Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE     Direct Submission
SUBMITTED (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA

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RESULT 4
AF458344/c
LOCUS      West Nile virus strain 68856 nonstructural protein 5 gene, partial
DEFINITION cds.
ACCESSION AF458344
VERSION   AF458344.1 GI:21636467
KEYWORDS
SOURCE    West Nile virus (WNV)
ORGANISM  West Nile virus
           Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
           Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 463)
AUTHORS   Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE     Mouse neuroinvasive phenotype of West Nile virus strains varies
           depending upon virus genotype
JOURNAL   Virology 296 (1), 17-23 (2002)
MEDLINE   22033887
PUBMED    12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS   Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE     Direct Submission
SUBMITTED (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA

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Db      404 TCCGAGACGGTCTTGAGGGCTTAC 381

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AF458344/c
LOCUS      West Nile virus strain 68856 nonstructural protein 5 gene, partial
DEFINITION cds.
ACCESSION AF458344
VERSION   AF458344.1 GI:21636467
KEYWORDS
SOURCE    West Nile virus (WNV)
ORGANISM  West Nile virus
           Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
           Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 463)
AUTHORS   Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE     Mouse neuroinvasive phenotype of West Nile virus strains varies
           depending upon virus genotype
JOURNAL   Virology 296 (1), 17-23 (2002)
MEDLINE   22033887
PUBMED    12036314
REFERENCE 2 (bases 1 to 462)
AUTHORS   Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE     Direct Submission
SUBMITTED (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA

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AF458350/c
LOCUS      West Nile virus strain And-27875 nonstructural protein 5 gene,
DEFINITION partial cds.
ACCESSION AF458350
VERSION   AF458350.1 GI:21636479
KEYWORDS
SOURCE    West Nile virus (WNV)
ORGANISM  West Nile virus
           Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
           Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 462)
AUTHORS   Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE     Mouse neuroinvasive phenotype of West Nile virus strains varies
           depending upon virus genotype
JOURNAL   Virology 296 (1), 17-23 (2002)
MEDLINE   22033887
PUBMED    12036314
REFERENCE 2 (bases 1 to 462)
AUTHORS   Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE     Direct Submission
SUBMITTED (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA

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depending upon virus genotype  
 JOURNAL Virology 296 (1), 17-23 (2002)  
 MEDLINE 22033887  
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 2 (bases 1 to 463)  
 Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.  
 Direct Submission  
 TITLE Submitted (14-DEC-2001) Department of Pathology and WHO  
 JOURNAL Collaborating Center for Tropical Diseases, The University of Texas  
 Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA  
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 DEFINITION partial cds.  
 ACCESSION AF458347.1 GI:21636473  
 VERSION  
 KEYWORDS  
 SOURCE West Nile virus (WNV)  
 ORGANISM  
 REFERENCE 1 (bases 1 to 463)  
 AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.  
 TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies  
 depending upon virus genotype  
 JOURNAL Virology 296 (1), 17-23 (2002)  
 MEDLINE 22033887  
 PUBMED 12036314  
 2 (bases 1 to 463)  
 Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.  
 Direct Submission  
 TITLE Submitted (14-DEC-2001) Department of Pathology and WHO  
 JOURNAL Collaborating Center for Tropical Diseases, The University of Texas  
 Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA  
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RESULT 6  
 AF458348/c  
 LOCUS West Nile virus strain IBAn7019 nonstructural protein 5 gene,  
 DEFINITION partial cds.  
 ACCESSION AF458348  
 VERSION AF458348.1 GI:21636475  
 KEYWORDS  
 SOURCE West Nile virus (WNV)  
 ORGANISM  
 REFERENCE 1 (bases 1 to 463)  
 AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.  
 TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies  
 depending upon virus genotype  
 JOURNAL Virology 296 (1), 17-23 (2002)  
 MEDLINE 22033887  
 PUBMED 12036314  
 2 (bases 1 to 463)  
 Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.  
 Direct Submission  
 TITLE Submitted (14-DEC-2001) Department of Pathology and WHO  
 JOURNAL Collaborating Center for Tropical Diseases, The University of Texas  
 Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA  
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RESULT 7  
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 LOCUS West Nile virus strain Egypt101 nonstructural protein 5 gene,  
 DEFINITION partial cds.  
 ACCESSION AF458355  
 VERSION AF458355.1 GI:21636477  
 KEYWORDS  
 SOURCE West Nile virus (WNV)  
 ORGANISM  
 REFERENCE 1 (bases 1 to 463)  
 AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.  
 TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies  
 depending upon virus genotype  
 JOURNAL Virology 296 (1), 17-23 (2002)  
 MEDLINE 22033887  
 PUBMED 12036314  
 2 (bases 1 to 463)  
 Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.  
 Direct Submission  
 TITLE Submitted (14-DEC-2001) Department of Pathology and WHO  
 JOURNAL Collaborating Center for Tropical Diseases, The University of Texas  
 Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA  
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QY 1 TCCGAGACGGTTCGAGGGCTTAC 24
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Db 106 TCCGAGACGGTTCGAGGGCTTAC 83

RESULT 12
AY590192/c
LOCUS AY590192 464 bp RNA linear VRL 30-MAY-2004
DEFINITION West Nile virus strain 03001087 3' UTR, partial sequence.
ACCESSION AY590192
VERSION AY590192.1 GI:47121679
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5658 State Farm Rd., Slingerlands, NY 12159, USA
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Db 106 TCCGAGACGGTTCGAGGGCTTAC 83

RESULT 13
AY590193/c
LOCUS AY590193 464 bp RNA linear VRL 30-MAY-2004
DEFINITION West Nile virus strain 03001426 3' UTR, partial sequence.
ACCESSION AY590193
VERSION AY590193.1 GI:47121680
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus

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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.

REFERENCE 1 (bases 1 to 464)  
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.

TITLE Genetic and phenotypic variation of West Nile virus in New York, 2000-2003

JOURNAL Am. J. Trop. Med. Hyg. (2004) In press  
REFERENCE 2 (bases 1 to 464)  
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.

TITLE Direct Submission  
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA

FEATURES Location/Qualifiers

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Db 106 TCCGAGACGGTCTGAGGGCTTAC 83

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DEFINITION  
ACCESSION AY590194  
VERSION AY590194.1 GI:47121681

KEYWORDS West Nile virus (WNV)  
SOURCE West Nile virus

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.

REFERENCE 1 (bases 1 to 464)  
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.

TITLE Genetic and phenotypic variation of West Nile virus in New York, 2000-2003

JOURNAL Am. J. Trop. Med. Hyg. (2004) In press  
REFERENCE 2 (bases 1 to 464)  
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.

TITLE Direct Submission  
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA

FEATURES Location/Qualifiers

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Db 106 TCCGAGACGGTCTGAGGGCTTAC 83

RESULT 15  
AY590195/c

LOCUS West Nile virus strain 03001543 3' UTR, partial sequence.  
DEFINITION  
ACCESSION AY590195

VERSION AY590195.1 GI:47121682  
KEYWORDS West Nile virus (WNV)

SOURCE West Nile virus

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.

REFERENCE 1 (bases 1 to 464)  
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.

TITLE Genetic and phenotypic variation of West Nile virus in New York, 2000-2003

JOURNAL Am. J. Trop. Med. Hyg. (2004) In press  
REFERENCE 2 (bases 1 to 464)  
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.

TITLE Direct Submission  
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA

FEATURES Location/Qualifiers

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Db 106 TCCGAGACGGTCTGAGGGCTTAC 83

RESULT 16  
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LOCUS West Nile virus strain 03001619 3' UTR, partial sequence.  
DEFINITION  
ACCESSION AY590196

VERSION AY590196.1 GI:47121683  
KEYWORDS West Nile virus (WNV)

SOURCE West Nile virus

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.

REFERENCE 1 (bases 1 to 464)  
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.

TITLE Genetic and phenotypic variation of West Nile virus in New York, 2000-2003

JOURNAL Am. J. Trop. Med. Hyg. (2004) In press  
REFERENCE 2 (bases 1 to 464)  
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.

TITLE Direct Submission  
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA



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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 VERSION AY590200.1 GI:47121687  
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 West Nile virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Flavivirus; Japanese encephalitis virus group.  
 1 (bases 1 to 464)  
 Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and  
 Kramer,L.D.  
 TITLE Genetic and phenotypic variation of West Nile virus in New York,  
 2000-2003  
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press  
 REFERENCE 2 (bases 1 to 464)  
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and  
 Kramer,L.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth  
 Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA

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QY 1 TCCGAGACGGTCTTGAGGGCTTAC 24  
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RESULT 21  
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 ACCESSION AY590201  
 VERSION AY590201.1 GI:47121688  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 West Nile virus (WNV)  
 West Nile virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Flavivirus; Japanese encephalitis virus group.  
 1 (bases 1 to 464)  
 Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and  
 Kramer,L.D.  
 TITLE Genetic and phenotypic variation of West Nile virus in New York,  
 2000-2003  
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press  
 REFERENCE 2 (bases 1 to 464)  
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and  
 Kramer,L.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth  
 Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA

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 Db 106 TCCGAGACGGTCTTGAGGGCTTAC 83

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 LOCUS  
 DEFINITION West Nile virus strain 03001895 3' UTR, partial sequence.  
 ACCESSION AY590202  
 VERSION AY590202.1 GI:47121689  
 KEYWORDS  
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 ORGANISM  
 West Nile virus (WNV)  
 West Nile virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Flavivirus; Japanese encephalitis virus group.  
 1 (bases 1 to 464)  
 Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and  
 Kramer,L.D.  
 TITLE Genetic and phenotypic variation of West Nile virus in New York,  
 2000-2003  
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press  
 REFERENCE 2 (bases 1 to 464)  
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and  
 Kramer,L.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth  
 Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA

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RESULT 23  
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 ACCESSION AY590203  
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Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA

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 Db 106 TCCGAGACGGTCTTGAGGGCTTAC 83

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 ACCESSION AY590202  
 VERSION AY590202.1 GI:47121689  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 West Nile virus (WNV)  
 West Nile virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Flavivirus; Japanese encephalitis virus group.  
 1 (bases 1 to 464)  
 Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and  
 Kramer,L.D.  
 TITLE Genetic and phenotypic variation of West Nile virus in New York,  
 2000-2003  
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press  
 REFERENCE 2 (bases 1 to 464)  
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and  
 Kramer,L.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth  
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 Best Local Similarity 100.0%; Pred. No. 0.43;  
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QY 1 TCCGAGACGGTCTTGAGGGCTTAC 24  
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 Db 106 TCCGAGACGGTCTTGAGGGCTTAC 83

RESULT 23  
 AY590203/c  
 LOCUS  
 DEFINITION West Nile virus strain 03001956 3' UTR, partial sequence.  
 ACCESSION AY590203  
 VERSION AY590203.1 GI:47121690  
 KEYWORDS

SOURCE West Nile virus (WNV)  
 ORGANISM West Nile virus  
 REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 AUTHORS Flavivirus; Japanese encephalitis virus group.  
 1 (bases 1 to 464)  
 Ebner, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and  
 Kramer, L.D.  
 TITLE Genetic and phenotypic variation of West Nile virus in New York,  
 2000-2003  
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press  
 REFERENCE 2 (bases 1 to 464)  
 AUTHORS Ebner, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and  
 Kramer, L.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth  
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 Db 106 TCCGAGACGGTCTCGAGGCTTAC 83  
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 LOCUS West Nile virus strain 03001956 464 bp RNA linear VRL 30-MAY-2004  
 DEFINITION  
 ACCESSION AY590204  
 VERSION AY590204.1 GI:47121691  
 KEYWORDS  
 ORGANISM West Nile virus (WNV)  
 REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 AUTHORS Flavivirus; Japanese encephalitis virus group.  
 1 (bases 1 to 464)  
 Ebner, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and  
 Kramer, L.D.  
 TITLE Genetic and phenotypic variation of West Nile virus in New York,  
 2000-2003  
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press  
 REFERENCE 2 (bases 1 to 464)  
 AUTHORS Ebner, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and  
 Kramer, L.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth  
 Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA  
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 Db 106 TCCGAGACGGTCTCGAGGCTTAC 83  
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 AY590206/c  
 LOCUS West Nile virus strain 03002031 464 bp RNA linear VRL 30-MAY-2004  
 DEFINITION  
 ACCESSION AY590206  
 VERSION AY590206.1 GI:47121693  
 KEYWORDS  
 ORGANISM West Nile virus (WNV)  
 REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 AUTHORS Flavivirus; Japanese encephalitis virus group.  
 1 (bases 1 to 464)  
 Ebner, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and  
 Kramer, L.D.  
 TITLE Genetic and phenotypic variation of West Nile virus in New York,  
 2000-2003  
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press  
 REFERENCE 2 (bases 1 to 464)  
 AUTHORS Ebner, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and  
 Kramer, L.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth  
 Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA  
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 Db 106 TCCGAGACGGTCTCGAGGCTTAC 83

Best Local Similarity 100.0%; Pred. No. 0.43;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGAGACGGTCTCGAGGCTTAC 24  
 Db 106 TCCGAGACGGTCTCGAGGCTTAC 83  
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 AY590205/c  
 LOCUS West Nile virus strain 03002018 464 bp RNA linear VRL 30-MAY-2004  
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 ACCESSION AY590205  
 VERSION AY590205.1 GI:47121692  
 KEYWORDS  
 ORGANISM West Nile virus (WNV)  
 REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 AUTHORS Flavivirus; Japanese encephalitis virus group.  
 1 (bases 1 to 464)  
 Ebner, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and  
 Kramer, L.D.  
 TITLE Genetic and phenotypic variation of West Nile virus in New York,  
 2000-2003  
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press  
 REFERENCE 2 (bases 1 to 464)  
 AUTHORS Ebner, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and  
 Kramer, L.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth  
 Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA  
 FEATURES Location/Qualifiers  
 source  
 1..464  
 /organism="West Nile virus"  
 /mol\_type="genomic RNA"  
 /strain="03002018"  
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 /country="USA"  
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 Best Local Similarity 100.0%; Pred. No. 0.43;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGAGACGGTCTCGAGGCTTAC 24  
 Db 106 TCCGAGACGGTCTCGAGGCTTAC 83  
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 AY590206/c  
 LOCUS West Nile virus strain 03002031 464 bp RNA linear VRL 30-MAY-2004  
 DEFINITION  
 ACCESSION AY590206  
 VERSION AY590206.1 GI:47121693  
 KEYWORDS  
 ORGANISM West Nile virus (WNV)  
 REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 AUTHORS Flavivirus; Japanese encephalitis virus group.  
 1 (bases 1 to 464)  
 Ebner, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and  
 Kramer, L.D.  
 TITLE Genetic and phenotypic variation of West Nile virus in New York,  
 2000-2003  
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press  
 REFERENCE 2 (bases 1 to 464)  
 AUTHORS Ebner, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and  
 Kramer, L.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth  
 Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA  
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 QY 1 TCCGAGACGGTCTCGAGGCTTAC 24  
 Db 106 TCCGAGACGGTCTCGAGGCTTAC 83

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JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
FEATURES Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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/virion
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCAGGGCTTAC 24
Db 106 TCCGAGACGGTTCAGGGCTTAC 83

RESULT 27
AY590207/c
LOCUS West Nile virus (WNV)
DEFINITION 464 bp RNA linear VRL 30-MAY-2004
ACCESSION West Nile virus strain 03002035 3' UTR, partial sequence.
VERSION AY590207.1 GI:47121694
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
Genetic and phenotypic variation of West Nile virus in New York,
Kramer, L.D.
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
Ebel, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and
Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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/organism="West Nile virus"
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/specific_host="American crow"
/db_xref="taxon:11082"
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QY 1 TCCGAGACGGTTCAGGGCTTAC 24
Db 106 TCCGAGACGGTTCAGGGCTTAC 83

RESULT 29
AY590209/c
LOCUS West Nile virus (WNV)
DEFINITION 464 bp RNA linear VRL 30-MAY-2004
ACCESSION West Nile virus strain 03002086 3' UTR, partial sequence.
VERSION AY590209.1 GI:47121696
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
Genetic and phenotypic variation of West Nile virus in New York,
Kramer, L.D.
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
Ebel, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and
Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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/virion
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCAGGGCTTAC 24
Db 106 TCCGAGACGGTTCAGGGCTTAC 83

RESULT 28
AY590208/c
LOCUS West Nile virus (WNV)
DEFINITION 464 bp RNA linear VRL 30-MAY-2004
ACCESSION West Nile virus strain 03002066 3' UTR, partial sequence.
VERSION AY590208.1 GI:47121695

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KEYWORDS West Nile virus (WNV)
SOURCE West Nile virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 464)
AUTHORS Ebel, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and
Kramer, L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and
Kramer, L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
FEATURES Location/Qualifiers
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/organism="West Nile virus"
/virion
/mol_type="genomic RNA"
/strain="03002066"
/specific_host="American crow"
/db_xref="taxon:11082"
/country="USA"
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Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCAGGGCTTAC 24
Db 106 TCCGAGACGGTTCAGGGCTTAC 83

RESULT 29
AY590209/c
LOCUS West Nile virus (WNV)
DEFINITION 464 bp RNA linear VRL 30-MAY-2004
ACCESSION West Nile virus strain 03002086 3' UTR, partial sequence.
VERSION AY590209.1 GI:47121696
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
Genetic and phenotypic variation of West Nile virus in New York,
Kramer, L.D.
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and
Kramer, L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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/virion
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/specific_host="American crow"
/db_xref="taxon:11082"
/country="USA"
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3'UTR
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.43; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0;

QY 1 TCCGAGACGGTCTCGAGGGCTTAC 24
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Db 106 TCCGAGACGGTCTCGAGGGCTTAC 83

RESULT 30
AF458349/c
LOCUS
DEFINITION
West Nile virus strain ArB3575/82 nonstructural protein 5 gene,
partial cds.
ACCESSION
AF458349
VERSION
AF458349.1 GI:21636477
SOURCE
West Nile virus (WNV)
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 481)
AUTHORS
Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE
Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL
Virology 296 (1), 17-23 (2002)
MEDLINE
22033887
PUBMED
12036314
REFERENCE
2 (bases 1 to 481)
AUTHORS
Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE
Direct Submission
Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
JOURNAL
Location/Qualifiers
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/protein_id="AAM70025.1"
/db_xref="GI:21636478"
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RYEDTIVVEDTVL"
175. .>481
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Best Local Similarity 100.0%; Pred. No. 0.43; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0;

QY 1 TCCGAGACGGTCTCGAGGGCTTAC 24
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RESULT 32
AF458345/c
LOCUS
DEFINITION
West Nile virus strain ArD-76104 nonstructural protein 5 gene,
partial cds.
ACCESSION
AF458345
VERSION
AF458345.1 GI:21636469
KEYWORDS
West Nile virus (WNV)
SOURCE
West Nile virus
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 483)
AUTHORS
Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE
Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL
Virology 296 (1), 17-23 (2002)
MEDLINE
22033887
PUBMED
12036314
REFERENCE
2 (bases 1 to 483)
AUTHORS
Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE
Direct Submission
Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
JOURNAL
Location/Qualifiers
FEATURES
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Matches 24; Conservative 0;

QY 1 TCCGAGACGGTCTCGAGGGCTTAC 24
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Db 423 TCCGAGACGGTCTCGAGGGCTTAC 400

RESULT 31
AF458359/c
LOCUS
DEFINITION
West Nile virus strain H-442 nonstructural protein 5 gene, partial
cds.
ACCESSION
AF458359
VERSION
AF458359.1 GI:21636497
KEYWORDS
West Nile virus (WNV)
SOURCE
West Nile virus
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.

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/product="nonstructural protein 5"
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RYEDTIVVEDTVL"
175. .>483

3'UTR
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTAC 24
|||||
Db 425 TCCGAGACGGTTCTGAGGGCTTAC 402

RESULT 33
AF458357/c
LOCUS
DEFINITION
West Nile virus strain SPU-116/89 nonstructural protein 5 gene,
partial cds.
ACCESSION
AF458357
VERSION
AF458357.1 GI:21636493
KEYWORDS
SOURCE
ORGANISM
West Nile virus (WNV)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 483)
Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
Virology 296 (1), 17-23 (2002)
MEDLINE
22033887
PUBMED
12036314
REFERENCE
2 (bases 1 to 483)
Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
Direct Submission
Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
Location/Qualifiers
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RYEDTIVVEDTVL"
175. .>483

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Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTAC 24
|||||
Db 425 TCCGAGACGGTTCTGAGGGCTTAC 402

RESULT 34
AF458354/c
LOCUS
DEFINITION
West Nile virus strain ArMg979 nonstructural protein 5 gene,
partial cds.
ACCESSION
AF458354
VERSION
AF458354.1 GI:21636487
KEYWORDS
SOURCE
ORGANISM
West Nile virus (WNV)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 484)
Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
Virology 296 (1), 17-23 (2002)
MEDLINE
22033887
PUBMED
12036314
REFERENCE
2 (bases 1 to 484)
Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
Direct Submission
Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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/translation="DIWCGSLGTRTRATWAENIHVAINQVRSVIGEEKYVDYMSSLR
RYEDTIVVEDTVL"
175. .>484

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ORIGIN
Query Match 100.0%; Score 24; DB 14; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTAC 24
|||||
Db 426 TCCGAGACGGTTCTGAGGGCTTAC 403

RESULT 35
AF297854/c
LOCUS
DEFINITION
Kunjin virus isolate WK436 nonstructural protein 5 gene, partial
cds.
ACCESSION
AF297854
VERSION
AF297854.1 GI:11991998
KEYWORDS
SOURCE
ORGANISM
Kunjin virus
Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 542)
Scherrer,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Brisse,T., Gould,E.A. and Hall,R.A.
The relationships between West Nile and Kunjin viruses
Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE
21469816
PUBMED
11585335
REFERENCE
2 (bases 1 to 542)
Scherrer,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Definitive studies of the relationships between West Nile and

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Kunjin viruses
Unpublished
3 (bases 1 to 542)
Scherreret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE
JOURNAL
Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
FEATURES
source
1..542
Location/Qualifiers
/organism="Kunjin virus"
/mol_type="genomic RNA"
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/db_xref="taxon:11077"
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/notes="NS5"
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/db_xref="GI:11991999"
/translation="NEWEDKTPVEKWSDPYSGKREDIWCGSLIGTRARATWAENIQ
VAINQVRSIIIGDEKYVDYMSWKRYEDTTLVEDTVL"
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Best Local Similarity 100.0%; Pred. No. 0.42; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGCTTAC 24
Db 469 TCCGAGACGGTTCGAGGCTTAC 446

RESULT 36
KUNNS5GAA/c
LOCUS
Kunjin virus nonstructural protein (NS5) gene, 3' end of cds.
VRL 07-JUN-1996
DEFINITION
L48978
ACCESSION
L48978
VERSION
L48978.1 GI:1066802
KEYWORDS
NS5 gene; nonstructural protein.
SOURCE
Kunjin virus
ORGANISM
Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 587)
Poldinger,M., Hall,R.A. and Mackenzie,J.S.
AUTHORS
Molecular characterization of the Japanese encephalitis serocomplex
of the flavivirus genus
TITLE
Virology 218 (2), 417-421 (1996)
JOURNAL
MEDLINE
96193756
PUBMED
8610471
COMMENT
Original source text: Kunjin virus (strain MRM61C) cDNA to genomic
RNA.
FEATURES
source
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.42; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGCTTAC 24
Db 461 TCCGAGACGGTTCGAGGCTTAC 438

RESULT 37
KUNNS5GAB/c
LOCUS
Kunjin virus nonstructural protein (NS5) gene, 3' end of cds.
VRL 07-JUN-1996
DEFINITION
L48979
ACCESSION
L48979
VERSION
L48979.1 GI:1066804
KEYWORDS
NS5 gene; nonstructural protein.
SOURCE
Kunjin virus
ORGANISM
Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 587)
Poldinger,M., Hall,R.A. and Mackenzie,J.S.
AUTHORS
Molecular characterization of the Japanese encephalitis serocomplex
of the flavivirus genus
TITLE
Virology 218 (2), 417-421 (1996)
JOURNAL
MEDLINE
96193756
PUBMED
8610471
COMMENT
Original source text: Kunjin virus (strain MRM16) cDNA to genomic
RNA.
FEATURES
source
Location/Qualifiers
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/db_xref="GI:1066805"
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INQVRSIIIGDEKYVDYMSWKRYEDTTLVEDTVL"
ORIGIN
Query Match 100.0%; Score 24; DB 14; Length 587;
Best Local Similarity 100.0%; Pred. No. 0.42; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGCTTAC 24
Db 461 TCCGAGACGGTTCGAGGCTTAC 438

RESULT 38
AF196543/c
LOCUS
West Nile virus isolate Mgan798 polyprotein gene, partial cds.
VRL 05-MAR-2002
DEFINITION
AF196543
ACCESSION
AF196543
VERSION
AF196543.1 GI:15865595
KEYWORDS
West Nile virus
SOURCE
West Nile virus
ORGANISM
West Nile virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 591)
Scherreret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
AUTHORS
The relationships between West Nile and Kunjin viruses
TITLE
Emerging Infect. Dis. 7 (4), 697-705 (2001)
JOURNAL
MEDLINE
21469816
PUBMED
11585535
REFERENCE
2 (bases 1 to 591)

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AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.  
and Hall,R.A.  
TITLE Definitive studies of the relationships between West Nile and  
Kunjin viruses  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 591)  
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.  
and Hall,R.A.  
TITLE Direct Submission  
JOURNAL Submitted (20-OCT-1999) Department of Microbiology and  
Parasitology, University of Queensland, St. Lucia, Brisbane, QLD  
4072, Australia

FEATURES  
source Location/Qualifiers  
1..591  
/organism="West Nile virus"  
/mol\_type="genomic RNA"  
/isolate="Mgan798"  
/db\_xref="taxon:11082"  
CDS  
1..250  
/codon\_start=1  
/product="polyprotein"  
/protein\_id="AAU09961.1"  
/db\_xref="GI:15865596"  
mat\_peptide  
1..252  
ENHAINQVRSVIGEEKYVDYMSLRREYEDTTVVEDTVL"  
3'UTR  
256..591  
/product="non-structural protein NS5"  
ORIGIN  
Query Match 100.0%; Score 24; DB 14; Length 591;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGAGACGGTCTCTGAGGCTTAC 24  
Db 419 TCCGAGACGGTCTCTGAGGCTTAC 396

RESULT 39  
WNFNS5GAA/c  
LOCUS West Nile virus nonstructural protein (NS5) gene, 3' end of cds.  
DEFINITION  
ACCESSION L48977  
VERSION 148977.1 GI:1066867  
KEYWORDS NS5 gene; nonstructural protein.  
SOURCE West Nile virus  
ORGANISM West Nile virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Flavivirus; Japanese encephalitis virus group.  
REFERENCE 1 (bases 1 to 593)  
AUTHORS Poidinger,M., Hall,R.A. and Mackenzie,J.S.  
TITLE Molecular characterization of the Japanese encephalitis serocomplex  
of the flavivirus genus  
JOURNAL Virology 218 (2), 417-421 (1996)  
MEDLINE 96193756  
PUBMED 8610471  
COMMENT Original source text: West Nile virus (strain Sarafend) cDNA to  
genomic RNA.

FEATURES  
source Location/Qualifiers  
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/strain="Sarafend"  
/db\_xref="taxon:11082"  
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/gene="NS5"  
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/codon\_start=2  
/product="nonstructural protein"  
/protein\_id="AA02101.1"  
/db\_xref="GI:1066868"

ORIGIN  
Query Match 100.0%; Score 24; DB 14; Length 593;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGAGACGGTCTCTGAGGCTTAC 24  
Db 426 TCCGAGACGGTCTCTGAGGCTTAC 403

RESULT 40  
AF297844/c  
LOCUS Kunjin virus isolate CH16549E nonstructural protein 5 gene, partial  
DEFINITION cds.  
ACCESSION AF297844  
VERSION AF297844.1 GI:11991978  
KEYWORDS Kunjin virus  
SOURCE Kunjin virus  
ORGANISM Kunjin virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Flavivirus; Japanese encephalitis virus group.  
REFERENCE 1 (bases 1 to 601)  
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,  
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.  
TITLE The relationships between West Nile and Kunjin viruses  
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)  
MEDLINE 21469816  
PUBMED 11585535  
REFERENCE 2 (bases 1 to 601)  
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.  
and Hall,R.A.  
TITLE Definitive studies of the relationships between West Nile and  
Kunjin viruses  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 601)  
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.  
and Hall,R.A.  
TITLE Direct Submission  
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University  
of Queensland, St Lucia, QLD 4072, Australia

FEATURES  
source Location/Qualifiers  
1..601  
/organism="Kunjin virus"  
/mol\_type="genomic RNA"  
/isolate="CH16549E"  
/db\_xref="taxon:11077"  
CDS  
1..242  
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/codon\_start=3  
/product="nonstructural protein 5"  
/protein\_id="AAG42382.1"  
/db\_xref="GI:11991979"  
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Query Match 100.0%; Score 24; DB 14; Length 601;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGAGACGGTCTCTGAGGCTTAC 24  
Db 468 TCCGAGACGGTCTCTGAGGCTTAC 445

RESULT 41  
KUNNS5/c  
LOCUS Kunjin virus (strain Sarawak) nonstructural protein (NS5) gene, 3'  
DEFINITION

end of cds.

ACCESSION L49311  
 VERSION L49311.1 GI:1100210  
 KEYWORDS NS5 gene; nonstructural protein.  
 SOURCE Kunjin virus  
 ORGANISM Kunjin virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.

REFERENCE Poidinger, M.  
 AUTHORS Poidinger, M., Hall, R.A. and Mackenzie, J.S.  
 TITLE Molecular characterization of the JE serogroup of flaviviruses  
 JOURNAL Unpublished (1995)  
 REFERENCE 2 (sites)  
 AUTHORS Poidinger, M., Hall, R.A. and Mackenzie, J.S.  
 TITLE Molecular characterization of the Japanese encephalitis serocomplex of the flavivirus genus  
 JOURNAL Virology 218 (2), 417-421 (1996)  
 MEDLINE 96193756  
 PUBMED 8610471  
 COMMENT Original source text: Kunjin virus (strain Sarawak) cDNA to genomic RNA.

FEATURES  
 source Location/Qualifiers  
 1..604  
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 /mol\_type="genomic RNA"  
 /strain="Sarawak"  
 /db\_xref="taxon:11077"  
 1..260  
 /gene="NS5"  
 <1..260  
 /genes="NS5"  
 /codon\_start=3  
 /protein\_id="AAB02076.1"  
 /db\_xref="GI:1100211"  
 /translation="VMIEENXWMDKTPVRSWSDVPYSGKREDIMCGSLIGTRARATW  
 AENIQVAINQVRSIIIGDEKFDVMSLSRKYEDITLVEDSVL"  
 mat\_peptide 1..257  
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 /product="NS5 gene, 3' end; putative"

ORIGIN  
 Query Match 100.0%; Score 24; DB 14; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 0.42;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTAC 24  
 |||||  
 Db 446 TCCGAGACGGTTCTGAGGGCTTAC 423

RESULT 42  
 AF297841/c  
 LOCUS Kunjin virus isolate CH16465C nonstructural protein 5 gene, partial  
 DEFINITION cds.

ACCESSION AF297841  
 VERSION AF297841.1 GI:11991972  
 KEYWORDS Kunjin virus  
 SOURCE Kunjin virus  
 ORGANISM Kunjin virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.

REFERENCE 1 (bases 1 to 607)  
 AUTHORS Scherret, J.H., Poidinger, M., Mackenzie, J.S., Broom, A.K., Deubel, V., Lipkin, W.I., Briese, T., Gould, E.A. and Hall, R.A.  
 TITLE The relationships between West Nile and Kunjin viruses  
 JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)  
 MEDLINE 21469816  
 PUBMED 11585535  
 REFERENCE 2 (bases 1 to 607)  
 AUTHORS Scherret, J.H., Poidinger, M., Mackenzie, J.S., Broom, A.K., Deubel, V. and Hall, R.A.  
 TITLE Definitive studies of the relationships between West Nile and Kunjin viruses

Kunjin viruses  
 Unpublished  
 3 (bases 1 to 607)  
 Scherret, J.H., Poidinger, M., Mackenzie, J.S., Broom, A.K., Deubel, V. and Hall, R.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia  
 FEATURES Location/Qualifiers  
 source 1..607  
 /organism="Kunjin virus"  
 /mol\_type="genomic RNA"  
 /isolate="CH16465C"  
 /db\_xref="taxon:11077"  
 <1..255  
 /note="NS5"  
 /codon\_start=1  
 /product="nonstructural protein 5"  
 /protein\_id="AAG42379.1"  
 /db\_xref="GI:11991973"  
 /translation="WIEENWMDKTPVRSWSDVPYSGKREDIMCGSLIGTRARATWA  
 ENIQVAINQVRSIIIGDEKFDVMSLSRKYEDITLVEDVL"

CDS  
 1 TCCGAGACGGTTCTGAGGGCTTAC 24  
 |||||  
 481 TCCGAGACGGTTCTGAGGGCTTAC 458

RESULT 43  
 AF297856/c  
 LOCUS Kunjin virus isolate PI553 nonstructural protein 5 gene, partial  
 DEFINITION cds.

ACCESSION AF297856  
 VERSION AF297856.1 GI:11992002  
 KEYWORDS Kunjin virus  
 SOURCE Kunjin virus  
 ORGANISM Kunjin virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.

REFERENCE 1 (bases 1 to 609)  
 AUTHORS Scherret, J.H., Poidinger, M., Mackenzie, J.S., Broom, A.K., Deubel, V., Lipkin, W.I., Briese, T., Gould, E.A. and Hall, R.A.  
 TITLE The relationships between West Nile and Kunjin viruses  
 JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)  
 MEDLINE 21469816  
 PUBMED 11585535  
 REFERENCE 2 (bases 1 to 609)  
 AUTHORS Scherret, J.H., Poidinger, M., Mackenzie, J.S., Broom, A.K., Deubel, V. and Hall, R.A.  
 TITLE Definitive studies of the relationships between West Nile and Kunjin viruses

REFERENCE 3 (bases 1 to 609)  
 AUTHORS Scherret, J.H., Poidinger, M., Mackenzie, J.S., Broom, A.K., Deubel, V. and Hall, R.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia  
 FEATURES Location/Qualifiers  
 source 1..609  
 /organism="Kunjin virus"  
 /mol\_type="genomic RNA"  
 /isolate="PI553"  
 /db\_xref="taxon:11077"  
 <1..257  
 /note="NS5"  
 /codon\_start=3

CDS  
 1 TCCGAGACGGTTCTGAGGGCTTAC 24  
 |||||  
 481 TCCGAGACGGTTCTGAGGGCTTAC 458

/product="nonstructural protein 5"  
/protein\_id="AAG42394.1"  
/db\_xref="GI:11992003"  
/translations="WIDENEMEDKTPVEKWSDPYSGKREDIWCGSLIGTRARATWA  
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## ORIGIN

Query Match 100.0%; Score 24; DB 14; Length 609;  
Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCCGAGACGGTTCTGAGGGCTTAC 24  
Db 490 TCCGAGACGGTTCTGAGGGCTTAC 467

## RESULT 44

AF297845/c  
LOCUS  
Kunjin virus isolate CX255 nonstructural protein 5 gene, partial  
cds.

ACCESSION AF297845  
VERSION AF297845.1  
KEYWORDS GI:11991980

SOURCE  
ORGANISM Kunjin virus

REFERENCE  
AUTHORS Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Flavivirus; Japanese encephalitis virus group.

TITLE  
JOURNAL Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,  
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.  
The relationships between West Nile and Kunjin viruses  
MEDLINE Emerging Infect. Dis. 7 (4), 697-705 (2001)  
PUBMED 21469816

REFERENCE  
AUTHORS 11585535

TITLE  
JOURNAL Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,  
and Hall,R.A.  
Definitive studies of the relationships between West Nile and  
Kunjin viruses

REFERENCE  
AUTHORS 3 (bases 1 to 616)  
Unpublished  
JOURNAL Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,  
and Hall,R.A.

TITLE  
JOURNAL Direct Submission  
Submitted (22-AUG-2000) Microbiology and Parasitology, University  
of Queensland, St Lucia, QLD 4072, Australia

## FEATURES

source  
1..616  
/organism="Kunjin virus"  
/mol\_type="genomic RNA"  
/isolate="CX255"  
/db\_xref="taxon:11077"  
<1..226

## CDS

/notes="NS5"  
/codon\_start=2  
/product="nonstructural protein 5"  
/protein\_id="AAG42393.1"  
/db\_xref="GI:11991981"  
/translations="TTPVEKWSDPYSGKPEDIWCGSLIGTRARATWAENIQVAVTQV  
RSIIIGDEKYVDYMSLSKRYEDTILVEDTVL"

## ORIGIN

Query Match 100.0%; Score 24; DB 14; Length 616;  
Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCTGAGGGCTTAC 24

Db 452 TCCGAGACGGTTCTGAGGGCTTAC 429

## RESULT 45

AF297859/c  
LOCUS  
Kunjin virus isolate MRM5373 nonstructural protein 5 gene, partial  
cds.

ACCESSION AF297859  
VERSION AF297859.1  
KEYWORDS GI:11992008

SOURCE  
ORGANISM Kunjin virus

REFERENCE  
AUTHORS Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Flavivirus; Japanese encephalitis virus group.

TITLE  
JOURNAL Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,  
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.  
The relationships between West Nile and Kunjin viruses  
MEDLINE Emerging Infect. Dis. 7 (4), 697-705 (2001)  
PUBMED 21469816

REFERENCE  
AUTHORS 2 (bases 1 to 620)  
11585535

TITLE  
JOURNAL Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,  
and Hall,R.A.  
Definitive studies of the relationships between West Nile and  
Kunjin viruses

REFERENCE  
AUTHORS 3 (bases 1 to 620)  
Unpublished  
JOURNAL Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,  
and Hall,R.A.

TITLE  
JOURNAL Direct Submission  
Submitted (22-AUG-2000) Microbiology and Parasitology, University  
of Queensland, St Lucia, QLD 4072, Australia

## FEATURES

source  
1..620  
/organism="Kunjin virus"  
/mol\_type="genomic RNA"  
/isolate="MRM5373"  
/db\_xref="taxon:11077"  
<1..251  
/note="NS5"  
/codon\_start=3  
/product="nonstructural protein 5"  
/protein\_id="AAG42397.1"  
/db\_xref="GI:11992009"  
/translation="EENEMEDKTPVEKWSDPYSGKREDIWCGSLIGTRARATWAEN  
IQVAINQVRSIIIGDEKYVDYMSLSKRYEDTILVEDTVL"

## CDS

/notes="NS5"  
/codon\_start=3  
/product="nonstructural protein 5"  
/protein\_id="AAG42397.1"  
/db\_xref="GI:11992009"  
/translation="EENEMEDKTPVEKWSDPYSGKREDIWCGSLIGTRARATWAEN  
IQVAINQVRSIIIGDEKYVDYMSLSKRYEDTILVEDTVL"

## ORIGIN

Query Match 100.0%; Score 24; DB 14; Length 620;  
Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCTGAGGGCTTAC 24

Db 477 TCCGAGACGGTTCTGAGGGCTTAC 454

## RESULT 46

AF297842/c  
LOCUS  
Kunjin virus isolate CHI6514C nonstructural protein 5 gene, partial  
cds.

ACCESSION AF297842  
VERSION AF297842.1  
KEYWORDS GI:11991974

SOURCE  
ORGANISM Kunjin virus

REFERENCE  
AUTHORS Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Flavivirus; Japanese encephalitis virus group.

TITLE  
JOURNAL Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,  
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.  
The relationships between West Nile and Kunjin viruses  
MEDLINE Emerging Infect. Dis. 7 (4), 697-705 (2001)  
PUBMED 21469816

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PUBMED
REFERENCE
AUTHORS
Scherreret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE
Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL
Unpublished
REFERENCE
AUTHORS
Scherreret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE
Direct Submission
JOURNAL
Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
FEATURES
source
1. .622
/organism="Kunjin virus"
/mol_type="genomic RNA"
/isolate="CH16514C"
/db_xref="taxon:11077"
<1..245
/notes="NS5"
/codon_start=3
/product="nonstructural protein 5"
/protein_id="AAG42380.1"
/db_xref="GI:11991975"
/translation="NS5MEDKTPVEKWDVPSGKREDIWCGSLIGTRARATWAENIQ
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGCGTTAC 24
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Db 471 TCCGAGACGGTTCTGAGGCGTTAC 448

RESULT 47
AF297843/c
LOCUS
DEFINITION
Kunjin virus isolate CH16532C nonstructural protein 5 gene, partial
cds.
ACCESSION
AF297843
VERSION
AF297843.1 GI:11991976
KEYWORDS
Kunjin virus
ORGANISM
Kunjin virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 623)
Scherreret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE
The relationships between West Nile and Kunjin viruses
JOURNAL
Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE
21469816
PUBMED
11955535
REFERENCE
2 (bases 1 to 623)
Scherreret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE
Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL
Unpublished
REFERENCE
3 (bases 1 to 623)
Scherreret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE
Direct Submission
JOURNAL
Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
FEATURES
source
1. .623
/organism="Kunjin virus"
/mol_type="genomic RNA"

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/isolate="CH16532C"
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<1..245
/notes="NS5"
/codon_start=1
/product="nonstructural protein 5"
/protein_id="AAG42381.1"
/db_xref="GI:11991977"
/translation="EYEMWEDTTPVEKWDVPSGKREDIWCGSLIGTRARATWAEDI
QVAINQVRSIIIGDEKIVYMSSLKRYEDTTLVEDTVL"

CDS
Query Match 100.0%; Score 24; DB 14; Length 623;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGCGTTAC 24
|||||
Db 472 TCCGAGACGGTTCTGAGGCGTTAC 449

RESULT 48
KUNNONCODB/c
LOCUS
DEFINITION
Kunjin virus 3' UTR.
ACCESSION
L24512
VERSION
L24512.1 GI:403464
KEYWORDS
Kunjin virus
ORGANISM
Kunjin virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 627)
Coia,G., Parker,M.D., Speight,G., Byrne,M.E. and Westaway,E.G.
Nucleotide and complete amino acid sequences of Kunjin virus:
definitive gene order and characteristics of the virus-specified
proteins
JOURNAL
J. Gen. Virol. 69 (Pt 1), 1-21 (1988)
MEDLINE
88089524
PUBMED
2826659
REFERENCE
2 (bases 1 to 627)
Khromykh,A.A. and Westaway,E.G.
TITLE
Completion of Kunjin virus RNA sequence and recovery of an
infectious RNA transcribed from stably cloned full-length cDNA
JOURNAL
J. Virol. 68 (7), 4580-4588 (1994)
MEDLINE
94267921
PUBMED
8207832
COMMENT
Original source text: Kunjin virus (strain MRM 61C) mature RNA.
FEATURES
source
1. .627
/organism="Kunjin virus"
/mol_type="genomic RNA"
/strain="MRM 61C"
/db_xref="taxon:11077"
/dev_stage="mature"
4. .627
/notes="putative"
/citation={2}

3'UTR
Query Match 100.0%; Score 24; DB 14; Length 627;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGCGTTAC 24
|||||
Db 227 TCCGAGACGGTTCTGAGGCGTTAC 204

RESULT 49
AF297858/c
LOCUS
DEFINITION
Kunjin virus isolate OR205 nonstructural protein 5 gene, partial

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TITLE      The relationships between West Nile and Kunjin viruses
JOURNAL    Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE    21469816
PUBMED     11585535
REFERENCE  3 (bases 1 to 644)
AUTHORS    Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
           and Hall,R.A.
TITLE      Definitive studies of the relationships between West Nile and
JOURNAL    Kunjin viruses
REFERENCE  4 (bases 1 to 644)
AUTHORS    Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
           and Hall,R.A.
TITLE      Direct Submission
JOURNAL    Submitted (20-OCT-1999) Department of Microbiology and
           Parasitology, University of Queensland, St. Lucia, Brisbane, QLD
           4072, Australia
FEATURES   Location/Qualifiers
            source          1..644
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                        /mol_type="genomic RNA"
                        /isolate="G22886"
                        /db_xref="taxon:11082"
                        <1..270
CDS        /codon_start=1
            /product="polyprotein"
            /protein_id="AAG47646.1"
            /db_xref="GI:12043780"
            /translation="GVQRVMIENWEMDKTPVERWSDVPYSKREDIWCGSLIGTRA
            RATAWENIQVAINQVRAIGEEKYVDYMSLRREYETLVEDSVL"
            mat_peptide     <1..267
            /product="non-structural protein NS5"
            3'UTR          271..>644
ORIGIN
Query Match      100.0%; Score 24; DB 14; Length 644;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1      TCCGAGACGGTCTTGAGGGCTTAC 24
           |||||||||||||||||||
Db      489    TCCGAGACGGTCTTGAGGGCTTAC 466

Search completed: March 25, 2005, 11:41:18
Job time : 928.571 secs

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|  |                  |                              |              |   |
|--|------------------|------------------------------|--------------|---|
| AF297858   | AF297858.1       | GI:11992006                  | Kunjin virus | Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group. |
| 1  | (bases 1 to 633) |                              |              |   |
| Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A. |                  |                              |              |   |
| The relationships between West Nile and Kunjin viruses   |                  |                              |              |   |
| Emerging Infect. Dis. 7 (4), 697-705 (2001)  |                  |                              |              |   |
| 21469816   |                  |                              |              |   |
| 1158535  |                  |                              |              |   |
| 2  | (bases 1 to 633) |                              |              |   |
| Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.                                     |                  |                              |              |   |
| Definitive studies of the relationships between West Nile and Kunjin viruses   |                  |                              |              |   |
| Unpublished  |                  |                              |              |   |
| 3  | (bases 1 to 633) |                              |              |   |
| Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.                                     |                  |                              |              |   |
| Direct Submission  |                  |                              |              |   |
| Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia       |                  |                              |              |   |
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| ACCESSION  |                  |                              |              |   |
| VERSION  |                  |                              |              |   |
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| West Nile virus isolate G22886 polyprotein gene, partial cds.  |                  |                              |              |   |
| 644 bp RNA linear  |                  |                              |              |   |
| VRL 05-MAR-2002  |                  |                              |              |   |
| Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.    |                  |                              |              |   |
| 1  | (bases 1 to 644) |                              |              |   |
| Jia,X.Y., Briese,T., Jordan,I., Rambaut,A., Chi,H.C., Mackenzie,J.S., Hall,R.A., Scherret,J. and Lipkin,W.I.         |                  |                              |              |   |
| Genetic analysis of West Nile New York 1999 encephalitis virus   |                  |                              |              |   |
| Lancet 354 (9194), 1971-1972 (1999)  |                  |                              |              |   |
| 20086017   |                  |                              |              |   |
| 10622305   |                  |                              |              |   |
| 2  | (bases 1 to 644) |                              |              |   |
| Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A. |                  |                              |              |   |

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 09:32:36 ; Search time 229.143 Seconds  
(without alignments)  
620.023 Million cell updates/sec

Title: US-10-688-489-75

Perfect score: 24

Sequence: 1 tcgcgacggtcttgagggtcttac 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 500 summaries

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8: Geneseqn2003s:\*

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13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| C 73 | 16.2 | 67.5 | 1836   | 10 | ABE42297 Toxicity              |
| C 74 | 16.2 | 67.5 | 2082   | 2  | AAAT05901 Human IL-            |
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| c 252 | 15.6 | 65.0 | 3877 | 9  | ABD60790 | Abd60790 Connectiv  | 3877 | 15.6 | 65.0 | 5368   | 10 | AD598328 | Cancer-li           |
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| c 256 | 15.6 | 65.0 | 3943 | 6  | AAS16294 | Aas16294 cDNA enco  | 3943 | 15.6 | 65.0 | 5390   | 13 | ADS88604 | Ad588604 Human hou  |
| c 257 | 15.6 | 65.0 | 3961 | 12 | AD116314 | Adi16314 Human nuc  | 3961 | 15.6 | 65.0 | 5407   | 10 | AD598347 | Ad598347 Leukaemia  |
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| c 294 | 15.6 | 65.0 | 4992 | 10 | AD598312 | Ad598312 Cancer-li  | 4992 | 15.6 | 65.0 | 110000 | 12 | ADN47591 | Adn47591            |
| c 295 | 15.6 | 65.0 | 4997 | 10 | AD598310 | Ad598310 Cancer-li  | 4997 | 15.6 | 65.0 | 110000 | 12 | ADN46123 | Adn46123            |
| c 296 | 15.6 | 65.0 | 5008 | 10 | AD598338 | Ad598338 Cancer-li  | 5008 | 15.6 | 65.0 | 110000 | 12 | ADN47209 | Adn47209            |
| c 297 | 15.6 | 65.0 | 5062 | 10 | AD598383 | Ad598383 Cancer-li  | 5062 | 15.6 | 65.0 | 110000 | 12 | ADN46464 | Adn46464            |
| c 298 | 15.6 | 65.0 | 5069 | 10 | AD598330 | Ad598330 Cancer-li  | 5069 | 15.6 | 65.0 | 110000 | 12 | ADN47960 | Adn47960            |
| c 299 | 15.6 | 65.0 | 5073 | 10 | AD598315 | Ad598315 Cancer-li  | 5073 | 15.6 | 65.0 | 110000 | 13 | ABD32721 | Abd32721 Human can  |
| c 300 | 15.6 | 65.0 | 5076 | 10 | AD598341 | Ad598341 Cancer-li  | 5076 | 15.6 | 65.0 | 146733 | 12 | ADQ97410 | Adq97410 Mouse can  |
| c 301 | 15.6 | 65.0 | 5078 | 10 | AD598374 | Ad598374 Cancer-li  | 5078 | 15.6 | 65.0 | 185695 | 8  | ABQ77405 | Abq77405 Human THB  |
| c 302 | 15.6 | 65.0 | 5083 | 10 | AD598380 | Ad598380 Cancer-li  | 5083 | 15.6 | 65.0 | 219352 | 13 | ABD33098 | Abd33098 Murine ca  |
| c 303 | 15.6 | 65.0 | 5088 | 10 | AD598348 | Ad598348 Cancer-li  | 5088 | 15.6 | 65.0 | 219352 | 13 | ABD33098 | Abd33098 Murine ca  |
| c 304 | 15.6 | 65.0 | 5094 | 10 | AD598309 | Ad598309 Cancer-li  | 5094 | 15.6 | 65.0 | 229354 | 6  | ABQ74179 | Abq74179 Human cyt  |
| c 305 | 15.6 | 65.0 | 5137 | 10 | AD598333 | Ad598333 Cancer-li  | 5137 | 15.6 | 65.0 | 349980 | 3  | AAF21609 | Aaf21609 Neisseria  |
| c 306 | 15.6 | 65.0 | 5146 | 10 | AD598307 | Ad598307 Cancer-li  | 5146 | 15.6 | 65.0 | 349980 | 3  | AAF21608 | Aaf21608 Neisseria  |
| c 307 | 15.6 | 65.0 | 5169 | 10 | AD598377 | Ad598377 Cancer-li  | 5169 | 15.6 | 65.0 | 349980 | 6  | ABQ81849 | Abq81849 Bifidobac  |
| c 308 | 15.6 | 65.0 | 5175 | 10 | AD598352 | Ad598352 Cancer-li  | 5175 | 15.4 | 64.2 | 694    | 10 | ABV72906 | Abv72906 Human end  |
| c 309 | 15.6 | 65.0 | 5183 | 10 | AD598373 | Ad598373 Cancer-li  | 5183 | 15.4 | 64.2 | 1937   | 5  | ABV24796 | Abv24796 Human pro  |
| c 310 | 15.6 | 65.0 | 5185 | 10 | AD598385 | Ad598385 Cancer-li  | 5185 | 15.4 | 64.2 | 1968   | 9  | AD809644 | Ad809644 Allolococ  |
| c 311 | 15.6 | 65.0 | 5190 | 10 | AD598347 | Ad598347 Cancer-li  | 5190 | 15.4 | 64.2 | 1968   | 9  | AD809642 | Ad809642 Allolococ  |
| c 312 | 15.6 | 65.0 | 5232 | 10 | AD598335 | Ad598335 Cancer-li  | 5232 | 15.4 | 64.2 | 1968   | 12 | ADJ27112 | Adj27112 Allolococ  |
| c 313 | 15.6 | 65.0 | 5232 | 10 | AD598337 | Ad598337 Cancer-li  | 5232 | 15.4 | 64.2 | 5017   | 4  | AAH18661 | Aah18661 Human CDN  |

|       |      |      |        |    |             |                     |       |      |      |      |    |          |                    |
|-------|------|------|--------|----|-------------|---------------------|-------|------|------|------|----|----------|--------------------|
| C 386 | 15.4 | 64.2 | 92076  | 13 | ABD33368    | Abd33368 Murine ca  | C 459 | 15.2 | 63.3 | 1619 | 6  | ABL61992 | AbL61992 Colon ade |
| 387   | 15.4 | 64.2 | 110000 | 9  | ADBI2064_10 | Continuation (11 o  | C 460 | 15.2 | 63.3 | 1633 | 13 | ADS49320 | Ads49320 Bacterial |
| 388   | 15.2 | 63.3 | 160    | 6  | ABN42743    | Abn42743 Human spl  | C 461 | 15.2 | 63.3 | 1665 | 3  | AAA37070 | Aaa37070 Human PRO |
| 389   | 15.2 | 63.3 | 147    | 3  | AAC18009    | Aac18009 Human sec  | C 462 | 15.2 | 63.3 | 1665 | 4  | AAF54312 | Aaf54312 DNA encod |
| 390   | 15.2 | 63.3 | 221    | 3  | RAC16163    | Rac16163 Human sec  | C 463 | 15.2 | 63.3 | 1665 | 4  | AAS46067 | Aas46067 Human DNA |
| 391   | 15.2 | 63.3 | 251    | 12 | ACH85841    | Ach85841 Human gen  | C 464 | 15.2 | 63.3 | 1665 | 4  | AAS92100 | Aas92100 Human PRO |
| 392   | 15.2 | 63.3 | 344    | 6  | ABK29694    | Abk29694 Colon ade  | C 465 | 15.2 | 63.3 | 1665 | 6  | ABS74420 | Abs74420 Human cDN |
| 393   | 15.2 | 63.3 | 348    | 5  | ABN13864    | Abn13864 Human ner  | C 466 | 15.2 | 63.3 | 1665 | 8  | ACA89517 | Aca89517 cDNA enco |
| 394   | 15.2 | 63.3 | 375    | 2  | AAV88984    | Aav88984 Human dig  | C 467 | 15.2 | 63.3 | 1665 | 8  | ACA73527 | Aca73527 Human sec |
| C 395 | 15.2 | 63.3 | 421    | 4  | ABA07054    | Aba07054 Human pan  | C 468 | 15.2 | 63.3 | 1665 | 8  | ACA05842 | Aca05842 Human sec |
| C 396 | 15.2 | 63.3 | 421    | 4  | AAK88795    | Aak88795 Human dig  | C 469 | 15.2 | 63.3 | 1665 | 8  | ACA66676 | Aca66676 cDNA enco |
| 397   | 15.2 | 63.3 | 429    | 10 | ABZ37842    | Abz37842 N. gonorr  | C 470 | 15.2 | 63.3 | 1665 | 8  | ACA91206 | Aca91206 Novel hum |
| 398   | 15.2 | 63.3 | 429    | 10 | ABZ39565    | Abz39565 N. gonorr  | C 471 | 15.2 | 63.3 | 1665 | 8  | ACD81583 | Acd81583 Human cDN |
| C 399 | 15.2 | 63.3 | 437    | 6  | AAV97768    | Aav97768 EST clone  | C 472 | 15.2 | 63.3 | 1665 | 8  | ACF20251 | Acf20251 Human sec |
| C 400 | 15.2 | 63.3 | 441    | 6  | ABN77830    | Abn77830 Human ORF  | C 473 | 15.2 | 63.3 | 1665 | 8  | ACF19637 | Acf19637 Human sec |
| C 401 | 15.2 | 63.3 | 442    | 9  | ACH50617    | Ach50617 Human mam  | C 474 | 15.2 | 63.3 | 1665 | 8  | ACD21925 | Acd21925 Human sec |
| C 402 | 15.2 | 63.3 | 457    | 8  | ACA23582    | Aca23582 Prokaryot  | C 475 | 15.2 | 63.3 | 1665 | 8  | ACF13090 | Acf13090 Human sec |
| C 403 | 15.2 | 63.3 | 459    | 9  | ACH29596    | Ach29596 Human adu  | C 476 | 15.2 | 63.3 | 1665 | 8  | ACD25193 | Acd25193 Human sec |
| C 404 | 15.2 | 63.3 | 468    | 9  | ACH38754    | Ach38754 Human foe  | C 477 | 15.2 | 63.3 | 1665 | 8  | ACF00242 | Acf00242 Human sec |
| C 405 | 15.2 | 63.3 | 489    | 9  | ACH16066    | Ach16066 Human adu  | C 478 | 15.2 | 63.3 | 1665 | 8  | ACA60405 | Aca60405 Novel hum |
| C 406 | 15.2 | 63.3 | 513    | 4  | ABA60756    | Aba60756 Human adu  | C 479 | 15.2 | 63.3 | 1665 | 8  | ACA72299 | Aca72299 Novel hum |
| C 407 | 15.2 | 63.3 | 513    | 4  | AAI40648    | Aai40648 Probe #93  | C 480 | 15.2 | 63.3 | 1665 | 8  | ACD04823 | Acd04823 Novel hum |
| C 408 | 15.2 | 63.3 | 513    | 4  | AAK34932    | Aak34932 Human bon  | C 481 | 15.2 | 63.3 | 1665 | 8  | ACD18284 | Acd18284 Human sec |
| C 409 | 15.2 | 63.3 | 513    | 4  | AAK09041    | Aak09041 Human bra  | C 482 | 15.2 | 63.3 | 1665 | 8  | ACD08291 | Acd08291 Human sec |
| C 410 | 15.2 | 63.3 | 547    | 4  | AAI61295    | Aai61295 Human pol  | C 483 | 15.2 | 63.3 | 1665 | 8  | ACA88725 | Aca88725 Novel hum |
| 411   | 15.2 | 63.3 | 555    | 12 | ACH72085    | Ach72085 Human gen  | C 484 | 15.2 | 63.3 | 1665 | 8  | ACA70167 | Aca70167 Human sec |
| 412   | 15.2 | 63.3 | 557    | 12 | ACH76980    | Ach76980 Human gen  | C 485 | 15.2 | 63.3 | 1665 | 8  | ACD12389 | Acd12389 Novel hum |
| 413   | 15.2 | 63.3 | 576    | 8  | ABS55823    | Abs55823 Human Ank  | C 486 | 15.2 | 63.3 | 1665 | 8  | ACC74304 | Acc74304 Human sec |
| 414   | 15.2 | 63.3 | 576    | 12 | ADE91297    | Ade91297 cDNA clon  | C 487 | 15.2 | 63.3 | 1665 | 8  | ACD15932 | Acd15932 Human sec |
| C 415 | 15.2 | 63.3 | 583    | 2  | AAK21005    | Aak21005 Polynucle  | C 488 | 15.2 | 63.3 | 1665 | 8  | ACD25500 | Acd25500 Novel hum |
| 416   | 15.2 | 63.3 | 672    | 8  | AAK25931    | Aak25931 Human cDN  | C 489 | 15.2 | 63.3 | 1665 | 8  | ACD17977 | Acd17977 Human sec |
| 417   | 15.2 | 63.3 | 672    | 8  | ABX73272    | Abx73272 Human nov  | C 490 | 15.2 | 63.3 | 1665 | 8  | ACC88264 | Acc88264 Human sec |
| C 418 | 15.2 | 63.3 | 818    | 8  | ABX05210    | Abx05210 Human nov  | C 491 | 15.2 | 63.3 | 1665 | 8  | ACD21618 | Acd21618 Human sec |
| C 419 | 15.2 | 63.3 | 942    | 3  | AAC34540    | Aac34540 Arabidops  | C 492 | 15.2 | 63.3 | 1665 | 8  | ACA58852 | Aca58852 cDNA enco |
| C 420 | 15.2 | 63.3 | 956    | 4  | AAS33313    | Aas33313 DNA encod  | C 493 | 15.2 | 63.3 | 1665 | 8  | ABX98295 | Abx98295 Human cDN |
| C 421 | 15.2 | 63.3 | 969    | 6  | ABZ14641    | Abz14641 Arabidops  | C 494 | 15.2 | 63.3 | 1665 | 8  | ABX98295 | Abx98295 Human cDN |
| C 422 | 15.2 | 63.3 | 1002   | 4  | AAS12452    | Aas12452 DNA encod  | C 495 | 15.2 | 63.3 | 1665 | 8  | ACD14046 | Acd14046 Human PRO |
| C 423 | 15.2 | 63.3 | 1035   | 12 | ADL03456    | Adl03456 DNA encod  | C 496 | 15.2 | 63.3 | 1665 | 8  | ACD09826 | Acd09826 Human sec |
| C 424 | 15.2 | 63.3 | 1078   | 4  | AAK51908    | Aak51908 Human pol  | C 497 | 15.2 | 63.3 | 1665 | 8  | ACC88571 | Acc88571 Human sec |
| C 425 | 15.2 | 63.3 | 1158   | 6  | ABD42889    | Abd42889 Human DNA  | C 498 | 15.2 | 63.3 | 1665 | 8  | ACD21311 | Acd21311 Human sec |
| C 426 | 15.2 | 63.3 | 1158   | 6  | ABS55822    | Abs55822 Human cDN  | C 499 | 15.2 | 63.3 | 1665 | 8  | ABX75683 | Abx75683 Human cDN |
| C 427 | 15.2 | 63.3 | 1158   | 8  | ADH62620    | Adh62620 Human tel  | C 500 | 15.2 | 63.3 | 1665 | 8  | ACA64028 | Aca64028 cDNA enco |
| C 428 | 15.2 | 63.3 | 1158   | 12 | ADK91296    | Adk91296 cDNA enco  |       |      |      |      |    |          |                    |
| C 429 | 15.2 | 63.3 | 1202   | 4  | AAS33131    | Aas33131 DNA encod  |       |      |      |      |    |          |                    |
| C 430 | 15.2 | 63.3 | 1208   | 4  | AAI59509    | Aai59509 Human pol  |       |      |      |      |    |          |                    |
| C 431 | 15.2 | 63.3 | 1244   | 3  | AAK40734    | Aak40734 Arabidops  |       |      |      |      |    |          |                    |
| C 432 | 15.2 | 63.3 | 1286   | 4  | AAH99099    | Aah99099 Human EST  |       |      |      |      |    |          |                    |
| C 433 | 15.2 | 63.3 | 1368   | 11 | ACH99857    | Ach99857 Klebsiell  |       |      |      |      |    |          |                    |
| C 434 | 15.2 | 63.3 | 1392   | 6  | AAH48351    | Aah48351 Human FOA  |       |      |      |      |    |          |                    |
| C 435 | 15.2 | 63.3 | 1392   | 6  | ABA96942    | Abas96942 Human den |       |      |      |      |    |          |                    |
| C 436 | 15.2 | 63.3 | 1392   | 13 | ADS59699    | Ads59699 Bacterial  |       |      |      |      |    |          |                    |
| C 437 | 15.2 | 63.3 | 1400   | 4  | AAH21249    | Aah21249 Human KCN  |       |      |      |      |    |          |                    |
| C 438 | 15.2 | 63.3 | 1416   | 8  | ACA23300    | Aca23300 Prokaryot  |       |      |      |      |    |          |                    |
| C 439 | 15.2 | 63.3 | 1449   | 5  | AAK65954    | Aak65954 DNA encod  |       |      |      |      |    |          |                    |
| C 440 | 15.2 | 63.3 | 1452   | 10 | ADA53677    | Ada53677 Human cod  |       |      |      |      |    |          |                    |
| C 441 | 15.2 | 63.3 | 1466   | 4  | AAH32618    | Aah32618 Human sec  |       |      |      |      |    |          |                    |
| C 442 | 15.2 | 63.3 | 1475   | 12 | ADQ22740    | Adq22740 Human sof  |       |      |      |      |    |          |                    |
| C 443 | 15.2 | 63.3 | 1475   | 12 | ADQ23254    | Adq23254 Human sof  |       |      |      |      |    |          |                    |
| C 444 | 15.2 | 63.3 | 1492   | 2  | AAZ00814    | Aaz00814 Human sec  |       |      |      |      |    |          |                    |
| C 445 | 15.2 | 63.3 | 1492   | 8  | ADA39903    | Ada39903 Human sec  |       |      |      |      |    |          |                    |
| C 446 | 15.2 | 63.3 | 1492   | 8  | ACC50492    | Acc50492 Human sec  |       |      |      |      |    |          |                    |
| C 447 | 15.2 | 63.3 | 1492   | 8  | ABZ71274    | Abz71274 Human sec  |       |      |      |      |    |          |                    |
| C 448 | 15.2 | 63.3 | 1492   | 9  | ADB91180    | Abd91180 Human sec  |       |      |      |      |    |          |                    |
| C 449 | 15.2 | 63.3 | 1492   | 10 | ADC73557    | Adc73557 Human sec  |       |      |      |      |    |          |                    |
| C 450 | 15.2 | 63.3 | 1492   | 10 | ADD37614    | Add37614 Human sec  |       |      |      |      |    |          |                    |
| C 451 | 15.2 | 63.3 | 1492   | 10 | ADA56093    | Ada56093 Gene enco  |       |      |      |      |    |          |                    |
| C 452 | 15.2 | 63.3 | 1504   | 10 | ADD46911    | Add46911 Rat gene   |       |      |      |      |    |          |                    |
| C 453 | 15.2 | 63.3 | 1504   | 10 | ADE56589    | Ade56589 Rat gene   |       |      |      |      |    |          |                    |
| C 454 | 15.2 | 63.3 | 1504   | 10 | ADD46915    | Add46915 Rat gene   |       |      |      |      |    |          |                    |
| C 455 | 15.2 | 63.3 | 1504   | 10 | ADE56593    | Ade56593 Rat gene   |       |      |      |      |    |          |                    |
| C 456 | 15.2 | 63.3 | 1508   | 11 | ADM02282    | Adm02282 Human cDN  |       |      |      |      |    |          |                    |
| C 457 | 15.2 | 63.3 | 1588   | 10 | ADC30473    | Adc30473 Human nov  |       |      |      |      |    |          |                    |
| C 458 | 15.2 | 63.3 | 1616   | 5  | AAS73650    | Aas73650 DNA encod  |       |      |      |      |    |          |                    |

## ALIGNMENTS

## RESULT 1

## ADN36752

ID ADN36752 standard; DNA; 24 BP.

XX ADN36752;

XX 15-JUL-2004 (first entry)

DE West Nile virus detection-related oligonucleotide probe SeqID74.

XX hybridisation assay probe; nucleic acid detection;

KW target-complementary sequence; flavivirus; West Nile virus; WNV;

KW RNA virus; infection; meningitis; encephalitis;

XX high throughput screening; probe; ss.

OS West Nile virus.

XX WO2004036190-A2.

XX 29-APR-2004.

PD 10-OCT-2003; 2003WO-US033639.

PF 16-OCT-2002; 2002US-0418891P.

XX 25-NOV-2002; 2002US-0429006P.

PR 24-FEB-2003; 2003US-0449810P.

XX PA (GENP-) GEN-PROBE INC.  
 XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;  
 XX DR WPI; 2004-389590/36.  
 XX PT New hybridization assay probe comprising target-complementary sequence of  
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
 XX PS Claim 27; SEQ ID NO 74; 135pp; English.  
 XX CC This invention relates to a novel hybridisation assay probe, for  
 CC detecting a nucleic acid, which is a probe sequence that comprises a  
 CC target-complementary sequence of bases, and optionally one or more base  
 CC sequences that are not complementary to the nucleic acid that is to be  
 CC detected. The hybridisation assay probes and the kits are useful in  
 CC detecting and amplifying a target nucleic acid sequence, for example  
 CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC birds and culex mosquitoes, with humans and horses serving as incidental  
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
 CC invention may allow for accurate and efficient high throughput screening.  
 CC The present sequence is that of an oligonucleotide probe which is related  
 CC to the invention.  
 XX SQ Sequence 24 BP; 4 A; 6 C; 8 G; 6 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 24; DB 12; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.08; Indels 0; Gaps 0;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGAGACGGTTCCTGAGGGCTTAC 24  
 DB 1 TCCGAGACGGTTCCTGAGGGCTTAC 24  
 RESULT 2  
 ADN36753  
 ID ADN36753 standard; DNA; 24 BP.  
 AC ADN36753;  
 XX 15-JUL-2004 (first entry)  
 XX West Nile virus detection-related oligonucleotide probe SeqID75.  
 XX hybridisation assay probe; nucleic acid detection;  
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;  
 KW RNA virus; infection; meningitis; encephalitis;  
 KW high throughput screening; probe; ss.  
 XX West Nile virus.  
 OS WO2004036190-A2.  
 XX 29-APR-2004.  
 XX 10-OCT-2003; 2003WO-US033639.  
 XX 16-OCT-2002; 2002US-0418891P.  
 PR 25-NOV-2002; 2002US-0429006P.  
 PR 24-FEB-2003; 2003US-0449810P.  
 XX (GENP-) GEN-PROBE INC.  
 XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;  
 XX WPI; 2004-389590/36.  
 XX New hybridization assay probe comprising target-complementary sequence of  
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
 XX

PS Claim 26; SEQ ID NO 75; 135pp; English.  
 XX This invention relates to a novel hybridisation assay probe, for  
 CC detecting a nucleic acid, which is a probe sequence that comprises a  
 CC target-complementary sequence of bases, and optionally one or more base  
 CC sequences that are not complementary to the nucleic acid that is to be  
 CC detected. The hybridisation assay probes and the kits are useful in  
 CC detecting and amplifying a target nucleic acid sequence, for example  
 CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC birds and culex mosquitoes, with humans and horses serving as incidental  
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
 CC invention may allow for accurate and efficient high throughput screening.  
 CC The present sequence is that of an oligonucleotide probe which is related  
 CC to the invention.  
 XX SQ Sequence 24 BP; 4 A; 6 C; 8 G; 6 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 24; DB 12; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.08; Indels 0; Gaps 0;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGAGACGGTTCCTGAGGGCTTAC 24  
 DB 1 TCCGAGACGGTTCCTGAGGGCTTAC 24  
 RESULT 3  
 ADN36751  
 ID ADN36751 standard; DNA; 48 BP.  
 AC ADN36751;  
 XX 15-JUL-2004 (first entry)  
 XX West Nile virus detection-related oligonucleotide probe SeqID73.  
 XX hybridisation assay probe; nucleic acid detection;  
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;  
 KW RNA virus; infection; meningitis; encephalitis;  
 KW high throughput screening; probe; ss.  
 XX West Nile virus.  
 OS WO2004036190-A2.  
 XX 29-APR-2004.  
 XX 10-OCT-2003; 2003WO-US033639.  
 XX 16-OCT-2002; 2002US-0418891P.  
 PR 25-NOV-2002; 2002US-0429006P.  
 PR 24-FEB-2003; 2003US-0449810P.  
 XX (GENP-) GEN-PROBE INC.  
 XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;  
 XX WPI; 2004-389590/36.  
 XX New hybridization assay probe comprising target-complementary sequence of  
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
 XX Claim 18; SEQ ID NO 73; 135pp; English.  
 XX This invention relates to a novel hybridisation assay probe, for  
 CC detecting a nucleic acid, which is a probe sequence that comprises a  
 CC target-complementary sequence of bases, and optionally one or more base  
 CC sequences that are not complementary to the nucleic acid that is to be  
 CC detected. The hybridisation assay probes and the kits are useful in  
 CC detecting and amplifying a target nucleic acid sequence, for example  
 CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC

CC birds and culex mosquitoes, with humans and horses serving as incidental  
CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
CC invention may allow for accurate and efficient high throughput screening.  
CC The present sequence is that of an oligonucleotide probe which is related  
CC to the invention.

XX  
SQ Sequence 48 BP; 8 A; 12 C; 13 G; 15 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 12; Length 48;  
Best Local Similarity 100.0%; Pred. No. 0.096;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGCTTAC 24  
|||||  
Db 1 TCCGAGACGGTTCTGAGGCTTAC 24

RESULT 4  
ADN36762  
ID ADN36762 standard; DNA; 51 BP.

XX AC ADN36762;

XX DT 15-JUL-2004 (first entry)

XX DE West Nile virus detection-related oligonucleotide probe SeqID84.

XX KW hybridisation assay probe; nucleic acid detection;

XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;

XX KW RNA virus; infection; meningitis; encephalitis;

XX KW high throughput screening; probe; ss.

XX OS West Nile virus.

XX OS Enterobacteria phage T7.

XX FH Key Location/Qualifiers

FT misc\_feature 1..27

FT /\*tag= a

FT /\*note= "T7 promoter sequence"

FT 28..51

FT /\*tag= b

FT /\*note= "WNV-complimentary sequence"

XX WO2004036190-A2.

XX PD 29-APR-2004.

XX PF 10-OCT-2003; 2003WO-US033639.

XX PR 16-OCT-2002; 2002US-0418891P.

XX PR 25-NOV-2002; 2002US-0429006P.

XX PR 24-FEB-2003; 2003US-0449810P.

XX PA (GENP-) GEN-PROBE INC.

XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX WPI; 2004-389590/36.

XX DR  
XX PT New hybridization assay probe comprising target-complementary sequence of  
XX PT bases, useful in detecting flavivirus, e.g. West Nile virus.

XX PS Disclosure; SEQ ID NO 84; 135pp; English.

XX CC This invention relates to a novel hybridisation assay probe, for  
XX CC detecting a nucleic acid, which is a probe sequence that comprises a  
XX CC target-complementary sequence of bases, and optionally one or more base  
XX CC sequences that are not complementary to the nucleic acid that is to be  
XX CC detected. The hybridisation assay probes and the kits are useful in  
XX CC detecting and amplifying a target nucleic acid sequence, for example  
XX CC flavivirus like West Nile virus, that may be present in a biological  
XX CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
XX CC birds and culex mosquitoes, with humans and horses serving as incidental

CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
CC invention may allow for accurate and efficient high throughput screening.  
CC The present sequence is that of an oligonucleotide probe which is related  
CC to the invention.

XX SQ Sequence 51 BP; 15 A; 10 C; 13 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 12; Length 51;  
Best Local Similarity 100.0%; Pred. No. 0.088;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGCTTAC 24  
|||||  
Db 28 TCCGAGACGGTTCTGAGGCTTAC 51

RESULT 5  
ADN36750

ID ADN36750 standard; DNA; 70 BP.

XX AC ADN36750;

XX DT 15-JUL-2004 (first entry)

XX DE West Nile virus detection-related oligonucleotide probe SeqID72.

XX KW hybridisation assay probe; nucleic acid detection;

XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;

XX KW RNA virus; infection; meningitis; encephalitis;

XX KW high throughput screening; probe; ss.

XX OS West Nile virus.

XX PN WO2004036190-A2.

XX PD 29-APR-2004.

XX PF 10-OCT-2003; 2003WO-US033639.

XX PR 16-OCT-2002; 2002US-0418891P.

XX PR 25-NOV-2002; 2002US-0429006P.

XX PR 24-FEB-2003; 2003US-0449810P.

XX PA (GENP-) GEN-PROBE INC.

XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX WPI; 2004-389590/36.

XX PT New hybridization assay probe comprising target-complementary sequence of  
XX PT bases, useful in detecting flavivirus, e.g. West Nile virus.

XX PS Disclosure; SEQ ID NO 72; 135pp; English.

XX CC This invention relates to a novel hybridisation assay probe, for  
XX CC detecting a nucleic acid, which is a probe sequence that comprises a  
XX CC target-complementary sequence of bases, and optionally one or more base  
XX CC sequences that are not complementary to the nucleic acid that is to be  
XX CC detected. The hybridisation assay probes and the kits are useful in  
XX CC detecting and amplifying a target nucleic acid sequence, for example  
XX CC flavivirus like West Nile virus, that may be present in a biological  
XX CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
XX CC birds and culex mosquitoes, with humans and horses serving as incidental  
XX CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
XX CC invention may allow for accurate and efficient high throughput screening.  
XX CC The present sequence is that of an oligonucleotide probe which is related  
XX CC to the invention.

XX SQ Sequence 70 BP; 11 A; 19 C; 20 G; 20 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 12; Length 70;  
Best Local Similarity 100.0%; Pred. No. 0.092;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTAC 24  
 Db 1 TCCGAGACGGTCTGAGGGCTTAC 24

RESULT 6  
 ADR32078/c  
 ID ADR32078 standard; DNA; 10945 BP.  
 XX  
 AC ADR32078;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Genomic DNA of a West Nile virus.  
 XX  
 KW analysis; target; real time PCR; ds; genomic.  
 XX  
 OS West Nile virus.  
 XX  
 PN WO2004072230-A2.  
 XX  
 PD 26-AUG-2004.  
 XX  
 PF 10-FEB-2004; 2004WO-US0002012.  
 XX  
 PR 10-FEB-2003; 2003US-00361004.  
 XX  
 PA (CLEA-) CLEARANT INC.  
 XX  
 PI Mckenney K, Gillmeister L, Marlowe K, Armistead D;  
 XX  
 XX WPI; 2004-625843/60.  
 XX  
 PT Analyzing a target nucleic acid sequence in a biological material by real  
 PT time PCR using nucleic acid primers that are separated by at least 750  
 PT nucleic acid residues in the target sequence.  
 XX  
 PS Disclosure; SEQ ID NO 5; 96pp; English.  
 XX  
 CC The invention relates to a novel method for analysing a target nucleic  
 CC acid sequence in a biological material. The method comprises adding at  
 CC least two nucleic acid primers that hybridise under stringent conditions  
 CC to predetermined nucleic acid sequences of the target nucleic acid  
 CC sequence that are separated by at least 750 nucleic acid residues,  
 CC amplifying the target nucleic acid sequence by PCR, and detecting and  
 CC quantifying the target nucleic acid sequence. The methods and  
 CC compositions of the present invention are useful for analysing a target  
 CC nucleic acid sequence in a biological material by real time PCR using  
 CC nucleic acid primers that are separated by at least 750 nucleic acid  
 CC residues in the target sequence. This polynucleotide sequence represents  
 CC the genomic DNA of a West Nile virus used in the target analysis method  
 CC of the invention.  
 XX  
 SQ Sequence 10945 BP; 2999 A; 2457 C; 3143 G; 2346 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 24; DB 13; Length 10945;  
 Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTAC 24  
 Db 10587 TCCGAGACGGTCTGAGGGCTTAC 10564

RESULT 7  
 ADR67768/c  
 ID ADR67768 standard; DNA; 10945 BP.  
 XX  
 AC ADR67768;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX

DE West Nile virus DNA detected by novel detection method.  
 XX ds; detection; pathogen.  
 XX  
 OS West Nile virus.  
 XX  
 PN WO2004072231-A2.  
 XX  
 PD 26-AUG-2004.  
 XX  
 PF 10-FEB-2004; 2004WO-US0002013.  
 XX  
 PR 10-FEB-2003; 2003US-00361002.  
 XX  
 PA (CLEA-) CLEARANT INC.  
 XX  
 PI Mckenney K, Gillmeister L, Marlowe K, Armistead D;  
 XX  
 XX WPI; 2004-625844/60.  
 XX  
 CC Determining level of potentially active biological pathogens in  
 CC biological material, by adding nucleic acid primer pairs to biological  
 CC material, amplifying target nucleic acid by PCR, detecting and  
 CC quantifying target nucleic acid.  
 XX  
 PS Disclosure; SEQ ID NO 5; 111pp; English.  
 XX  
 CC The invention relates to a method of determining (MI) level of  
 CC potentially active biological pathogens in biological material, involves  
 CC adding at least two nucleic acid primer pairs to biological material,  
 CC amplifying target nucleic acid sequences by PCR, and detecting and  
 CC quantifying target nucleic acid sequences, where quantity of the nucleic  
 CC acid sequences is proportional to number of biological pathogens in  
 CC biological material. (MI) is useful for determining level of potentially  
 CC active biological pathogens in a biological material such as cells,  
 CC tissues, blood or blood components, proteins, enzymes, immunoglobulins,  
 CC botanicals, food, ligaments, tendons, nerves, bone, teeth, skin grafts,  
 CC bone marrow, heart valves, cartilage, corneas, arteries, veins, organs,  
 CC lipids, carbohydrates, collagen, chitin and its derivatives, forensic  
 CC samples, mummified material, human or animal remains, stem cells, islet  
 CC of Langerhans cells, cells for transplantation, red blood cells, white  
 CC blood cells or platelets. The biological pathogen is chosen from  
 CC bacteria, viruses, fungi and single cell parasites. The biological  
 CC pathogen is chosen from Aspergillus, Candida, Histoplasma,  
 CC Saccharomyces, Coccidioides, Cryptococcus, Escherichia, Bacillus,  
 CC Campylobacter, Helicobacter, Listeria, Clostridium, Streptococcus,  
 CC Enterococcus, Staphylococcus, Brucella, Haemophilus, Salmonella,  
 CC Yersinia, Pseudomonas, Serratia, Enterobacter, Klebsiella, Proteus,  
 CC Citrobacter, Corynebacterium, Propionibacterium and Coxiella. The  
 CC biological pathogen is chosen from Adeno-associated virus (AAV),  
 CC California encephalitis virus, Coronavirus, Coxsackievirus-A,  
 CC Coxsackievirus-B, Eastern equine encephalitis virus (EEEV), Echovirus,  
 CC Hantavirus, Hepatitis A virus (HAV), Hepatitis C virus (HCV), Hepatitis  
 CC delta virus (HDV), Hepatitis E virus (HEV), Hepatitis G virus (HGV), HIV,  
 CC Human T-lymphotrophic virus (HTLV), Influenza virus (Flu virus), Measles  
 CC virus (Rubella), Mumps virus, Norwalk virus, Parainfluenza virus, Polio  
 CC virus, Rabies virus, Respiratory Syncytial virus, Rhinovirus, Rubella  
 CC virus, Saint Louis encephalitis virus, Western equine encephalitis virus  
 CC (WEEV), yellow fever virus, Adenovirus, Cytomegalovirus (CMV), Epstein-  
 CC Barr virus (EBV), Hepatitis B virus (HBV), Herpes simplex virus 1, Herpes  
 CC simplex virus 2, Molluscum contagiosum, Papilloma virus (HPV), Smallpox  
 CC virus (Variola), Vaccinia virus, Venezuelan equine encephalitis virus  
 CC (VEEV), Ebola virus, West Nile virus, Human parvovirus B19 and Rotavirus.  
 CC (MI) is useful for determining the effectiveness of a sterilization  
 CC process applied to a biological material. (MI) is useful in determining  
 CC whether the biological pathogen is inactive or active. (MI) enables  
 CC determination of whether the particular biological pathogen is present in  
 CC a biological material as shown by amplification of first target sequence  
 CC and whether the biological pathogen is inactive or active. (MI) enables  
 CC evaluation of the effectiveness of sterilization processes, and  
 CC determination of both the original level and the residual level of  
 CC potentially active biological pathogens. This sequence corresponds to a  
 CC West Nile virus DNA detected by the method of the invention.

XX SQ Sequence 10945 BP; 2959 A; 2457 C; 3143 G; 2346 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 24; DB 13; Length 10945;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGCTTAC 24  
 |||||  
 Db 10587 TCCGAGACGGTTCTGAGGCTTAC 10564

RESULT 8  
 ADK13681/C  
 ID ADK13681 standard; DNA; 10962 BP.  
 XX AC ADK13681;  
 XX AC  
 XX DT 20-MAY-2004 (first entry)  
 XX DE West Nile Virus DNA sequence, SEQ ID 1.  
 XX KW Virucide; Immunosuppressant; flavivirus;  
 XX KW envelope protein domain III polypeptide; envelope protein; gene; ss.  
 XX OS West Nile virus.  
 XX FH Key Location/Qualifiers  
 XX CDS 97..10389  
 XX FT /\*tag= a  
 XX FT /product= "West Nile Virus protein"  
 XX PN WO2004016586-A2.  
 XX PD 26-FEB-2004.  
 XX PF 18-AUG-2003; 2003WO-US025681.  
 XX PR 16-AUG-2002; 2002US-0403893P.  
 XX PR 06-FEB-2003; 2003US-0445581P.  
 XX PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX PI Barrett A, Beasley D, Holbrook M;  
 XX WPI; 2004-203756/19.  
 XX DR P-PSDB; ADK13682.  
 XX PT Diagnosing flavivirus infection by contacting a sample from a human or  
 PT animal with a flavivirus envelope protein domain III polypeptide, and  
 PT detecting formation of an immunocomplex between the envelope protein and  
 PT antibodies in the sample.  
 XX PS Disclosure; SEQ ID NO 1; 110pp; English.  
 XX CC The present invention relates to a method for screening for a flavivirus  
 CC in a subject or animal host. The method comprises: contacting a sample  
 CC from the subject with a composition comprising a flavivirus envelope  
 CC protein domain III polypeptide (ADK13683-ADK13701) under conditions that  
 CC permit formation of specific immunocomplex between an antibody in the  
 CC sample and the envelope protein domain III polypeptide; and detecting  
 CC whether a specific immunocomplex is formed. The present sequence is the  
 CC coding sequence for West Nile Virus protein, from which E protein  
 CC envelope protein domain III polypeptide (ADK13683) is derived.  
 XX SQ Sequence 10962 BP; 2997 A; 2497 C; 3100 G; 2368 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 24; DB 12; Length 10962;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGCTTAC 24  
 |||||

Db 10564 TCCGAGACGGTTCTGAGGCTTAC 10541

RESULT 9  
 ADN98022/C  
 ID ADN98022 standard; DNA; 10975 BP.  
 XX AC ADN98022;  
 XX AC  
 XX DT 29-JUL-2004 (first entry)  
 XX DE West Nile Virus isolate 2741 complete genome sequence.  
 XX KW ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;  
 XX KW Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.  
 XX OS West Nile virus.  
 XX PN WO2004040263-A2.  
 XX PD 13-MAY-2004.  
 XX PF 31-OCT-2003; 2003WO-US034823.  
 XX PR 31-OCT-2002; 2002US-0422755P.  
 XX PR 06-JUN-2003; 2003US-0476513P.  
 XX PA (HEAL-) HEALTH RES INC.  
 XX PI Wong SJ, Pei-Yong S;  
 XX WPI; 2004-400223/37.  
 XX DR GENBANK; AF206518.  
 XX PT New diagnostic kit comprising West Nile Virus (WNV) envelope protein  
 PT reactive with antibody against WNV and cross-reactive with antibody  
 PT against a flavivirus, useful in diagnosing flavivirus infection caused by  
 PT DENV, WNV, JEV or SLEV.  
 XX PS Disclosure; Fig 37; 212pp; English.  
 XX CC The invention relates to a diagnostic kit comprising at least one  
 CC isolated and purified polypeptide comprising a West Nile Virus (WNV)  
 CC envelope (E) protein or its immunogenic fragment having a native  
 CC conformation or non-denatured structure and that is reactive with  
 CC antibodies against WNV and cross-reactive with antibodies against a  
 CC flavivirus. The diagnostic kit is useful in diagnosing flavivirus  
 CC infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to  
 CC the complete nucleotide sequence of the WNV isolate 2741.  
 XX SQ Sequence 10975 BP; 3007 A; 2460 C; 3149 G; 2359 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 24; DB 12; Length 10975;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGCTTAC 24  
 |||||  
 Db 10611 TCCGAGACGGTTCTGAGGCTTAC 10588

RESULT 10  
 ABZ68481/C  
 ID ABZ68481 standard; DNA; 11029 BP.  
 XX AC ABZ68481;  
 XX AC  
 XX DT 22-APR-2003 (first entry)  
 XX DE Nucleotide sequence of the genome of West Nile virus IS-98-ST1.  
 XX KW WNV; IS-98-ST1; Flavivirus; infection; encephalitis; gene; ss.  
 XX XX





XX 31-OCT-2002; 2002US-0422755P.  
 PR 06-JUN-2003; 2003US-0476513P.  
 XX (HEAL-) HEALTH RES INC.  
 XX Wong SJ, Pei-Yong S;  
 XX WPI; 2004-400223/37.  
 DR GENBANK; AF404756.  
 XX New diagnostic kit comprising West Nile Virus (WNV) envelope protein  
 PT reactive with antibody against WNV and cross-reactive with antibody  
 PT against a flavivirus, useful in diagnosing flavivirus infection caused by  
 XX DENV, WNV, JEV or SLEV.  
 XX Disclosure; Fig 38; 212pp; English.  
 XX The invention relates to a diagnostic kit comprising at least one  
 CC isolated and purified polypeptide comprising a West Nile Virus (WNV)  
 CC envelope (E) protein or its immunogenic fragment having a native  
 CC conformation or non-denatured structure and that is reactive with  
 CC antibodies against WNV and cross-reactive with antibodies against a  
 CC flavivirus. The diagnostic kit is useful in diagnosing flavivirus  
 CC infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to  
 CC the complete nucleotide sequence of the WNV isolate 3356.  
 XX SQ Sequence 11029 BP; 3017 A; 2466 C; 3172 G; 2374 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 24; DB 12; Length 11029;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGAGACGGTTCTGAGGGCTTAC 24  
 DB 10629 TCCGAGACGGTTCTGAGGGCTTAC 10606  
 RESULT 13  
 ADN36754  
 ID ADN36754 standard; DNA; 23 BP.  
 XX AC ADN36754;  
 XX 15-JUL-2004 (first entry)  
 XX West Nile virus detection-related oligonucleotide probe SeqID76.  
 DE hybridisation assay probe; nucleic acid detection;  
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;  
 KW RNA virus; infection; meningitis; encephalitis;  
 KW high throughput screening; probe; ss.  
 XX West Nile virus.  
 OS WO2004036190-A2.  
 XX 29-APR-2004.  
 XX 10-OCT-2003; 2003WO-US033639.  
 XX 16-OCT-2002; 2002US-0418891P.  
 PR 25-NOV-2002; 2002US-0429006P.  
 PR 24-FEB-2003; 2003US-0449810P.  
 XX (GENP-) GEN-PROBE INC.  
 XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;  
 XX WPI; 2004-389590/36.  
 XX New hybridization assay probe comprising target-complementary sequence of  
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.

XX Claim 26; SEQ ID NO 76; 135pp; English.  
 PS This invention relates to a novel hybridisation assay probe, for  
 CC detecting a nucleic acid, which is a probe sequence that comprises a  
 CC target-complementary sequence of bases, and optionally one or more base  
 CC sequences that are not complementary to the nucleic acid that is to be  
 CC detected. The hybridisation assay probes and the kits are useful in  
 CC detecting and amplifying a target nucleic acid sequence, for example  
 CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC birds and culex mosquitoes, with humans and horses serving as incidental  
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
 CC invention may allow for accurate and efficient high throughput screening.  
 CC The present sequence is that of an oligonucleotide probe which is related  
 CC to the invention.  
 XX SQ Sequence 23 BP; 4 A; 5 C; 8 G; 6 T; 0 U; 0 Other;  
 Query Match 95.8%; Score 23; DB 12; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 0.24;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGAGACGGTTCTGAGGGCTTA 23  
 DB 1 TCCGAGACGGTTCTGAGGGCTTA 23  
 RESULT 14  
 ADN36763  
 ID ADN36763 standard; DNA; 50 BP.  
 XX AC ADN36763;  
 XX 15-JUL-2004 (first entry)  
 XX West Nile virus detection-related PCR primer SeqID85.  
 DE hybridisation assay probe; nucleic acid detection;  
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;  
 KW RNA virus; infection; meningitis; encephalitis;  
 KW high throughput screening; PCR; primer; ss.  
 XX West Nile virus.  
 OS Enterobacteria phage T7.  
 XX Key Location/Qualifiers  
 FH misc\_feature 1..27  
 FT /\*tag= a  
 FT /note= "T7 promoter sequence"  
 FT misc\_feature 28..50  
 FT /\*tag= b  
 FT /note= "WNV-complimentary sequence"  
 XX WO2004036190-A2.  
 XX 29-APR-2004.  
 XX 10-OCT-2003; 2003WO-US033639.  
 XX 16-OCT-2002; 2002US-0418891P.  
 PR 25-NOV-2002; 2002US-0429006P.  
 PR 24-FEB-2003; 2003US-0449810P.  
 XX (GENP-) GEN-PROBE INC.  
 XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;  
 XX WPI; 2004-389590/36.  
 XX New hybridization assay probe comprising target-complementary sequence of  
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.

PS Example 4; SEQ ID NO 85; 135pp; English.

XX This invention relates to a novel hybridisation assay probe, for  
CC detecting a nucleic acid, which is a probe sequence that comprises a  
CC target-complementary sequence of bases, and optionally one or more base  
CC sequences that are not complementary to the nucleic acid that is to be  
CC detected. The hybridisation assay probes and the kits are useful in  
CC detecting and amplifying a target nucleic acid sequence, for example  
CC flavivirus like West Nile virus, that may be present in a biological  
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
CC birds and culex mosquitoes, with humans and horses serving as incidental  
CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
CC invention may allow for accurate and efficient high throughput screening.  
CC The present sequence is that of a PCR primer which is related to the  
CC invention.

SQ Sequence 50 BP; 15 A; 9 C; 13 G; 13 T; 0 U; 0 Other;

Query Match 95.8%; Score 23; DB 12; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.27; Length 50;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTA 23

DB 28 TCCGAGACGGTCTGAGGGCTTA 50

RESULT 15

ADO07431/C  
ID ADO07431 standard; DNA; 10818 BP.

XX  
AC ADO07431;

XX 15-JUL-2004 (first entry)

DE Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 9.

XX antiinflammatory; neuroprotective; gene therapy;  
KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;  
KW Japanese encephalitis.

OS Japanese encephalitis virus.

XX WO2004033690-A1.

XX 22-APR-2004.

XX 09-OCT-2003; 2003WO-KR002081.

XX 09-OCT-2002; 2002KR-00061589.

XX (CIBC-) CID CO LTD.

XX (LEES/) LEE S H.

XX Lee SH, Lee Y, Yun S;

XX WPI; 2004-340933/31.

PT New Japanese encephalitis virus genomic RNA, useful in developing  
PT vaccines for and in diagnosing and treating Japanese encephalitis.

XX Example 2; Page 145-152; 265pp; English.

XX The present invention relates to a genomic RNA of the Korean Japanese  
CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated  
CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,  
CC JEV cDNA and reagents are useful in developing vaccines for and in  
CC diagnosing and treating Japanese encephalitis. The present sequence is a  
CC sequence of the invention.

XX Sequence 10818 BP; 2991 A; 2491 C; 3075 G; 2261 T; 0 U; 0 Other;

SQ Sequence 93.3%; Score 22.4; DB 12; Length 10818;

Query Match

Best Local Similarity 95.8%; Pred. No. 1.1;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTAC 24

DB 10523 TCCGAGACGGTCTGAGGGCTTTC 10500

RESULT 16

ADO07437/C

ID ADO07437 standard; DNA; 10968 BP.

XX ADO07437;

XX 15-JUL-2004 (first entry)

DE Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 15.

XX antiinflammatory; neuroprotective; gene therapy;  
KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;  
KW Japanese encephalitis.

OS Japanese encephalitis virus.

XX WO2004033690-A1.

XX 22-APR-2004.

XX 09-OCT-2003; 2003WO-KR002081.

XX 09-OCT-2002; 2002KR-00061589.

XX (CIBC-) CID CO LTD.

XX (LEES/) LEE S H.

XX Lee SH, Lee Y, Yun S;

XX WPI; 2004-340933/31.

PT New Japanese encephalitis virus genomic RNA, useful in developing  
PT vaccines for and in diagnosing and treating Japanese encephalitis.

XX Claim 3; Page 154-161; 265pp; English.

XX The present invention relates to a genomic RNA of the Korean Japanese  
CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated  
CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,  
CC JEV cDNA and reagents are useful in developing vaccines for and in  
CC diagnosing and treating Japanese encephalitis. The present sequence is a  
CC sequence of the invention.

SQ Sequence 10968 BP; 3032 A; 2518 C; 3117 G; 2301 T; 0 U; 0 Other;

Query Match 93.3%; Score 22.4; DB 12; Length 10968;

Best Local Similarity 95.8%; Pred. No. 1.1;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTAC 24

DB 10573 TCCGAGACGGTCTGAGGGCTTTC 10550

RESULT 17

ADO07466/C

ID ADO07466 standard; DNA; 18563 BP.

XX ADO07466;

XX 15-JUL-2004 (first entry)

DE Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 44.

XX antiinflammatory; neuroprotective; gene therapy;

KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;  
 KW Japanese encephalitis.  
 XX  
 OS Japanese encephalitis virus.  
 XX  
 XX WO2004033690-A1.  
 XX  
 XX PD 22-APR-2004.  
 XX  
 XX PF 09-OCT-2003; 2003WO-KR002081.  
 XX  
 XX PR 09-OCT-2002; 2002KR-00061589.  
 XX  
 XX PA (CIBC-) CID CO LTD.  
 XX PA (LEES/) LEE S H.  
 XX  
 XX PI Lee SH, Lee Y, Yun S;  
 XX WPI; 2004-340933/31.  
 XX  
 XX PT New Japanese encephalitis virus genomic RNA, useful in developing  
 PT vaccines for and in diagnosing and treating Japanese encephalitis.  
 XX  
 XX Claim 12; Page 193-206; 265pp; English.  
 XX  
 XX CC The present invention relates to a genomic RNA of the Korean Japanese  
 CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated  
 CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,  
 CC JEV cDNA and reagents are useful in developing vaccines for and in  
 CC diagnosing and treating Japanese encephalitis. The present sequence is a  
 CC sequence of the invention.  
 XX  
 XX SQ Sequence 18563 BP; 4943 A; 4211 C; 4929 G; 4480 T; 0 U; 0 Other;  
 Query Match 93.3%; Score 22.4; DB 12; Length 18563;  
 Best Local Similarity 95.8%; Pred. No. 1.2;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX QY 1 TCCGAGACGGTCTCGAGGCTTAC 24  
 DB 10573 TCCGAGACGGTCTCGAGGCTTTC 10550  
 RESULT 18  
 ID ADO07465/C  
 ID ADO07465 standard; DNA; 18563 BP.  
 XX  
 XX AC ADO07465;  
 XX  
 XX DT 15-JUL-2004 (first entry)  
 XX  
 XX DE Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 43.  
 XX  
 XX KW antiinflammatory; neuroprotective; gene therapy;  
 KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;  
 KW Japanese encephalitis.  
 XX  
 XX OS Japanese encephalitis virus.  
 XX  
 XX PN WO2004033690-A1.  
 XX PD 22-APR-2004.  
 XX  
 XX PF 09-OCT-2003; 2003WO-KR002081.  
 XX  
 XX PR 09-OCT-2002; 2002KR-00061589.  
 XX  
 XX PA (CIBC-) CID CO LTD.  
 XX PA (LEES/) LEE S H.  
 XX  
 XX PI Lee SH, Lee Y, Yun S;  
 XX WPI; 2004-340933/31.  
 XX  
 XX PT New Japanese encephalitis virus genomic RNA, useful in developing  
 PT vaccines for and in diagnosing and treating Japanese encephalitis.  
 XX  
 XX Claim 12; Page 193-206; 265pp; English.  
 XX  
 XX CC The present invention relates to a genomic RNA of the Korean Japanese  
 CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated  
 CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,  
 CC JEV cDNA and reagents are useful in developing vaccines for and in  
 CC diagnosing and treating Japanese encephalitis. The present sequence is a  
 CC sequence of the invention.  
 XX  
 XX SQ Sequence 18563 BP; 4943 A; 4211 C; 4929 G; 4480 T; 0 U; 0 Other;  
 Query Match 93.3%; Score 22.4; DB 12; Length 18563;  
 Best Local Similarity 95.8%; Pred. No. 1.2;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX QY 1 TCCGAGACGGTCTCGAGGCTTAC 24  
 DB 10573 TCCGAGACGGTCTCGAGGCTTTC 10550  
 RESULT 19  
 ID ADO07467/C  
 ID ADO07467 standard; DNA; 18565 BP.  
 XX  
 XX AC ADO07467;  
 XX  
 XX DT 15-JUL-2004 (first entry)  
 XX  
 XX DE Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 45.  
 XX  
 XX KW antiinflammatory; neuroprotective; gene therapy;  
 KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;  
 KW Japanese encephalitis.  
 XX  
 XX OS Japanese encephalitis virus.  
 XX  
 XX PN WO2004033690-A1.  
 XX PD 22-APR-2004.  
 XX  
 XX PF 09-OCT-2003; 2003WO-KR002081.  
 XX  
 XX PR 09-OCT-2002; 2002KR-00061589.  
 XX  
 XX PA (CIBC-) CID CO LTD.  
 XX PA (LEES/) LEE S H.  
 XX  
 XX PI Lee SH, Lee Y, Yun S;  
 XX WPI; 2004-340933/31.  
 XX  
 XX PT New Japanese encephalitis virus genomic RNA, useful in developing  
 PT vaccines for and in diagnosing and treating Japanese encephalitis.  
 XX  
 XX Claim 12; Page 206-219; 265pp; English.  
 XX  
 XX CC The present invention relates to a genomic RNA of the Korean Japanese  
 CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated  
 CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,  
 CC JEV cDNA and reagents are useful in developing vaccines for and in  
 CC diagnosing and treating Japanese encephalitis. The present sequence is a  
 CC sequence of the invention.  
 XX  
 XX SQ Sequence 18565 BP; 4944 A; 4211 C; 4929 G; 4481 T; 0 U; 0 Other;  
 Query Match 93.3%; Score 22.4; DB 12; Length 18565;  
 Best Local Similarity 95.8%; Pred. No. 1.2;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX QY 1 TCCGAGACGGTCTCGAGGCTTAC 24  
 DB 10573 TCCGAGACGGTCTCGAGGCTTTC 10550  
 RESULT 19  
 ID ADO07467/C  
 ID ADO07467 standard; DNA; 18565 BP.  
 XX  
 XX AC ADO07467;  
 XX  
 XX DT 15-JUL-2004 (first entry)  
 XX  
 XX DE Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 45.  
 XX  
 XX KW antiinflammatory; neuroprotective; gene therapy;  
 KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;  
 KW Japanese encephalitis.  
 XX  
 XX OS Japanese encephalitis virus.  
 XX  
 XX PN WO2004033690-A1.  
 XX PD 22-APR-2004.  
 XX  
 XX PF 09-OCT-2003; 2003WO-KR002081.  
 XX  
 XX PR 09-OCT-2002; 2002KR-00061589.  
 XX  
 XX PA (CIBC-) CID CO LTD.  
 XX PA (LEES/) LEE S H.  
 XX  
 XX PI Lee SH, Lee Y, Yun S;  
 XX WPI; 2004-340933/31.  
 XX  
 XX PT New Japanese encephalitis virus genomic RNA, useful in developing  
 PT vaccines for and in diagnosing and treating Japanese encephalitis.  
 XX  
 XX Claim 12; Page 206-219; 265pp; English.  
 XX  
 XX CC The present invention relates to a genomic RNA of the Korean Japanese  
 CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated  
 CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,  
 CC JEV cDNA and reagents are useful in developing vaccines for and in  
 CC diagnosing and treating Japanese encephalitis. The present sequence is a  
 CC sequence of the invention.  
 XX  
 XX SQ Sequence 18565 BP; 4944 A; 4211 C; 4929 G; 4481 T; 0 U; 0 Other;  
 Query Match 93.3%; Score 22.4; DB 12; Length 18565;  
 Best Local Similarity 95.8%; Pred. No. 1.2;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX QY 1 TCCGAGACGGTCTCGAGGCTTAC 24  
 DB 10573 TCCGAGACGGTCTCGAGGCTTTC 10550

```

Qy 1 TCCGAGACGGTCTCTGAGGGCTTAC 24
Db 10573 TCCGAGACGGTCTCTGAGGGCTTTC 10550

RESULT 20
ADO07468/c
ID ADO07468 standard; DNA; 19038 BP.
AC ADO07468;
XX
XX 15-JUL-2004 (first entry)
XX Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 46.
DE
XX
XX antiinflammatory; neuroprotective; gene therapy;
KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;
KW Japanese encephalitis.
XX
XX Japanese encephalitis virus.
OS
XX WO2004033690-A1.
XX
XX 22-APR-2004.
XX
XX 09-OCT-2003; 2003WO-KR002081.
XX
XX 09-OCT-2002; 2002KR-00061589.
XX
XX (CIBC-) CID CO LTD.
XX (LEES/) LEE S H.
XX
XX Lee SH, Lee Y, Yun S;
XX WPI; 2004-340933/31.
XX New Japanese encephalitis virus genomic RNA, useful in developing
PT vaccines for and in diagnosing and treating Japanese encephalitis.
XX
XX Claim 12; Page 232-245; 265pp; English.
XX
XX The present invention relates to a genomic RNA of the Korean Japanese
CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
CC JEV cDNA and reagents are useful in developing vaccines for and in
CC diagnosing and treating Japanese encephalitis. The present sequence is a
CC sequence of the invention.
XX
XX Sequence 19038 BP; 5059 A; 4310 C; 5055 G; 4614 T; 0 U; 0 Other;
SQ

Query Match 93.3%; Score 22.4; DB 12; Length 19038;
Best Local Similarity 95.8%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTCTGAGGGCTTAC 24
Db 10573 TCCGAGACGGTCTCTGAGGGCTTTC 10550

RESULT 22
ADO07470/c
ID ADO07470 standard; DNA; 19040 BP.
XX
XX ADO07470;
XX
XX 15-JUL-2004 (first entry)
XX
XX Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 48.
DE
XX
XX antiinflammatory; neuroprotective; gene therapy;
KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;
KW Japanese encephalitis.
XX
XX Japanese encephalitis virus.
OS
XX WO2004033690-A1.
XX
XX 22-APR-2004.
XX
XX 09-OCT-2003; 2003WO-KR002081.
XX
XX 09-OCT-2002; 2002KR-00061589.
XX
XX (CIBC-) CID CO LTD.
XX (LEES/) LEE S H.
XX
XX Lee SH, Lee Y, Yun S;
XX WPI; 2004-340933/31.
XX New Japanese encephalitis virus genomic RNA, useful in developing
PT vaccines for and in diagnosing and treating Japanese encephalitis.
XX
XX Claim 12; Page 219-232; 265pp; English.
XX
XX The present invention relates to a genomic RNA of the Korean Japanese
CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
CC JEV cDNA and reagents are useful in developing vaccines for and in
CC diagnosing and treating Japanese encephalitis. The present sequence is a
CC sequence of the invention.
XX
XX Sequence 19038 BP; 5060 A; 4310 C; 5055 G; 4613 T; 0 U; 0 Other;
SQ

Query Match 93.3%; Score 22.4; DB 12; Length 19038;
Best Local Similarity 95.8%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTCTGAGGGCTTAC 24
Db 10573 TCCGAGACGGTCTCTGAGGGCTTTC 10550

RESULT 21
ADO07469/c
ID ADO07469 standard; DNA; 19038 BP.
XX
XX ADO07469;
XX
XX 15-JUL-2004 (first entry)
XX Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 47.
DE
XX
XX antiinflammatory; neuroprotective; gene therapy;
KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;
KW Japanese encephalitis.
XX
XX

```

```
XX PS Claim 12; Page 245-258; 265pp; English.
XX CC The present invention relates to a genomic RNA of the Korean Japanese
XX CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
XX CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
XX CC JEV cDNA and reagents are useful in developing vaccines for and in
XX CC diagnosing and treating Japanese encephalitis. The present sequence is a
XX CC sequence of the invention.
XX SQ Sequence 19040 BP; 5060 A; 4310 C; 5055 G; 4615 T; 0 U; 0 Other;

Query Match          93.3%; Score 22.4; DB 12; Length 19040;
Best Local Similarity 95.8%; Pred. No. 1-2;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGGCTTAC 24
Db 10573 TCCGAGACGGTTCGAGGGCTTC 10550

RESULT 23
ADN36755
ID ADN36755 standard; DNA; 22 BP.
XX AC ADN36755;
XX DT 15-JUL-2004 (first entry)
XX DE West Nile virus detection-related oligonucleotide probe SeqID77.
XX KW hybridisation assay probe; nucleic acid detection;
XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;
XX KW RNA virus; infection; meningitis; encephalitis;
XX KW high throughput screening; probe; ss.
XX OS West Nile virus.
XX OS WO2004036190-A2.
XX PN 29-APR-2004.
XX PD 10-OCT-2003; 2003WO-US033639.
XX PF 16-OCT-2002; 2002US-0418891P.
XX PR 25-NOV-2002; 2002US-0429006P.
XX PR 24-FEB-2003; 2003US-0449810P.
XX XX (GENP-) GEN-PROBE INC.
XX XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX XX WPI; 2004-389590/36.
XX XX New hybridization assay probe comprising target-complementary sequence of
XX XX bases, useful in detecting flavivirus, e.g. West Nile virus.
XX PS Claim 26; SEQ ID NO 77; 135pp; English.
XX CC This invention relates to a novel hybridisation assay probe, for
XX CC detecting a nucleic acid, which is a probe sequence that comprises a
XX CC target-complementary sequence of bases, and optionally one or more base
XX CC sequences that are not complementary to the nucleic acid that is to be
XX CC detected. The hybridisation assay probes and the kits are useful in
XX CC detecting and amplifying a target nucleic acid sequence, for example
XX CC flavivirus like West Nile virus, that may be present in a biological
XX CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX CC birds and culex mosquitoes, with humans and horses serving as incidental
XX CC hosts. Infection of humans can lead to meningitis or encephalitis. The
XX CC invention may allow for accurate and efficient high throughput screening.
XX CC The present sequence is that of an oligonucleotide probe which is related
XX CC to the invention.
```

```
XX SQ Sequence 22 BP; 3 A; 5 C; 8 G; 6 T; 0 U; 0 Other;

Query Match          91.7%; Score 22; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGGCTT 22
Db 1 TCCGAGACGGTTCGAGGGCTT 22

RESULT 24
ADN36764
ID ADN36764 standard; DNA; 49 BP.
XX AC ADN36764;
XX DT 15-JUL-2004 (first entry)
XX DE West Nile virus detection-related oligonucleotide probe SeqID86.
XX KW hybridisation assay probe; nucleic acid detection;
XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;
XX KW RNA virus; infection; meningitis; encephalitis;
XX KW high throughput screening; probe; ss.
XX OS West Nile virus.
XX OS Enterobacteria phage T7.
XX FH Key Location/Qualifiers
XX FT misc_feature 1..27
XX FT /*tag= a
XX FT /note= "T7 promoter sequence"
XX FT misc_feature 28..49
XX FT /*tag= b
XX FT /note= "WNV-complimentary sequence"
XX XX WO2004036190-A2.
XX XX 29-APR-2004.
XX XX 10-OCT-2003; 2003WO-US033639.
XX XX 16-OCT-2002; 2002US-0418891P.
XX XX 25-NOV-2002; 2002US-0429006P.
XX XX 24-FEB-2003; 2003US-0449810P.
XX XX (GENP-) GEN-PROBE INC.
XX XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX XX WPI; 2004-389590/36.
XX XX New hybridization assay probe comprising target-complementary sequence of
XX XX bases, useful in detecting flavivirus, e.g. West Nile virus.
XX PS Disclosure; SEQ ID NO 86; 135pp; English.
XX CC This invention relates to a novel hybridisation assay probe, for
XX CC detecting a nucleic acid, which is a probe sequence that comprises a
XX CC target-complementary sequence of bases, and optionally one or more base
XX CC sequences that are not complementary to the nucleic acid that is to be
XX CC detected. The hybridisation assay probes and the kits are useful in
XX CC detecting and amplifying a target nucleic acid sequence, for example
XX CC flavivirus like West Nile virus, that may be present in a biological
XX CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX CC birds and culex mosquitoes, with humans and horses serving as incidental
XX CC hosts. Infection of humans can lead to meningitis or encephalitis. The
XX CC invention may allow for accurate and efficient high throughput screening.
XX CC The present sequence is that of an oligonucleotide probe which is related
XX CC to the invention.
XX SQ Sequence 49 BP; 14 A; 9 C; 13 G; 13 T; 0 U; 0 Other;
```







CC detecting and amplifying a target nucleic acid sequence, for example  
CC flavivirus like West Nile virus, that may be present in a biological  
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
CC birds and culex mosquitoes, with humans and horses serving as incidental  
CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
CC invention may allow for accurate and efficient high throughput screening.  
CC The present sequence is that of an oligonucleotide probe which is related  
CC to the invention.

XX SQ Sequence 87 BP; 23 A; 25 C; 26 G; 13 T; 0 U; 0 Other;

Query Match: 79.2%; Score 19; DB 12; Length 87;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACGGTCTCGAGGGCTTAC 24

|||||  
DB 87 GACGGTCTCGAGGGCTTAC 69

RESULT 29

ADD31012/c

ID ADD31012 standard; cDNA; 1661 BP.

XX AC ADD31012;

XX DT 15-JAN-2004 (first entry)

XX DE Plant yield-related polynucleotide clone G631.

XX db; transcription factor; transgenic plant; growth rate; senescence;

XX KW seed germination rate; plant vigor; seedling vigor.

XX OS Arabidopsis thaliana.

XX PN WO2003013227-A2.

XX PD 20-FEB-2003.

XX PF 09-AUG-2002; 2002WO-US025805.

XX PR 09-AUG-2001; 2001US-0310847P.

XX PR 19-NOV-2001; 2001US-0336049P.

XX PR 11-DEC-2001; 2001US-0338692P.

XX PR 14-JUN-2002; 2002US-00171468.

XX PA (MEND-) MENDEL BIOTECHNOLOGY INC.

XX PI Ratcliffe O, Riechmann JL, Adam LJ, Dubell AT, Heard JE;

XX PI Pilgrim ML, Jiang C, Reuber TL, Creelman RA, Pineda O, Yu G;

XX PI Broun PE;

XX DR WPI; 2003-248221/24.

XX DR P-PSDB; ADD31013.

XX PT New plant transcription factor polynucleotides and polypeptides, useful

XX PT in producing transgenic plants with commercially valuable properties,

XX PT such as an alteration in a plant growth characteristic, e.g. growth rate

XX PT or apomixis.

XX PS Disclosure; SEQ ID NO 1041; 454pp; English.

XX CC The invention relates to a number of isolated Arabidopsis thaliana cDNA

XX CC sequences and their encoded proteins which are especially transcription

XX CC factor related cDNAs and proteins. The isolated or recombinant plant

XX CC transcription factor polynucleotides and polypeptides are useful in

XX CC producing transgenic plants with commercially valuable properties, i.e.

XX CC modified or altered desirable traits as compared to a reference plant,

XX CC such as an alteration in a plant growth characteristic, e.g. growth rate,

XX CC germination rate of seeds, vigor of plants and seedlings, or leaf and

XX CC flower senescence. Sequence information related to the polynucleotides

XX CC and polypeptides can also be used in bioinformatic search methods. The

XX CC transgenic plant is useful for growing a progeny plant from a parent

CC plant. This sequence represents one of the cDNAs of the invention.

XX SQ Sequence 1661 BP; 474 A; 379 C; 344 G; 464 T; 0 U; 0 Other;

Query Match: 73.3%; Score 17.6; DB 10; Length 1661;

Best Local Similarity 83.3%; Pred. No. 1.8e+02;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGGCTTAC 24

|||||  
DB 610 TCCAGTCGGTCTCGATGGCTCAC 587

RESULT 30

ADI43924/c

ID ADI43924 standard; DNA; 1661 BP.

XX AC ADI43924;

XX DT 22-APR-2004 (first entry)

XX DE Plant transcription factor related polynucleotide #1551.

XX KW transgenic; plant; enhanced tolerance to abiotic stress;

XX KW glycosphate tolerance; hormone sensitivity; disease resistance;

XX KW sugar sensing; flowering; flower structure; stem bifurcation;

XX KW branching pattern; apical dominance; trichome; stem morphology;

XX KW root growth; root hair; seed development; cell proliferation;

XX KW cell differentiation; premature senescence; necrosis; plant size;

XX KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;

XX KW plant anthocyanin; light response; shade avoidance; bioinformatic;

XX KW transcription factor; ds.

XX OS Unidentified.

XX PN US2004019927-A1.

XX PD 29-JAN-2004.

XX PF 25-FEB-2003; 2003US-00374780.

XX PR 18-APR-2001; 2001US-00837944.

XX PA (SHER/) SHERMAN B K.

XX PA (RIEC/) RIECHMANN J L.

XX PA (JIAN/) JIANG C.

XX PA (HEAR/) HEARD J E.

XX PA (HAAR/) HAAKE V.

XX PA (CREE/) CREELMAN R A.

XX PA (RATC/) RATCLIFFE O.

XX PA (ADAM/) ADAM L J.

XX PA (REUB/) REUBER T L.

XX PA (KEDD/) KEDDIE J.

XX PA (BROU/) BROUN P E.

XX PA (PILG/) PILGRIM M L.

XX PA (DUBE/) DUBELL A N.

XX PA (PINE/) PINEDA O.

XX PA (YUGG/) YU G.

XX PI Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V;

XX PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE;

XX PI Pilgrim ML, Dubell AN, Pineda O, Yu G;

XX DR WPI; 2004-132245/13.

XX DR P-PSDB; ADI43925.

XX PT New transgenic plant comprising a recombinant polynucleotide of any one

XX PT of more than 500 nucleotide sequences, useful in bioinformatic search

XX PT methods.

XX PS Disclosure; SEQ ID NO 2387; 435pp; English.

XX CC The invention describes a transgenic plant comprising a recombinant

CC polynucleotide of any one of more than 500 nucleotide sequences fully  
 CC defined in the specification or its complement. The method of the  
 CC invention can be used to produce a plant having altered traits such as:  
 CC enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone  
 CC sensitivity; disease resistance; sugar sensing; early or late flowering;  
 CC altered flower structure, change in stem bifurcations, altered branching  
 CC pattern, reduced apical dominance, reduced trichome density; lack of  
 CC trichomes; reduced ectopic trichome development; altered trichome  
 CC development; increase in trichome number; altered stem morphology;  
 CC increased root growth; increased root hairs; altered seed development;  
 CC altered cell proliferation or cell differentiation; rapid development;  
 CC premature senescence; increased necrosis; increase in seedling or plant  
 CC size; decreased plant size; leaf morphology; seed morphology; seed  
 CC biochemistry; increase in root anthocyanins; increase in plant  
 CC anthocyanins, or alteration in light response or shade avoidance. The  
 CC transgenic plant, polynucleotides and polypeptides are useful in  
 CC bioinformatic search methods. This sequence represents a plant  
 CC transcription factor related polynucleotide.  
 XX  
 SQ Sequence 1661 BP; 474 A; 379 C; 344 G; 464 T; 0 U; 0 Other;  
 Query Match 73.3%; Score 17.6; DB 12; Length 1661;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 TCCGAGACGGTCTGAGGGCTTAC 24  
 Db 610 TCCAAATCGGTCTGATGGCTCAC 587  
 RESULT 31  
 ADI61330/c  
 ID ADI61330 standard; cDNA; 1661 BP.  
 XX  
 AC ADI61330;  
 XX  
 XX  
 DT 22-APR-2004 (first entry)  
 DE  
 DE cDNA encoding A. thaliana novel transcription factor (TF) #15.  
 XX  
 XX Plant; transcription factor; TF; plant trait; gene; ss.  
 KW  
 XX Arabidopsis thaliana.  
 XX  
 XX US2003229915-A1.  
 XX  
 PD 11-DEC-2003.  
 XX  
 PF 22-NOV-2002; 2002US-00302267.  
 XX  
 PR 18-FEB-1999; 99US-0120880P.  
 PR 22-FEB-1999; 99US-0121037P.  
 PR 11-MAR-1999; 99US-0124278P.  
 PR 15-APR-1999; 99US-0129450P.  
 PR 20-MAY-1999; 99US-0135134P.  
 PR 15-JUL-1999; 99US-0144153P.  
 PR 22-OCT-1999; 99US-0161143P.  
 PR 01-NOV-1999; 99US-0162556P.  
 PR 17-FEB-2000; 2000US-00506720.  
 XX  
 PA (KEDD/) KEDDIE J.  
 PA (FROM/) FROMM M.  
 PA (HEAR/) HEARD J.  
 PA (RIEC/) RIECHMANN J L.  
 PA (ADAM/) ADAM L.  
 PA (BROU/) BROUN P.  
 PA (PINE/) PINEDA O.  
 PA (REUB/) REUBER L.  
 PA (ZHAN/) ZHANG J.  
 PA (YUGG/) YU G.  
 PA (JIAN/) JIANG C.  
 PA (SAMA/) SAMAHA R.  
 PA (PILG/) PILGRIM M.

PA (CREE/) CREELMAN R.  
 XX  
 PI Keddle J, Fromm M, Heard J, Riechmann JL, Adam L, Broun P;  
 PI Pineda O, Reuber L, Zhang J, Yu G, Jiang C, Samaha R, Pilgrim M;  
 PI Creelman R;  
 XX  
 DR WPI: 2004-052052/05.  
 DR P-PSDB; ADI61331.  
 XX  
 PT New polynucleotide, useful in screening for a transcription factor that  
 PT modifies a plant trait.  
 PT  
 PS Claim 1; SEQ ID NO 29; 16pp; English.  
 XX  
 CC The present invention relates to the isolation of novel plant  
 CC (arabidopsis thaliana) polynucleotide sequences that encode transcription  
 CC factors (TFs), and the polypeptide sequences for the TFs. The  
 CC polynucleotide sequences are useful in screening for a transcription  
 CC factor that modifies a plant trait. Also disclosed is an expression  
 CC vector comprising a TF polynucleotide sequence, a host cell comprising  
 CC the expression vector, a transgenic plant comprising or ectopically  
 CC expressing an isolated TF polynucleotide sequence, a method for screening  
 CC for a molecule that modifies a plant trait, a method for producing a  
 CC transgenic plant, a method for identifying a sequence homologous to a TF  
 CC polynucleotide or polypeptide sequence, and a method for screening for a  
 CC transcription factor that modifies a plant trait. The present sequence  
 CC encodes a novel A. thaliana TF of the invention. Note: The sequence data  
 CC for this patent did not form part of the printed specification. The  
 CC complete sequence data for this patent was obtained in electronic format  
 CC directly from the USPTO web site at seqdata.uspto.gov.  
 XX  
 SQ Sequence 1661 BP; 474 A; 379 C; 344 G; 464 T; 0 U; 0 Other;  
 Query Match 73.3%; Score 17.6; DB 12; Length 1661;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 TCCGAGACGGTCTGAGGGCTTAC 24  
 Db 610 TCCAAATCGGTCTGATGGCTCAC 587  
 RESULT 32  
 ADO01998/c  
 ID ADO01998 standard; cDNA; 1661 BP.  
 XX  
 AC ADO01998;  
 XX  
 DT 01-JUL-2004 (first entry)  
 DE  
 DE Thalecress transcription factor cDNA #206.  
 XX  
 KW Thalecress; transcription factor; ss; gene; plant; transgenic;  
 KW abiotic stress; cold tolerance; heat tolerance; drought; osmotic stress;  
 KW phosphate limitation; potassium limitation; nitrogen limitation;  
 KW hormone sensitivity; disease resistance; sugar sensing; seed germination;  
 KW flowering; inflorescence architectural change;  
 KW meristem cell differentiation; phyllotaxy; apical dominance;  
 KW trichome development; seed development; premature senescence;  
 KW delayed senescence; lethality; necrosis; plant size; leaf morphology;  
 KW seed morphology; secondary metabolism; light response; shade avoidance.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 XX US2004045049-A1.  
 XX  
 PD 04-MAR-2004.  
 XX  
 PF 10-APR-2003; 2003US-00412699.  
 XX  
 PR 13-SEP-1999; 99US-00394519.  
 PR 21-JAN-2000; 2000US-00489376.  
 PR 17-FEB-2000; 2000US-00506720.

PR 22-MAR-2000; 2000US-00532591.  
 PR 22-MAR-2000; 2000US-00533029.  
 PR 22-MAR-2000; 2000US-00533030.  
 PR 22-MAR-2000; 2000US-00533392.  
 PR 22-MAR-2000; 2000US-00533648.  
 PR 06-APR-2000; 2000WO-US009448.  
 PR 16-NOV-2000; 2000US-00713394.  
 PR 27-MAR-2001; 2001US-00819142.  
 PR 17-APR-2001; 2001US-00837444.  
 PR 30-JAN-2002; 2002US-00958131.  
 PR 14-JUN-2002; 2002US-00171468.  
 PR 09-AUG-2002; 2002US-00225066.  
 PR 09-AUG-2002; 2002US-00225067.  
 PR 09-AUG-2002; 2002US-00225068.  
 PR 17-DEC-2002; 2002US-0434166P.  
 PR 25-FEB-2003; 2003US-00374780.  
 XX  
 PA (ZHAN/) ZHANG J.  
 PA (FROM/) FROMM M E.  
 PA (HEAR/) HEARD J E.  
 PA (RIEC/) RIECHMANN J L.  
 PA (ADAM/) ADAM L J.  
 PA (BROU/) BROUN P E.  
 PA (PINE/) PINEDA O.  
 PA (REUB/) REUBER T L.  
 PA (KEDD/) KEDDIE J S.  
 PA (YUGG/) YU G.  
 PA (JIAN/) JIANG C.  
 PA (SAMA/) SAMAHA R S.  
 PA (FILG/) FILGRIM M L.  
 PA (CREE/) CREELMAN R A.  
 PA (DUBE/) DUBELL A N.  
 PA (RATC/) RATCLIFFE O.  
 PA (KIMI/) KUMIMOTO R.  
 PA (SHER/) SHERMAN B K.  
 XX  
 PI Zhang J, Fromm ME, Heard JE, Riechmann JL, Adam LJ, Broun PE,  
 PI Pineda O, Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS,  
 PI Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R,  
 PI Sherman BK;  
 XX  
 DR WPI; 2004-225755/21.  
 DR P-PSDB; ADO01999.  
 XX  
 PT New transgenic plant, useful in developing phenotypes with altered or  
 PT improved characteristics or traits.  
 XX  
 PS Claim 1; SEQ ID NO 411; 213pp; English.  
 XX  
 CC The invention relates to a transgenic plant comprises a recombinant  
 CC polynucleotide having a polynucleotide sequence or its complementary  
 CC sequence comprising a sequence encoding a polypeptide, that initiates  
 CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,  
 CC Rice, Rape or Corn, comprising any of the sequences appearing as ADO01588  
 CC -ADO03527 or ADO03530-ADO03559. Also included are using a transgenic  
 CC plant to grow a progeny plant, an expression cassette (comprising a  
 CC constitutive, inducible or tissue-specific promoter and a recombinant  
 CC polynucleotide described above), a host cell comprising the expression  
 CC cassette, producing a modified plant having a modified trait, identifying  
 CC a factor that is modulated by or interacts with a polypeptide encoded by  
 CC the polynucleotide sequence and identifying at least one downstream  
 CC polynucleotide sequence that is subject to a regulatory effect of any of  
 CC the polypeptides encoded by the polynucleotide described above. The  
 CC transgenic plant is useful for producing a plant that has an altered  
 CC trait e.g. an enhanced tolerance to abiotic stress (increased tolerance  
 CC to chilling, germination in cold conditions, freezing tolerance, tolerance  
 CC to heat, tolerance to drought, tolerance to osmotic stress, tolerance to  
 CC salt, tolerance to phosphate limitation, tolerance to potassium  
 CC limitation, decreased sensitivity to nitrogen limitation), altered  
 CC hormone sensitivity, reduced sensitivity to abscisic acid, an altered  
 CC response to ethylene, disease resistance, altered susceptibility to  
 CC Botrytis, altered susceptibility to Fusarium, altered susceptibility to  
 CC Erysiphe, altered susceptibility to Pseudomonas syringae, altered

CC susceptibility to Sclerotinia, altered sugar sensing, improved seed  
 CC germination and seedling vigor, early flowering, late flowering, extended  
 CC period of flowering, an inflorescence architectural change, a change in  
 CC stem bifurcations, a lack of a shoot meristem, reduced meristem cell  
 CC differentiation, altered phyllotaxy, altered branching pattern, reduced  
 CC apical dominance, reduced trichome density, ectopic trichome development,  
 CC altered trichome development, altered stem morphology, increased root  
 CC growth, increased root hairs, altered seed development, delayed cell  
 CC proliferation/cell differentiation, premature senescence, increased  
 CC senescence, lethality, increased necrosis, an increase in seedling or  
 CC plant size, decreased plant size, a change in leaf morphology, increased  
 CC altered leaf development, increased leaf size and mass, glossy leaves,  
 CC leaf cell expansion, change in seed morphology, altered seed coloration,  
 CC increased seed size, decreased seed size, altered seed shape, change in  
 CC leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid  
 CC content, increased leaf insoluble sugars, decreased leaf insoluble  
 CC sugars, increased leaf anthocyanins, an alteration of leaf fatty acid  
 CC content, an alteration of leaf glucosinolate content, change in seed  
 CC biochemistry, an increase in seed oil content, decrease in seed oil  
 CC content, increase in seed fatty acid content, decrease in seed fatty acid  
 CC content, increase in seed protein content, decrease in seed protein  
 CC content, alteration in seed prenyl lipid content, increase in seed  
 CC sterols, upregulation of genes involved in secondary metabolism, increase  
 CC in root anthocyanins, increase in plant anthocyanins, and alteration in  
 CC light response or shade avoidance. The present sequence encodes a  
 CC thalaeal transcription factor of the invention.  
 XX  
 SQ Sequence 1661 BP; 474 A; 379 C; 344 G; 464 T; 0 U; 0 Other;

Query Match 73.3%; Score 17.6; DB 12; Length 1661;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGCTTAC 24  
 |||||  
 Db 610 TCCAGTCGGTCTCTGATGGCTCAC 587

RESULT 33  
 AAC36549/C

ID AAC36549 standard; DNA; 1823 BP.

XX AAC36549;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 14214.

KW Hybridisation assay; genetic mapping; gene expression control;  
 KW protein identification; signal transduction pathway; metabolic pathway;  
 KW promoter; termination sequence; ss.

OS Arabidopsis thaliana.

XX EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 03-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 23-MAR-1999; 99US-0126264P.

PR 01-APR-1999; 99US-0126785P.

PR 06-APR-1999; 99US-0127462P.

PR 08-APR-1999; 99US-0128234P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.

PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-01322407P.  
PR 04-MAY-1999; 99US-01322485P.  
PR 05-MAY-1999; 99US-01322486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-01334256P.  
PR 14-MAY-1999; 99US-01334218P.  
PR 14-MAY-1999; 99US-01334219P.  
PR 14-MAY-1999; 99US-0134321P.  
PR 18-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-01343768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
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PR 18-JUN-1999; 99US-0139454P.  
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PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142820P.  
PR 12-JUL-1999; 99US-0142977P.  
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PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-01444632P.

PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
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PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 06-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
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PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
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PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
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PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
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PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
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PR 14-OCT-1999; 99US-0159638P.  
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 PR 21-OCT-1999; 99US-0160741P.  
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 PR 21-OCT-1999; 99US-0160814P.  
 PR 21-OCT-1999; 99US-0160815P.  
 PR 22-OCT-1999; 99US-0160980P.  
 PR 22-OCT-1999; 99US-0160981P.  
 PR 22-OCT-1999; 99US-0160989P.  
 PR 25-OCT-1999; 99US-0161404P.  
 PR 25-OCT-1999; 99US-0161405P.  
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 PR 26-OCT-1999; 99US-0161360P.  
 PR 26-OCT-1999; 99US-0161361P.  
 PR 28-OCT-1999; 99US-0161320P.  
 PR 28-OCT-1999; 99US-0161992P.  
 PR 28-OCT-1999; 99US-0161993P.  
 PR 29-OCT-1999; 99US-0162142P.

Query Match 73.3%; Score 17.6; DB 3; Length 1823;

Best Local Similarity 83.3%; Pred. No. 1.8e+02;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGGCTTAC 24

Db 673 TCCAGTCGGTTCGAGGGCTTAC 650

RESULT 34

AAC35016/c  
 ID AAC35016 standard; DNA; 1823 BP.

XX AAC35016;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 8703.

XX KW Hybridisation assay; genetic mapping; gene expression control;  
 KW protein identification; signal transduction pathway; metabolic pathway;  
 KW promoter; termination sequence; ss.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 23-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.

PR 23-APR-1999; 99US-0130891P.

PR 28-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.

PR 04-MAY-1999; 99US-0132484P.

PR 05-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.

PR 06-MAY-1999; 99US-0132487P.  
 PR 07-MAY-1999; 99US-0132863P.  
 PR 11-MAY-1999; 99US-0134256P.  
 PR 14-MAY-1999; 99US-0134218P.  
 PR 14-MAY-1999; 99US-0134219P.  
 PR 14-MAY-1999; 99US-0134221P.  
 PR 14-MAY-1999; 99US-0134370P.  
 PR 18-MAY-1999; 99US-0134768P.  
 PR 19-MAY-1999; 99US-0134941P.  
 PR 20-MAY-1999; 99US-0135124P.  
 PR 21-MAY-1999; 99US-0135353P.  
 PR 24-MAY-1999; 99US-0135629P.  
 PR 25-MAY-1999; 99US-0136021P.  
 PR 27-MAY-1999; 99US-0136392P.  
 PR 28-MAY-1999; 99US-0136782P.  
 PR 01-JUN-1999; 99US-0137222P.  
 PR 03-JUN-1999; 99US-0137528P.  
 PR 04-JUN-1999; 99US-0137502P.  
 PR 07-JUN-1999; 99US-0137724P.  
 PR 08-JUN-1999; 99US-0138094P.  
 PR 10-JUN-1999; 99US-0138540P.  
 PR 10-JUN-1999; 99US-0138847P.  
 PR 14-JUN-1999; 99US-0139119P.  
 PR 16-JUN-1999; 99US-0139452P.  
 PR 16-JUN-1999; 99US-0139453P.  
 PR 17-JUN-1999; 99US-0139492P.  
 PR 18-JUN-1999; 99US-0139454P.  
 PR 18-JUN-1999; 99US-0139455P.  
 PR 18-JUN-1999; 99US-0139456P.  
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 PR 18-JUN-1999; 99US-0139458P.  
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 PR 18-JUN-1999; 99US-0139460P.  
 PR 18-JUN-1999; 99US-0139461P.  
 PR 18-JUN-1999; 99US-0139462P.  
 PR 18-JUN-1999; 99US-0139463P.  
 PR 18-JUN-1999; 99US-0139750P.  
 PR 21-JUN-1999; 99US-0139817P.  
 PR 22-JUN-1999; 99US-0139899P.  
 PR 23-JUN-1999; 99US-0140353P.  
 PR 23-JUN-1999; 99US-0140354P.  
 PR 24-JUN-1999; 99US-0140695P.  
 PR 28-JUN-1999; 99US-0140823P.  
 PR 29-JUN-1999; 99US-0140991P.  
 PR 30-JUN-1999; 99US-0141287P.  
 PR 01-JUL-1999; 99US-0141842P.  
 PR 01-JUL-1999; 99US-0142154P.  
 PR 02-JUL-1999; 99US-0142055P.  
 PR 06-JUL-1999; 99US-0142390P.  
 PR 08-JUL-1999; 99US-0142803P.  
 PR 09-JUL-1999; 99US-0142920P.  
 PR 12-JUL-1999; 99US-0142977P.  
 PR 13-JUL-1999; 99US-0143542P.  
 PR 14-JUL-1999; 99US-0143624P.  
 PR 15-JUL-1999; 99US-0144005P.  
 PR 16-JUL-1999; 99US-0144085P.  
 PR 16-JUL-1999; 99US-0144086P.  
 PR 19-JUL-1999; 99US-0144325P.  
 PR 19-JUL-1999; 99US-0144331P.  
 PR 19-JUL-1999; 99US-0144332P.  
 PR 19-JUL-1999; 99US-0144333P.  
 PR 19-JUL-1999; 99US-0144334P.  
 PR 19-JUL-1999; 99US-0144335P.  
 PR 20-JUL-1999; 99US-0144352P.  
 PR 20-JUL-1999; 99US-0144632P.  
 PR 20-JUL-1999; 99US-0144884P.  
 PR 21-JUL-1999; 99US-0144814P.  
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 PR 22-JUL-1999; 99US-0145085P.  
 PR 22-JUL-1999; 99US-0145087P.  
 PR 22-JUL-1999; 99US-0145089P.

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|----|--------------|----------------|
| PR | 21-OCT-1999; | 99US-0160815P. |
| PR | 22-OCT-1999; | 99US-0160980P. |
| PR | 22-OCT-1999; | 99US-0160981P. |
| PR | 22-OCT-1999; | 99US-0160989P. |
| PR | 25-OCT-1999; | 99US-0161404P. |
| PR | 25-OCT-1999; | 99US-0161405P. |
| PR | 25-OCT-1999; | 99US-0161406P. |
| PR | 26-OCT-1999; | 99US-0161359P. |
| PR | 26-OCT-1999; | 99US-0161360P. |
| PR | 26-OCT-1999; | 99US-0161361P. |
| PR | 28-OCT-1999; | 99US-0161920P. |
| PR | 28-OCT-1999; | 99US-0161992P. |
| PR | 28-OCT-1999; | 99US-0161993P. |
| PR | 29-OCT-1999; | 99US-0162142P. |

|                       |        |              |
|-----------------------|--------|--------------|
| Query Match           | 73.3%; | Score 17     |
| Best Local Similarity | 83.3%; | Pred. Nucleo |
| Matches               | 20;    | Conservative |
|                       | 0;     | Mismat       |

|    |     |                           |     |
|----|-----|---------------------------|-----|
| Qy | 1   | TCCGAGACGGTCTTCGAGGGCTTAC | 24  |
| Db | 673 | TCCAGTCCGGTTCGATGGCTCAC   | 650 |

|   |
|---|
| RESULT 35                                 |
| ACN03369/c                                |
| ID ACN03369 standard; RNA; 17 BP.         |
| XX AC ACN03369;                           |
| XX AC ACN03369;                           |
| DT 22-APR-2004 (first entry)              |
| XX WNV Inozyme substrate SEQ ID NO 3372.  |
| DE WNV; West Nile Virus; antiinflammatory |
| XX virucide; neuroprotective; antibacter  |
| KW encephalitis; myocarditis; meningitis  |
| KW liver failure; cancer; cirrhosis; Ham  |
| KW Amberzyme; zincyme; ss.                |
| XX OS West Nile Virus.                    |
| XX WO200268637-A2.                        |
| PN 06-SEP-2002.                           |
| PD 19-OCT-2001; 2001WO-US048350.          |
| XX 20-OCT-2000; 2000US-0242411P.          |
| PR (RIBO-) RIBOZYME PHARM INC.            |
| PA (BLAT/) BLATT L.                       |
| PA (MCSW/) MCSWIGGEN J A.                 |
| XX Blatt L, Mcswiggen JA;                 |
| XX WPI; 2002-706994/76.                   |
| XX New nucleic acid molecule that modula  |
| PT (WNV), useful for treating a conditio  |
| PT pancreatitis, meningitis, hepatocellu  |
| XX Claim 23; SEQ ID NO 3372; 495pp; Engl  |
| XX The invention relates to nucleic acid  |
| CC of the West Nile Virus (WNV). The nuc  |
| CC treating a condition related to WNV i  |
| CC encephalitis, myocarditis, meningitis  |
| CC liver failure, hepatocellular carcino  |
| CC molecule is selected from the group o  |
| CC Hammerhead, Inozyme, G-cleaver, DNaz   |
| CC nucleic acid molecules further compr   |
| CC least ten 2'-O-methyl modifications.   |

**Qy**            1   TCCGAGACGGTTCTGAGGGCTTAC   24  
               |||||  
**Dβ**            673   TCCAAGTCGGTCTTGATGGCTCAC   650

ACN03369/c

XX  
22-APR-70

XX

OS West Nile Virus.

XX  
FN  
002000003 / -A2.

PF 19-OCT-2001; 2001WO-US048350.

(RTBO-) RTBOZYME PHARM INC

XX

DK WET; 2002-106994/10:  
XX

XX

the invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. encephalitis, hepatitis, myocarditis, meningitis, neurologic infection, hepatitis, and the like. In one embodiment, the nucleic acid molecules are selected from the category of antisense molecules, nucleic acid analogs, and nucleic acid derivatives. In another embodiment, the nucleic acid molecules comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at

CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX  
 SQ Sequence 17 BP; 4 A; 6 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 70.8%; Score 17; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGAGACGGTTCTGAG 17  
 DB 17 TCCGAGACGGTTCTGAG 1

RESULT 36

ACN05431/c  
 ID ACN05431 standard; RNA; 17 BP.

AC ACN05431;

DT 22-APR-2004 (first entry)

XX WNV DNzyme substrate SEQ ID NO 5434.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNzyme;  
 KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

PI Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 5434; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

XX Sequence 17 BP; 3 A; 8 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 70.8%; Score 17; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGAGACGGTTCTGAGG 19  
 DB 17 CGAGACGGTTCTGAGG 1

RESULT 37

ACN07305/c

ID ACN07305 standard; RNA; 17 BP.

XX AC ACN07305;

XX 22-APR-2004 (first entry)

XX WNV Amberzyme substrate SEQ ID NO 7308.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNzyme;  
 KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

PI Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 7308; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

XX Sequence 17 BP; 4 A; 7 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 70.8%; Score 17; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGACGGTTCTGAGGCT 21  
 ||||||||||||||||





KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyme; ss.  
 XX West Nile Virus.  
 OS  
 XX WO200268637-A2.  
 PN  
 XX 06-SEP-2002.  
 PD  
 XX 19-OCT-2001; 2001WO-US048350.  
 PP  
 XX 20-OCT-2000; 2000US-0242411P.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX  
 PI Blatt L, Mcswiggen JA;  
 DR WPI; 2002-706994/76.  
 XX  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX  
 PS Claim 23; SEQ ID NO 3371; 495pp; English.  
 XX  
 CC The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX  
 SQ Sequence 17 BP; 5 A; 7 C; 3 G; 0 T; 2 U; 0 Other;  
 Query Match 70.8%; Score 17; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GACGGTCTCGAGGCTT 22  
 Db 17 GACGGTCTCGAGGCTT 1  
 RESULT 41  
 ID ACN12333 standard; RNA; 17 BP.  
 XX  
 AC ACN12333;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE WNV minus strand Zinzyme substrate SEQ ID NO 12336.  
 XX  
 KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyme; ss.  
 XX  
 OS West Nile Virus.  
 XX

PN WO200268637-A2.  
 XX  
 PD 06-SEP-2002.  
 XX  
 PP 19-OCT-2001; 2001WO-US048350.  
 XX  
 PR 20-OCT-2000; 2000US-0242411P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX  
 PI Blatt L, Mcswiggen JA;  
 DR WPI; 2002-706994/76.  
 XX  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX  
 PS Claim 23; SEQ ID NO 12336; 495pp; English.  
 XX  
 CC The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX  
 SQ Sequence 17 BP; 3 A; 4 C; 7 G; 0 T; 3 U; 0 Other;  
 Query Match 70.8%; Score 17; DB 6; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 1.9e+02;  
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 CCGAGACGGTCTGAGG 18  
 Db 1 CCGAGACGGTCTGAGG 17  
 RESULT 42  
 ID ACN09607 standard; RNA; 17 BP.  
 XX  
 AC ACN09607;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE WNV minus strand Inozyme substrate SEQ ID NO 9610.  
 XX  
 KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyme; ss.  
 XX  
 OS West Nile Virus.  
 XX  
 PN WO200268637-A2.  
 XX  
 PD 06-SEP-2002.  
 XX  
 PP 19-OCT-2001; 2001WO-US048350.  
 XX  
 PR 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX Blatt L, Mcswiggen JA;  
 PI  
 XX WPI; 2002-706994/76.  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX Claim 23; SEQ ID NO 9610; 495pp; English.  
 XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX Sequence 17 BP; 2 A; 3 C; 7 G; 0 T; 5 U; 0 Other;  
 SQ Query Match 70.8%; Score 17; DB 6; Length 17;  
 Best Local Similarity 70.6%; Pred. No. 1.9e+02;  
 Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GACGGTTCGAGGGCTT 22  
 Db 1 GACGGUUCGAGGGCUU 17  
 RESULT 43  
 ACN03367/c  
 ID ACN03367 standard; RNA; 17 BP.  
 XX ACN03367;  
 XX 22-APR-2004 (first entry)  
 XX WNV Inozyme substrate SEQ ID NO 3370.  
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX West Nile Virus.  
 OS WO200268637-A2.  
 XX 06-SEP-2002.  
 XX 19-OCT-2001; 2001WO-US048350.  
 XX 20-OCT-2000; 2000US-0242411P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX Blatt L, Mcswiggen JA;  
 PI  
 XX WPI; 2002-706994/76.  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX Claim 23; SEQ ID NO 9610; 495pp; English.

DR WPI; 2002-706994/76.  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX Claim 23; SEQ ID NO 3370; 495pp; English.  
 XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX Sequence 17 BP; 5 A; 6 C; 4 G; 0 T; 2 U; 0 Other;  
 SQ Query Match 70.8%; Score 17; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 CGGTTCTGAGGGCTTAC 24  
 Db 17 CGGTTCTGAGGGCTTAC 1  
 RESULT 44  
 ACN07446  
 ID ACN07446 standard; RNA; 17 BP.  
 XX ACN07446;  
 XX 22-APR-2004 (first entry)  
 XX WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7449.  
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX West Nile Virus.  
 OS WO200268637-A2.  
 XX 06-SEP-2002.  
 XX 19-OCT-2001; 2001WO-US048350.  
 XX 20-OCT-2000; 2000US-0242411P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX Blatt L, Mcswiggen JA;  
 PI  
 XX WPI; 2002-706994/76.  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX Claim 23; SEQ ID NO 7449; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

XX Sequence 17 BP; 3 A; 3 C; 8 G; 0 T; 3 U; 0 Other;  
 SQ Query Match 70.8%; Score 17; DB 6; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 1.9e+02;  
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTCTGAGGGC 20  
 |||||:|:|:|:|:  
 Db 1 GAGACGGUUCUGAGGGC 17

RESULT 45  
 ACN07447  
 ID ACN07447 standard; RNA; 17 BP.  
 XX ACN07447;  
 AC ACN07447;  
 DT 22-APR-2004 (first entry)  
 XX WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7450.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.  
 OS  
 XX WO200268637-A2.  
 PN  
 XX 06-SEP-2002.  
 PD  
 XX 19-OCT-2001; 2001WO-US048350.  
 PF  
 XX 20-OCT-2000; 2000US-0242411P.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX Blatt L, Mcswiggen JA;  
 PI  
 XX WPI; 2002-706994/76.  
 DR  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 CC (WNV), useful for treating a condition related to WNV infection e.g.  
 CC pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 7450; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of

CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

XX Sequence 17 BP; 3 A; 3 C; 7 G; 0 T; 4 U; 0 Other;  
 SQ Query Match 70.8%; Score 17; DB 6; Length 17;  
 Best Local Similarity 76.5%; Pred. No. 1.9e+02;  
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGACGGTCTGAGGGCT 21  
 |||||:|:|:|:|:  
 Db 1 AGACGGUUCUGAGGGCU 17

RESULT 46  
 ACN01377/C  
 ID ACN01377 standard; RNA; 17 BP.  
 XX ACN01377;  
 AC ACN01377;  
 DT 22-APR-2004 (first entry)  
 XX WNV Hammerhead Ribozyme substrate SEQ ID NO 1367.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.  
 OS  
 XX WO200268637-A2.  
 PN  
 XX 06-SEP-2002.  
 PD  
 XX 19-OCT-2001; 2001WO-US048350.  
 PF  
 XX 20-OCT-2000; 2000US-0242411P.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX Blatt L, Mcswiggen JA;  
 PI  
 XX WPI; 2002-706994/76.  
 DR  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 CC (WNV), useful for treating a condition related to WNV infection e.g.  
 CC pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 1367; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

CC molecule of the invention  
XX Sequence 17 BP; 5 A; 6 C; 3 G; 0 T; 3 U; 0 Other;  
SQ Query Match 70.8%; Score 17; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACGGTTCTGAGGGCTTA 23  
DB 17 ACGGTTCTGAGGGCTTA 1

RESULT 47  
ACH18165/c  
ID ACH18165 standard; cDNA; 487 BP.  
XX AC ACH18165;  
XX DT 13-OCT-2003 (first entry)  
XX XX Human adult heart cDNA #2479.  
XX DE Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
XX KW genome mapping; biodiversity; genetic disorder.  
XX OS Homo sapiens.  
XX PN US2003073623-A1.  
XX PD 17-APR-2003.  
XX PF 30-JUL-2001; 2001US-00918995.  
XX PR 30-JUL-2001; 2001US-00918995.  
XX PA (DRMA/) DRMANAC R T.  
XX PA (LABAT/) LABAT I.  
XX PA (STAC/) STACHE-CRAIN B.  
XX PA (DICK/) DICKSON M C.  
XX PA (JONE/) JONES L W.  
XX PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
XX WPI; 2003-615964/58.  
XX DT New polynucleotide sequences obtained from various cDNA libraries, useful  
XX PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
XX PT mapping, in the recombinant production of protein, or in generating  
XX PT antisense DNA or RNA.  
XX PS Claim 1; SEQ ID NO 5377; 44pp; English.  
XX CC The invention relates to an isolated polynucleotide comprising any one of  
XX CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
XX CC determined by the technique of SBH (sequencing by hybridisation). Also  
XX CC included is a purified polypeptide comprising a sequence corresponding to  
XX CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
XX CC are useful in diagnostics as expressed sequence tags (EST) for  
XX CC identifying expressed genes or for physical mapping of the human genome,  
XX CC in forensics, in assessing biodiversity, or in identifying mutations  
XX CC responsible for genetic disorders and other traits. The nucleotide  
XX CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
XX CC for chromosome and gene mapping, in the recombinant production of  
XX CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
XX CC is useful for generating antibodies specific for it. The present sequence  
XX CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
XX CC for this patent did not form part of the printed specification, but was  
XX CC obtained in electronic format directly from USPTO at  
XX CC seqdata.uspto.gov/sequence.html?DocID=20030073623  
XX SQ Sequence 487 BP; 135 A; 140 C; 87 G; 122 T; 0 U; 3 Other;

Query Match 70.0%; Score 16.8; DB 9; Length 487;  
Best Local Similarity 90.0%; Pred. No. 3.8e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGCG 20  
DB 47 TCCGAGACGGTTCTGAGGCG 28

RESULT 48  
AAV20871  
ID AAV20871 standard; cDNA; 2799 BP.  
XX AC AAV20871;  
XX DT 16-JUL-1998 (first entry)  
XX XX Murine phospholipase D 2 (mPLD2) encoding cDNA.  
XX DE Phospholipase D; PLD; murine; PLD mediator; autoimmune disease;  
XX KW rheumatoid arthritis; psoriasis; ulcerative colitis; cancer; mPLD2;  
XX KW inflammatory disease; wound healing; ds.  
XX OS Mus sp.  
XX PH Key Location/Qualifiers  
XX FT CDS 1..2799  
XX FT /\*tag= a  
XX FT /product= "murine PLD2 protein"  
XX PN W09810076-A2.  
XX PD 12-MAR-1998.  
XX PF 06-AUG-1997; 97WO-US013919.  
XX PR 05-SEP-1996; 96US-0025469P.  
XX PA (ONYX-) ONYX PHARM INC.  
XX PI Frohman MA, Morris AJ;  
XX WPI; 1998-193626/17.  
XX DR P-PSDB; AAW53281.  
XX DT DNA sequence encoding phospholipase D - useful to identify modulators to  
XX PT treat auto-immune and inflammatory diseases.  
XX PS Claim 5; Page 57-58; 70pp; English.  
XX CC This cDNA encodes a murine phospholipase D (PLD) 2 (mPLD2) protein. This  
XX CC can be used in a method for identifying mediators of PLD, which comprises  
XX CC transfecting a cell line with an expression vector comprising nucleic  
XX CC acid sequences encoding a PLD protein and culturing the cell line in  
XX CC culture medium, where the PLD protein is expressed stably. An effective  
XX CC amount of a compound sufficient to cause a detectable loss in the loss in  
XX CC catalytic activity of PLD is added to the culture medium, and the loss in  
XX CC catalytic activity is detected. The PLD proteins are enzymes having  
XX CC phosphatidylcholine specific PLD activity. The PLD polypeptides which are  
XX CC perinuclear membrane associated require PI(4,5)P2 for in vitro activity  
XX CC and is activated by at least 1 G protein. The PLD polypeptides that are  
XX CC plasma membrane associated activates cytoskeletal reorganisation  
XX CC pathways, require PI(4,5)P2 for in vitro activity and does not require  
XX CC Rac1m cdc42, RhoA, PKC or ARF1 for activation. A PLD mediator can be used  
XX CC to treat autoimmune or inflammatory diseases, specifically rheumatoid  
XX CC arthritis, psoriasis and ulcerative colitis. The mediator can also be  
XX CC used in wound healing and for treating cancer and other diseases  
XX CC characterised by pathogenic mitogenicity  
XX SQ Sequence 2799 BP; 639 A; 766 C; 762 G; 632 T; 0 U; 0 Other;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCGAGACGGTTCTGAGGGCT 21  
 ||||| ||||| ||||| |||||  
 Db 444 CCGAGGAGGTTCTGAGGGCT 463

RESULT 49  
 ADJ67687  
 ID ADJ67687 standard; DNA; 2802 BP.  
 XX  
 AC ADJ67687;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Kiflc DNA #3.  
 XX  
 KW Kiflc; gene; ds; kinesin-like motor protein;  
 XX Bacillus anthracis infection; anthrax; antibacterial.  
 XX  
 OS Unidentified.  
 XX  
 PN US2004038222-A1.  
 XX  
 PD 26-FEB-2004.  
 XX  
 PF 30-SEP-2002; 2002US-00261175.  
 XX  
 PR 29-SEP-2001; 2001US-0325864P.  
 XX  
 PA (DIET/) DIETRICH W F.  
 XX (WATT/) WATERS J W.  
 XX  
 PI Dietrich WF, Waters JW;  
 XX  
 DR WPI; 2004-213930/20.  
 XX  
 XX Isolated Kiflc nucleic acids that confer resistance to Bacillus anthracis  
 PT Lethal Toxin, useful for detecting and conferring resistance to anthrax  
 PT infections.  
 XX  
 PS Claim 3; SEQ ID NO 3; 80pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid sequence or fragment  
 CC coding for a modified Kiflc polypeptide, a kinesin-like motor protein.  
 CC The invention also relates to a method of protecting a cell against  
 CC Bacillus anthracis infection, comprising administering the nucleic acid  
 CC to the cell and a method of treating a mammal affected by anthrax,  
 CC comprising administering the nucleic acid to the mammal or cells of the  
 CC mammal. The Kiflc nucleic acids may be used as hybridisation probes to  
 CC detect the presence of similar sequences in a sample and therefore detect  
 CC resistance to infection. They may also be used to produce the Kiflc  
 CC polypeptide which may be used in assays to identify modulators of anthrax  
 CC infection, a modified susceptible Kiflc amino acid sequence or a  
 CC functional fragment. This sequence represents a Kiflc nucleic acid of the  
 CC invention.  
 XX  
 SQ Sequence 2802 BP; 639 A; 769 C; 761 G; 633 T; 0 U; 0 Other;

Query Match 70.0%; Score 16.8; DB 12; Length 2802;  
 Best Local Similarity 90.0%; Pred. No. 4.8e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCGAGACGGTTCTGAGGGCT 21  
 ||||| ||||| ||||| |||||  
 Db 444 CCGAGGAGGTTCTGAGGGCT 463

RESULT 50  
 AAV20872  
 ID AAV20872 standard; cDNA; 3374 BP.  
 XX  
 AC AAV20872;

XX 16-JUL-1998 (first entry)  
 DT Murine phospholipase D 2 (mPLD2) encoding cDNA.  
 DE  
 DE  
 XX Phospholipase D; PLD; murine; PLD mediator; autoimmune disease;  
 KW rheumatoid arthritis; psoriasis; ulcerative colitis; cancer; mPLD2;  
 KW inflammatory disease; wound healing; ds.  
 XX  
 OS Mus sp.  
 XX  
 XX Key Location/Qualifiers  
 FH 139.2937  
 FT CDS /tag= a  
 FT /product= "murine PLD2 protein"  
 XX  
 XX WO9810076-A2.  
 PN  
 XX 12-MAR-1998.  
 PD  
 XX 06-AUG-1997; 97WO-US013919.  
 PF  
 XX 05-SEP-1996; 96US-0025469P.  
 PR  
 XX (ONYX-) ONYX PHARM INC.  
 PA  
 XX Frohman MA, Morris AJ;  
 PI  
 XX WPI; 1998-193626/17.  
 DR P-PSDB; AAW53281.  
 DR  
 XX DNA sequence encoding phospholipase D - useful to identify modulators to  
 PT treat auto-immune and inflammatory diseases.  
 PT  
 XX Claim 5; Page 62-66; 70pp; English.  
 PS  
 XX This cDNA encodes a murine phospholipase D (PLD) 2 (mPLD2) protein. This  
 CC can be used in a method for identifying mediators of PLD, which comprises  
 CC transfecting a cell line with an expression vector comprising nucleic  
 CC acid sequences encoding a PLD protein and culturing the cell line in  
 CC culture medium, where the PLD protein is expressed stably. An effective  
 CC amount of a compound sufficient to cause a detectable loss in the  
 CC catalytic activity of PLD is added to the culture medium, and the loss in  
 CC catalytic activity is detected. The PLD proteins are enzymes having  
 CC phosphatidylcholine specific PLD activity. The PLD polypeptides which are  
 CC perinuclear membrane associated require PI(4,5)P2 for in vitro activity  
 CC and is activated by at least 1 G protein. The PLD polypeptides that are  
 CC plasma membrane associated, activates cytoskeletal reorganisation  
 CC pathways, require PI(4,5)P2 for in vitro activity and does not require  
 CC Rac1m cdc42, RhoA, PKC or ARF1 for activation. A PLD mediator can be used  
 CC to treat autoimmune or inflammatory diseases, specifically rheumatoid  
 CC arthritis, psoriasis and ulcerative colitis. The mediator can also be  
 CC used in wound healing and for treating cancer and other diseases  
 CC characterised by pathogenic mitogenicity  
 XX  
 SQ Sequence 3374 BP; 753 A; 955 C; 905 G; 760 T; 0 U; 1 Other;

Query Match 70.0%; Score 16.8; DB 2; Length 3374;  
 Best Local Similarity 90.0%; Pred. No. 4.9e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCGAGACGGTTCTGAGGGCT 21  
 ||||| ||||| ||||| |||||  
 Db 582 CCGAGGAGGTTCTGAGGGCT 601

Search completed: March 25, 2005, 11:15:16  
 Job time : 269.143 secs

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|       |      |      |      |   |           |           |           |       |      |      |      |   |          |          |            |      |
|-------|------|------|------|---|-----------|-----------|-----------|-------|------|------|------|---|----------|----------|------------|------|
| C 98  | 17   | 70.8 | 612  | 9 | CE183667  | CE183667  | tigr-gss- | 171   | 16.6 | 69.2 | 518  | 2 | BE476414 | BE476414 | 159648     | BA   |
| C 99  | 17   | 70.8 | 627  | 9 | CE346969  | CE346969  | tigr-gss- | C 172 | 16.6 | 69.2 | 520  | 6 | CD296448 | CD296448 | StrPu691   |      |
| C 100 | 17   | 70.8 | 649  | 9 | CE89678   | CE89678   | tigr-gss- | 173   | 16.6 | 69.2 | 527  | 5 | BU672687 | BU672687 | TR48       | Leaf |
| C 101 | 17   | 70.8 | 668  | 9 | CE844747  | CE844747  | tigr-gss- | 174   | 16.6 | 69.2 | 536  | 8 | BH759830 | BH759830 | MC_H2M02   |      |
| C 102 | 17   | 70.8 | 689  | 9 | CE552243  | CE552243  | tigr-gss- | C 175 | 16.6 | 69.2 | 541  | 8 | AQ631597 | AQ631597 | RPCI-11-4  |      |
| C 103 | 17   | 70.8 | 709  | 9 | CE667057  | CE667057  | tigr-gss- | C 176 | 16.6 | 69.2 | 543  | 5 | BU226275 | BU226275 | 603401282  |      |
| C 104 | 17   | 70.8 | 716  | 9 | CE322509  | CE322509  | tigr-gss- | 177   | 16.6 | 69.2 | 545  | 6 | CB826313 | CB826313 | tw23h01.v  |      |
| C 105 | 16.8 | 70.0 | 712  | 2 | BF515880  | BF515880  | Reverse s | 178   | 16.6 | 69.2 | 557  | 2 | AW660621 | AW660621 | 99586      | MAR  |
| C 106 | 16.8 | 70.0 | 396  | 8 | CR078754  | CR078754  | Reverse s | 179   | 16.6 | 69.2 | 560  | 2 | BF415859 | BF415859 | UI-R-CAL   |      |
| C 107 | 16.8 | 70.0 | 412  | 6 | AZ648021  | AZ648021  | IM0514P16 | 180   | 16.6 | 69.2 | 561  | 4 | BZ844163 | BZ844163 | CH240_249  |      |
| C 108 | 16.8 | 70.0 | 412  | 6 | CA883559  | CA883559  | B0104A09- | 181   | 16.6 | 69.2 | 566  | 4 | BU661181 | BU661181 | BU661181   |      |
| C 109 | 16.8 | 70.0 | 428  | 1 | AV736641  | AV736641  | AV736641  | C 182 | 16.6 | 69.2 | 573  | 9 | CLJ11875 | CLJ11875 | 286435     | LB   |
| C 110 | 16.8 | 70.0 | 418  | 1 | AA603041  | AA603041  | AV10d08.s | 183   | 16.6 | 69.2 | 574  | 8 | AZ580518 | AZ580518 | 1M0368L18  |      |
| C 111 | 16.8 | 70.0 | 437  | 1 | AA470122  | AA470122  | zulla03.s | 184   | 16.6 | 69.2 | 579  | 5 | BP507338 | BP507338 | BP507338   |      |
| C 112 | 16.8 | 70.0 | 437  | 9 | CR0014120 | CR0014120 | AL003564  | 185   | 16.6 | 69.2 | 581  | 5 | AZ820286 | AZ820286 | 2M0092F23  |      |
| C 113 | 16.8 | 70.0 | 455  | 7 | CR390267  | CR390267  | F.rubripe | 186   | 16.6 | 69.2 | 587  | 5 | BU220755 | BU220755 | 603757726  |      |
| C 114 | 16.8 | 70.0 | 502  | 2 | BF600370  | BF600370  | K0817A05- | C 187 | 16.6 | 69.2 | 590  | 4 | BI538003 | BI538003 | 428349     | MA   |
| C 115 | 16.8 | 70.0 | 529  | 1 | A1810086  | A1810086  | wf65c11.x | 188   | 16.6 | 69.2 | 596  | 8 | AQ419600 | AQ419600 | RPCI-11-1  |      |
| C 116 | 16.8 | 70.0 | 531  | 1 | AJ637413  | AJ637413  | AJ637413  | 189   | 16.6 | 69.2 | 600  | 8 | AZ580421 | AZ580421 | 1M0368L16  |      |
| C 117 | 16.8 | 70.0 | 568  | 7 | CF296986  | CF296986  | 30DGS--07 | 190   | 16.6 | 69.2 | 604  | 6 | AZ580516 | AZ580516 | 1M0368L16  |      |
| C 118 | 16.8 | 70.0 | 588  | 9 | CE373065  | CE373065  | tigr-gss- | 191   | 16.6 | 69.2 | 608  | 6 | CB534500 | CB534500 | 767840     | MA   |
| C 119 | 16.8 | 70.0 | 609  | 8 | BH094141  | BH094141  | RPCI-24-3 | 192   | 16.6 | 69.2 | 610  | 2 | BE403332 | BE403332 | UI-R-CAL   |      |
| C 120 | 16.8 | 70.0 | 620  | 9 | CE002755  | CE002755  | tigr-gss- | 193   | 16.6 | 69.2 | 611  | 5 | BM238486 | BM238486 | EW238486   |      |
| C 121 | 16.8 | 70.0 | 668  | 5 | BU061624  | BU061624  | Fgr_10_G2 | 194   | 16.6 | 69.2 | 611  | 1 | AV439993 | AV439993 | AV439993   |      |
| C 122 | 16.8 | 70.0 | 686  | 9 | CE256623  | CE256623  | tigr-gss- | 195   | 16.6 | 69.2 | 622  | 7 | CK970701 | CK970701 | 4086554    | B    |
| C 123 | 16.8 | 70.0 | 698  | 7 | CR281380  | CR281380  | Forward s | 196   | 16.6 | 69.2 | 627  | 5 | BM228395 | BM228395 | EW228395   |      |
| C 124 | 16.8 | 70.0 | 735  | 4 | CG811991  | CG811991  | FSAAL57TR | 197   | 16.6 | 69.2 | 630  | 7 | CO221365 | CO221365 | WS01012.B  |      |
| C 125 | 16.8 | 70.0 | 757  | 4 | BI655860  | BI655860  | 603284878 | 198   | 16.6 | 69.2 | 632  | 7 | CO782672 | CO782672 | BL015D.F0  |      |
| C 126 | 16.8 | 70.0 | 851  | 8 | BZ745514  | BZ745514  | OGFAB527M | 199   | 16.6 | 69.2 | 636  | 6 | CB435808 | CB435808 | 616089     | MA   |
| C 127 | 16.8 | 70.0 | 861  | 8 | BZ139594  | BZ139594  | CH230_511 | 200   | 16.6 | 69.2 | 646  | 7 | CU814362 | CU814362 | 4079551    | B    |
| C 128 | 16.8 | 70.0 | 871  | 4 | BI554980  | BI554980  | 603236284 | 201   | 16.6 | 69.2 | 660  | 6 | BZ892747 | BZ892747 | Hm7_0174   |      |
| C 129 | 16.8 | 70.0 | 875  | 9 | CR236004  | CR236004  | Forward s | 202   | 16.6 | 69.2 | 667  | 9 | AG170821 | AG170821 | Pan-trog1  |      |
| C 130 | 16.8 | 70.0 | 898  | 5 | BQ713050  | BQ713050  | AGENCOURT | 203   | 16.6 | 69.2 | 671  | 7 | CF641513 | CF641513 | D40_G08.F  |      |
| C 131 | 16.8 | 70.0 | 960  | 9 | CNS01TAC  | CNS01TAC  | Tetraodon | 204   | 16.6 | 69.2 | 675  | 5 | BU815183 | BU815183 | N038C09.F  |      |
| C 132 | 16.8 | 70.0 | 1014 | 5 | BX341747  | BX341747  | Tetraodon | 205   | 16.6 | 69.2 | 686  | 1 | AV273704 | AV273704 | wr1.pk004  |      |
| C 133 | 16.8 | 70.0 | 1037 | 3 | CR687277  | CR687277  | Tetraodon | 206   | 16.6 | 69.2 | 686  | 5 | BU814362 | BU814362 | 4079551    | B    |
| C 134 | 16.8 | 70.0 | 1088 | 4 | BG391329  | BG391329  | 602417386 | 207   | 16.6 | 69.2 | 706  | 7 | CU814362 | CU814362 | 4079551    | B    |
| C 135 | 16.8 | 70.0 | 1336 | 5 | BM920585  | BM920585  | AGENCOURT | 208   | 16.6 | 69.2 | 710  | 5 | BM238395 | BM238395 | EW228395   |      |
| C 136 | 16.8 | 70.0 | 1465 | 2 | BF787901  | BF787901  | 602113685 | 209   | 16.6 | 69.2 | 723  | 8 | CG323957 | CG323957 | TAM32-8A1  |      |
| C 137 | 16.6 | 69.2 | 112  | 2 | BB576237  | BB576237  | BF787901  | 210   | 16.6 | 69.2 | 739  | 7 | CF872500 | CF872500 | tric031xj  |      |
| C 138 | 16.6 | 69.2 | 188  | 2 | AW477900  | AW477900  | 6X680908  | 211   | 16.6 | 69.2 | 749  | 4 | BU664214 | BU664214 | BJ664214   |      |
| C 139 | 16.6 | 69.2 | 200  | 5 | BX680908  | BX680908  | 6X680908  | 212   | 16.6 | 69.2 | 753  | 4 | BU667886 | BU667886 | BJ667886   |      |
| C 140 | 16.6 | 69.2 | 208  | 5 | BP944751  | BP944751  | BP944751  | 213   | 16.6 | 69.2 | 800  | 8 | BZ455928 | BZ455928 | BONOF23TR  |      |
| C 141 | 16.6 | 69.2 | 208  | 5 | BP948958  | BP948958  | BP948958  | 214   | 16.6 | 69.2 | 807  | 9 | AG312564 | AG312564 | Mus muscu  |      |
| C 142 | 16.6 | 69.2 | 220  | 8 | AQ074681  | AQ074681  | CTT-HSP-2 | 215   | 16.6 | 69.2 | 815  | 6 | CG902749 | CG902749 | tric031xj  |      |
| C 143 | 16.6 | 69.2 | 238  | 5 | BP947972  | BP947972  | BP947972  | 216   | 16.6 | 69.2 | 846  | 2 | BE618860 | BE618860 | 601462777  |      |
| C 144 | 16.6 | 69.2 | 241  | 2 | AW896572  | AW896572  | PM2-NN004 | 217   | 16.6 | 69.2 | 895  | 6 | CD796283 | CD796283 | EST667644  |      |
| C 145 | 16.6 | 69.2 | 258  | 5 | BP950081  | BP950081  | BP950081  | 218   | 16.6 | 69.2 | 895  | 6 | CD796285 | CD796285 | EST667646  |      |
| C 146 | 16.6 | 69.2 | 275  | 1 | AV533685  | AV533685  | AV533685  | 219   | 16.6 | 69.2 | 929  | 6 | CD796284 | CD796284 | EST667645  |      |
| C 147 | 16.6 | 69.2 | 277  | 9 | FR0029464 | FR0029464 | FR0029464 | 220   | 16.6 | 69.2 | 941  | 3 | CNS0A6LP | CNS0A6LP | Arabidops  |      |
| C 148 | 16.6 | 69.2 | 289  | 1 | AI130802  | AI130802  | Fugu rubr | 221   | 16.6 | 69.2 | 959  | 8 | AQ560624 | AQ560624 | HS_2066.B  |      |
| C 149 | 16.6 | 69.2 | 310  | 9 | TA381C08Q | TA381C08Q | TA381C08Q | 222   | 16.6 | 69.2 | 1001 | 5 | BQ894616 | BQ894616 | AGENCOURT  |      |
| C 150 | 16.6 | 69.2 | 322  | 9 | FR0029448 | FR0029448 | FR0029448 | 223   | 16.6 | 69.2 | 1032 | 5 | BQ894616 | BQ894616 | AGENCOURT  |      |
| C 151 | 16.6 | 69.2 | 323  | 2 | BF392661  | BF392661  | Fugu rubr | 224   | 16.6 | 69.2 | 1078 | 4 | BG331282 | BG331282 | 601465777  |      |
| C 152 | 16.6 | 69.2 | 324  | 1 | AI598840  | AI598840  | UI-R-CAO- | 225   | 16.6 | 69.2 | 1559 | 3 | CNS0A7BL | CNS0A7BL | 602432007  |      |
| C 153 | 16.6 | 69.2 | 327  | 2 | BF403427  | BF403427  | UI-R-CAO- | 226   | 16.6 | 69.2 | 1562 | 3 | CNS0A6UZ | CNS0A6UZ | Arabidops  |      |
| C 154 | 16.6 | 69.2 | 351  | 9 | CR051145  | CR051145  | Forward s | 227   | 16.6 | 69.2 | 1615 | 3 | CNS0A75Z | CNS0A75Z | Arabidops  |      |
| C 155 | 16.6 | 69.2 | 400  | 9 | FR0029455 | FR0029455 | FR0029455 | 228   | 16.6 | 69.2 | 1661 | 3 | CNS0A70W | CNS0A70W | Arabidops  |      |
| C 156 | 16.6 | 69.2 | 403  | 8 | AQ275445  | AQ275445  | PM2-NN004 | 229   | 16.6 | 69.2 | 1689 | 3 | CNS0A7AE | CNS0A7AE | Arabidops  |      |
| C 157 | 16.6 | 69.2 | 407  | 1 | BM430837  | BM430837  | 1du050G06 | 230   | 16.6 | 69.2 | 360  | 7 | D35016   | D35016   | CELK016AZP |      |
| C 158 | 16.6 | 69.2 | 417  | 2 | BF394710  | BF394710  | PM2-NN004 | 231   | 16.6 | 69.2 | 396  | 2 | BF645550 | BF645550 | NF037E01E  |      |
| C 159 | 16.6 | 69.2 | 421  | 1 | AV793896  | AV793896  | AV793896  | 232   | 16.6 | 69.2 | 427  | 1 | AV407673 | AV407673 | AV407673   |      |
| C 160 | 16.6 | 69.2 | 422  | 5 | BP940130  | BP940130  | BP940130  | 233   | 16.6 | 69.2 | 440  | 9 | CG554647 | CG554647 | OSN168485  |      |
| C 161 | 16.6 | 69.2 | 423  | 1 | AV805158  | AV805158  | AV805158  | 234   | 16.6 | 69.2 | 440  | 9 | CG554647 | CG554647 | OSN168485  |      |
| C 162 | 16.6 | 69.2 | 433  | 1 | AV792327  | AV792327  | AV792327  | 235   | 16.6 | 69.2 | 450  | 9 | CG554647 | CG554647 | OSN168485  |      |
| C 163 | 16.6 | 69.2 | 441  | 4 | BM430837  | BM430837  | 1du050G06 | 236   | 16.6 | 69.2 | 494  | 9 | CG554647 | CG554647 | OSN168485  |      |
| C 164 | 16.6 | 69.2 | 448  | 1 | AV791223  | AV791223  | AV791223  | 237   | 16.6 | 69.2 | 594  | 9 | CG554647 | CG554647 | OSN168485  |      |
| C 165 | 16.6 | 69.2 | 452  | 5 | BP610418  | BP610418  | BP610418  | 238   | 16.6 | 69.2 | 602  | 4 | BG453197 | BG453197 | NF089H12L  |      |
| C 166 | 16.6 | 69.2 | 468  | 7 | CV512835  | CV512835  | TGESTZV6  | 239   | 16.6 | 69.2 | 602  | 4 | BG453197 | BG453197 | NF089H12L  |      |
| C 167 | 16.6 | 69.2 | 472  | 7 | CO390605  | CO390605  | TGESTZV6  | 240   | 16.6 | 69.2 | 602  | 4 | BG453197 | BG453197 | NF089H12L  |      |
| C 168 | 16.6 | 69.2 | 486  | 6 | CD489397  | CD489397  | T22_G10.T | 241   | 16.6 | 69.2 | 611  | 6 | BI429967 | BI429967 | fqi18904.x |      |
| C 169 | 16.6 | 69.2 | 487  | 2 | BF776202  | BF776202  | 286586    | 242   | 16.6 | 69.2 | 612  | 7 | CN651794 | CN651794 | EG_CWGRS   |      |
| C 170 | 16.6 | 69.2 | 507  | 2 | BF046625  | BF046625  | BP250010A | 243   | 16.6 | 69.2 | 616  | 7 | CN813880 | CN813880 | FG06_01gl  |      |



|     |      |      |      |   |          |                     |       |      |      |      |   |           |                     |
|-----|------|------|------|---|----------|---------------------|-------|------|------|------|---|-----------|---------------------|
| 244 | 16.4 | 68.3 | 622  | 6 | CD008391 | CD008391 VVB074D11  | 317   | 16.2 | 67.5 | 648  | 8 | BZ182014  | BZ182014 CH230-473  |
| 245 | 16.4 | 68.3 | 630  | 6 | CD718095 | CD718095 VVB146D04  | C 318 | 16.2 | 67.5 | 660  | 7 | CF544576  | CF544576 Hd mx17.6  |
| 246 | 16.4 | 68.3 | 636  | 6 | CN881360 | CN881360 010427AAS  | C 319 | 16.2 | 67.5 | 663  | 6 | CD408676  | CD408676 Gm ck3517  |
| 247 | 16.4 | 68.3 | 639  | 1 | AU239615 | AU239615 VVB0239615 | C 320 | 16.2 | 67.5 | 663  | 8 | BH927892  | BH927892 odf24h01   |
| 248 | 16.4 | 68.3 | 680  | 6 | CD006857 | CD006857 VVB068A12  | C 321 | 16.2 | 67.5 | 667  | 6 | BY746797  | BY746797 BY746797   |
| 249 | 16.4 | 68.3 | 699  | 6 | CB255978 | CB255978 03-E01273  | C 322 | 16.2 | 67.5 | 669  | 7 | CO641109  | CO641109 USDA-FP1   |
| 250 | 16.4 | 68.3 | 745  | 8 | CC368431 | CC368431 PUEFF33TD  | C 323 | 16.2 | 67.5 | 672  | 2 | BB636114  | BB636114 BB636114   |
| 251 | 16.4 | 68.3 | 784  | 9 | CNS03AFQ | AL235151 Tetracodon | C 324 | 16.2 | 67.5 | 674  | 7 | CF075905  | CF075905 Hd mx17.6  |
| 252 | 16.4 | 68.3 | 806  | 9 | CC802540 | CC802540 ih31d01.b  | C 325 | 16.2 | 67.5 | 679  | 8 | AZ824022  | AZ824022 ZM0098J24  |
| 253 | 16.4 | 68.3 | 879  | 8 | BZ990549 | BZ990549 PUGIN43TB  | C 326 | 16.2 | 67.5 | 681  | 4 | BJ165269  | BJ165269 BJ165269   |
| 254 | 16.4 | 68.3 | 926  | 9 | CNS03NV1 | AL252658 Tetracodon | C 327 | 16.2 | 67.5 | 684  | 6 | CD399629  | CD399629 Gm ck2131  |
| 255 | 16.4 | 68.3 | 965  | 9 | CC734683 | CC734683 OGUKP67TV  | C 328 | 16.2 | 67.5 | 685  | 2 | BE974043  | BE974043 601680374  |
| 256 | 16.4 | 68.3 | 966  | 5 | EX834218 | EX834218 BX834218   | C 329 | 16.2 | 67.5 | 690  | 7 | CF544450  | CF544450 Hd mx17.6  |
| 257 | 16.4 | 68.3 | 978  | 9 | CNS037XG | BU851901 Tetracodon | C 330 | 16.2 | 67.5 | 690  | 7 | CV432049  | CV432049 56870.1 A  |
| 258 | 16.4 | 68.3 | 1138 | 5 | BUS55057 | BU855057 AGENCOURT  | C 331 | 16.2 | 67.5 | 694  | 9 | AG136438  | AG136438 Pan trogl  |
| 259 | 16.4 | 68.3 | 1977 | 3 | CNS0A4GP | BX827087 Arabidops  | C 332 | 16.2 | 67.5 | 695  | 4 | BG973504  | BG973504 602842195  |
| 260 | 16.2 | 67.5 | 180  | 8 | AF061628 | AF061628 AF061628   | C 333 | 16.2 | 67.5 | 699  | 7 | CF721155  | CF721155 CCANR43TF  |
| 261 | 16.2 | 67.5 | 219  | 2 | BF754757 | BF754757 MKO-CT045  | C 334 | 16.2 | 67.5 | 703  | 8 | CC358002  | CC358002 PUEHT14TD  |
| 262 | 16.2 | 67.5 | 271  | 5 | BP137457 | BP137457 BP137457   | C 335 | 16.2 | 67.5 | 705  | 9 | CL166555  | CL166555 104_362_1  |
| 263 | 16.2 | 67.5 | 276  | 5 | BQ344806 | BQ344806 ILS-NT022  | C 336 | 16.2 | 67.5 | 712  | 2 | BE264683  | BE264683 601192506  |
| 264 | 16.2 | 67.5 | 289  | 2 | BB719604 | BB719604 BB719604   | C 337 | 16.2 | 67.5 | 719  | 9 | AG326391  | AG326391 Mus muscu  |
| 265 | 16.2 | 67.5 | 315  | 1 | AV046497 | AV046497 AV046497   | C 338 | 16.2 | 67.5 | 731  | 5 | BU941141  | BU941141 AGENCOURT  |
| 266 | 16.2 | 67.5 | 318  | 7 | N85945   | N85945 J5660F Huna  | C 339 | 16.2 | 67.5 | 743  | 7 | CV105837  | CV105837 AGENCOURT  |
| 267 | 16.2 | 67.5 | 327  | 2 | BF705846 | BF705846 271495 WA  | C 340 | 16.2 | 67.5 | 744  | 9 | CL166554  | CL166554 104_362_1  |
| 268 | 16.2 | 67.5 | 330  | 1 | AI398013 | AI398013 NC5MIC12T  | C 341 | 16.2 | 67.5 | 745  | 7 | CK326228  | CK326228 Hd mx23_0  |
| 269 | 16.2 | 67.5 | 332  | 5 | CF836462 | CF836462 UCRC903_0  | C 342 | 16.2 | 67.5 | 750  | 5 | BU252574  | BU252574 603745432  |
| 270 | 16.2 | 67.5 | 361  | 5 | BP661230 | BP661230 BP661230   | C 343 | 16.2 | 67.5 | 756  | 7 | CN978584  | CN978584 29421_125  |
| 271 | 16.2 | 67.5 | 365  | 7 | CO741783 | CO741783 Hd mx23_2  | C 344 | 16.2 | 67.5 | 758  | 8 | BZ285161  | BZ285161 CH230-385  |
| 272 | 16.2 | 67.5 | 380  | 9 | CG833539 | CG833539 ZMWBC013   | C 345 | 16.2 | 67.5 | 762  | 9 | CC928076  | CC928076 ZMMBC053   |
| 273 | 16.2 | 67.5 | 386  | 7 | CO579549 | CO579549 ILLUMIGEN  | C 346 | 16.2 | 67.5 | 764  | 9 | CR794611  | CR794611 GROMA12A   |
| 274 | 16.2 | 67.5 | 400  | 8 | BZ243089 | BZ243089 CH230-362  | C 347 | 16.2 | 67.5 | 767  | 8 | BZ077316  | BZ077316 1kz45603_  |
| 275 | 16.2 | 67.5 | 417  | 1 | AA142396 | AA142396 ms08003.r  | C 348 | 16.2 | 67.5 | 768  | 6 | CB328413  | CB328413 UT-R-FSO-  |
| 276 | 16.2 | 67.5 | 430  | 2 | AW101794 | AW101794 sd70e05.Y  | C 349 | 16.2 | 67.5 | 774  | 5 | BU135280  | BU135280 AGENCOURT  |
| 277 | 16.2 | 67.5 | 432  | 8 | BH611219 | BH611219 SALK_0304  | C 350 | 16.2 | 67.5 | 776  | 5 | BU842034  | BU842034 AGENCOURT  |
| 278 | 16.2 | 67.5 | 433  | 1 | AA142414 | AA142414 ms08004.r  | C 351 | 16.2 | 67.5 | 779  | 8 | BH535812  | BH535812 BOHMY45TF  |
| 279 | 16.2 | 67.5 | 467  | 8 | AQ944329 | AQ944329 Sheared D  | C 352 | 16.2 | 67.5 | 783  | 6 | CD813757  | CD813757 BN15.0200  |
| 280 | 16.2 | 67.5 | 474  | 2 | BE415363 | BE415363 MWL028.E0  | C 353 | 16.2 | 67.5 | 785  | 9 | CG012872  | CG012872 ZUAD21TV   |
| 281 | 16.2 | 67.5 | 492  | 2 | BE210916 | BE210916 s05508.Y   | C 354 | 16.2 | 67.5 | 787  | 9 | CC537886  | CC537886 CH240_417  |
| 282 | 16.2 | 67.5 | 498  | 2 | BF836338 | BF836338 RC1-HT097  | C 355 | 16.2 | 67.5 | 787  | 9 | CC549746  | CC549746 CH240_434  |
| 283 | 16.2 | 67.5 | 503  | 4 | BG509990 | BG509990 sad26b11_  | C 356 | 16.2 | 67.5 | 810  | 6 | CD814702  | CD814702 BN15_023P  |
| 284 | 16.2 | 67.5 | 508  | 6 | CD395262 | CD395262 Gm ck1525  | C 357 | 16.2 | 67.5 | 819  | 8 | BZ979888  | BZ979888 PUF1063TB  |
| 285 | 16.2 | 67.5 | 527  | 5 | BQ296930 | BQ296930 sso36b01_  | C 358 | 16.2 | 67.5 | 836  | 8 | BZ824487  | BZ824487 PUFAP30TB  |
| 286 | 16.2 | 67.5 | 531  | 4 | BJ159999 | BJ159999 BJ159999   | C 359 | 16.2 | 67.5 | 839  | 7 | CF708922  | CF708922 CCAEC62TO  |
| 287 | 16.2 | 67.5 | 533  | 1 | AA496043 | AA496043 zv72e02.s  | C 361 | 16.2 | 67.5 | 854  | 7 | CF702036  | CF702036 CCAC231TO  |
| 288 | 16.2 | 67.5 | 533  | 7 | CO741197 | CO741197 Hd mx23_1  | C 362 | 16.2 | 67.5 | 854  | 7 | CF692015  | CF692015 CCANR54TR  |
| 289 | 16.2 | 67.5 | 533  | 8 | AQ778376 | AQ778376 HS_3161_B  | C 363 | 16.2 | 67.5 | 856  | 9 | CNS0211N  | AL117044 Tetracodon |
| 290 | 16.2 | 67.5 | 536  | 1 | AI460461 | AI460461 sa78g10.Y  | C 364 | 16.2 | 67.5 | 857  | 9 | CC676774  | CC676774 OSGEG14TV  |
| 291 | 16.2 | 67.5 | 536  | 7 | CF075895 | CF075895 Hd mx17_6  | C 365 | 16.2 | 67.5 | 863  | 9 | CW010325  | CW010325 ZMMBLA001  |
| 292 | 16.2 | 67.5 | 543  | 5 | EX474155 | EX474155 DKFP2686L  | C 366 | 16.2 | 67.5 | 868  | 7 | CF708909  | CF708909 CCAGQ68TR  |
| 293 | 16.2 | 67.5 | 546  | 7 | CN635434 | CN635434 116C03_54  | C 367 | 16.2 | 67.5 | 870  | 9 | CG971969  | CG971969 ZUAE68TH   |
| 294 | 16.2 | 67.5 | 553  | 2 | BE105666 | BE105666 sq63a04.Y  | C 368 | 16.2 | 67.5 | 871  | 9 | CG015132  | CG015132 ZUACS78TV  |
| 295 | 16.2 | 67.5 | 553  | 4 | BI472115 | BI472115 sh939f07_  | C 369 | 16.2 | 67.5 | 880  | 5 | EX459433  | EX459433 BX459433   |
| 296 | 16.2 | 67.5 | 565  | 2 | AW781890 | AW781890 sl98a03.Y  | C 370 | 16.2 | 67.5 | 882  | 7 | CF718681  | CF718681 CCADM51TF  |
| 297 | 16.2 | 67.5 | 565  | 4 | BJ174381 | BJ174381 BJ174381   | C 371 | 16.2 | 67.5 | 889  | 9 | CG104403  | CG104403 PUFQMA7TD  |
| 298 | 16.2 | 67.5 | 565  | 6 | BQ041481 | BQ041481 gd22f09.Y  | C 372 | 16.2 | 67.5 | 889  | 9 | CG049669  | CG049669 PUFXA44TD  |
| 299 | 16.2 | 67.5 | 581  | 6 | CD449699 | CD449699 Hd mx18_0  | C 373 | 16.2 | 67.5 | 900  | 7 | CF677989  | CF677989 CCAD551TF  |
| 300 | 16.2 | 67.5 | 581  | 7 | CF544544 | CF544544 Hd mx17_6  | C 374 | 16.2 | 67.5 | 907  | 7 | CF707989  | CF707989 CCAGQ68TF  |
| 301 | 16.2 | 67.5 | 589  | 9 | CE146227 | CE146227 t1gr-g88-  | C 375 | 16.2 | 67.5 | 912  | 4 | BI828914  | BI828914 603075075  |
| 302 | 16.2 | 67.5 | 592  | 4 | BG762856 | BG762856 602734788  | C 376 | 16.2 | 67.5 | 915  | 9 | ECA576659 | AJ576659 Equus cab  |
| 303 | 16.2 | 67.5 | 592  | 7 | CF544173 | CF544173 Hd mx17_7  | C 377 | 16.2 | 67.5 | 918  | 9 | CL071117  | CL071117 CH216-120  |
| 304 | 16.2 | 67.5 | 592  | 4 | CF075895 | CF075895 Hd mx17_6  | C 378 | 16.2 | 67.5 | 919  | 2 | BE974853  | BE974853 601680912  |
| 305 | 16.2 | 67.5 | 593  | 8 | CR022133 | CR022133 Reverse s  | C 379 | 16.2 | 67.5 | 920  | 7 | CF702569  | CF702569 CCACL59TO  |
| 306 | 16.2 | 67.5 | 594  | 8 | AQ946118 | AQ946118 Sheared D  | C 380 | 16.2 | 67.5 | 922  | 7 | CF707286  | CF707286 CCAEN07TO  |
| 307 | 16.2 | 67.5 | 597  | 7 | CF075811 | CF075811 Hd mx17_6  | C 381 | 16.2 | 67.5 | 922  | 9 | CNS04CJG  | AL284533 Tetracodon |
| 308 | 16.2 | 67.5 | 598  | 9 | CE584964 | CE584964 t1gr-g88-  | C 382 | 16.2 | 67.5 | 933  | 9 | CNS0771L  | AL432827 T3 end of  |
| 309 | 16.2 | 67.5 | 599  | 7 | CK326743 | CK326743 Hd mx24_0  | C 383 | 16.2 | 67.5 | 939  | 2 | BF343178  | BF343178 602015827  |
| 310 | 16.2 | 67.5 | 600  | 1 | AA151689 | AA151689 z029a05.s  | C 384 | 16.2 | 67.5 | 942  | 7 | CF702042  | CF702042 CCAC231TR  |
| 311 | 16.2 | 67.5 | 605  | 5 | BQ176832 | BQ176832 UT-M-DJ2-  | C 385 | 16.2 | 67.5 | 950  | 9 | CG049668  | CG049668 PUFXA44TB  |
| 312 | 16.2 | 67.5 | 606  | 1 | AI749573 | AI749573 at30f09.x  | C 386 | 16.2 | 67.5 | 984  | 5 | BX900888  | BX900888 BX900888   |
| 313 | 16.2 | 67.5 | 611  | 7 | CF544591 | CF544591 Hd mx17_6  | C 387 | 16.2 | 67.5 | 996  | 8 | BZ576964  | BZ576964 msh2_5183  |
| 314 | 16.2 | 67.5 | 625  | 2 | BB658589 | BB658589 BB658589   | C 388 | 16.2 | 67.5 | 1004 | 9 | CNS0449R  | CL018422 Tetracodon |
| 315 | 16.2 | 67.5 | 638  | 2 | AW349552 | AW349552 GM210007B  | C 389 | 16.2 | 67.5 | 1004 | 9 | CL018422  | CL018422 CH216-311  |
| 316 | 16.2 | 67.5 | 645  | 9 | CG984522 | CG984522 CH240_154  | C 389 | 16.2 | 67.5 | 1004 | 9 | CL018422  | CL018422 CH216-311  |

|       |      |      |      |   |           |           |            |             |       |    |      |     |   |          |          |
|-------|------|------|------|---|-----------|-----------|------------|-------------|-------|----|------|-----|---|----------|----------|
| C 390 | 16.2 | 67.5 | 1006 | 6 | CB686120  | Bn01b_03n | CB686120   | Bn01b_03n   | C 463 | 16 | 66.7 | 403 | 5 | BY393139 | BY393139 |
| C 391 | 16.2 | 67.5 | 1019 | 8 | BZ793260  | PUGCD29TD | BZ793260   | PUGCD29TD   | C 464 | 16 | 66.7 | 404 | 1 | AI501517 | AI501517 |
| C 392 | 16.2 | 67.5 | 1019 | 9 | CG104399  | PUPQ47TB  | CG104399   | PUPQ47TB    | C 465 | 16 | 66.7 | 404 | 1 | AI501592 | AI501592 |
| C 393 | 16.2 | 67.5 | 1033 | 5 | BQ061998  | AGENCOURT | BQ061998   | AGENCOURT   | C 466 | 16 | 66.7 | 410 | 9 | CR490521 | CR490521 |
| C 394 | 16.2 | 67.5 | 1038 | 9 | CNS03V04  | Tetraodon | AL261805   | Tetraodon   | C 467 | 16 | 66.7 | 414 | 2 | BE686676 | BE686676 |
| C 395 | 16.2 | 67.5 | 1061 | 4 | BQ296748  | 602394509 | BQ296748   | 602394509   | C 468 | 16 | 66.7 | 414 | 7 | CKS86309 | CKS86309 |
| C 396 | 16.2 | 67.5 | 1069 | 9 | CL071243  | CH216-120 | CL071243   | CH216-120   | C 469 | 16 | 66.7 | 414 | 7 | CKS86333 | CKS86333 |
| C 397 | 16.2 | 67.5 | 1072 | 2 | BF207337  | 601870554 | BF207337   | 601870554   | C 470 | 16 | 66.7 | 420 | 8 | AQ443271 | AQ443271 |
| C 398 | 16.2 | 67.5 | 1101 | 9 | CNS014ZL  | Li04811   | Drosophila | Li04811     | C 471 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 399 | 16.2 | 67.5 | 1250 | 9 | BQ879673  | AGENCOURT | BQ879673   | AGENCOURT   | C 472 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 400 | 16.2 | 67.5 | 1250 | 9 | CG752348  | P047-1-CO | CG752348   | P047-1-CO   | C 473 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 401 | 16.2 | 67.5 | 1280 | 6 | CA254479  | SCBFFL411 | CA254479   | SCBFFL411   | C 474 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 402 | 16.2 | 67.5 | 1400 | 3 | CR727462  | Tetraodon | CR727462   | Tetraodon   | C 475 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 403 | 16.2 | 67.5 | 1662 | 3 | AK054100  | Mus muscu | AK054100   | Mus muscu   | C 476 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 404 | 16.2 | 67.5 | 2148 | 3 | AY415076  | AY415076  | AY415076   | Mus muscu   | C 477 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 405 | 16.2 | 67.5 | 2289 | 9 | CL951370  | OsJURA001 | CL951370   | OsJURA001   | C 478 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 406 | 16.2 | 67.5 | 2403 | 3 | AK040452  | Mus muscu | AK040452   | Mus muscu   | C 479 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 407 | 16.2 | 67.5 | 3228 | 3 | AK088607  | Mus muscu | AK088607   | Mus muscu   | C 480 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 408 | 16.2 | 67.5 | 3489 | 3 | AK043798  | Mus muscu | AK043798   | Mus muscu   | C 481 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 409 | 16.2 | 67.5 | 157  | 7 | R57724    | BE120740  | BE120740   | UI-R-B51-   | C 482 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 410 | 16.2 | 67.5 | 170  | 9 | TA252E05Q | AL482614  | T. brucei  | AL482614    | C 483 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 411 | 16.2 | 67.5 | 188  | 1 | AA924374  | UI-R-Al-d | AA924374   | UI-R-Al-d   | C 484 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 412 | 16.2 | 67.5 | 225  | 2 | BB300363  | BB300363  | BB300363   | BB300363    | C 485 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 413 | 16.2 | 67.5 | 230  | 7 | CR468393  | CR468393  | CR468393   | CR468393    | C 486 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 414 | 16.2 | 67.5 | 262  | 8 | BH671592  | BH671592  | BH671592   | BH671592    | C 487 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 415 | 16.2 | 67.5 | 263  | 7 | BE120740  | BE120740  | BE120740   | UI-R-B51-   | C 488 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 416 | 16.2 | 67.5 | 290  | 2 | BE120740  | BE120740  | BE120740   | UI-R-B51-   | C 489 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 417 | 16.2 | 67.5 | 302  | 8 | AQ067354  | AQ067354  | AQ067354   | HS 2237 A   | C 490 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 418 | 16.2 | 67.5 | 311  | 1 | AL842281  | AL842281  | AL842281   | AL842281    | C 491 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 419 | 16.2 | 67.5 | 322  | 6 | CA877103  | CA877103  | CA877103   | K0953A09-   | C 492 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 420 | 16.2 | 67.5 | 330  | 7 | CK908488  | CK908488  | CK908488   | rhzm0.00    | C 493 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 421 | 16.2 | 67.5 | 338  | 2 | BF843353  | BF843353  | BF843353   | W11-HT113   | C 494 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 422 | 16.2 | 67.5 | 339  | 5 | BY180895  | BY180895  | BY180895   | BY180895    | C 495 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 423 | 16.2 | 67.5 | 340  | 7 | CK577122  | CK577122  | CK577122   | IST_W15_1   | C 496 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 424 | 16.2 | 67.5 | 340  | 7 | CK577122  | CK577122  | CK577122   | IST_W15_1   | C 497 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 425 | 16.2 | 67.5 | 341  | 2 | BF149493  | BF149493  | BF149493   | uy65f09-Y   | C 498 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 426 | 16.2 | 67.5 | 346  | 9 | CL169980  | CL169980  | CL169980   | 104_370_1   | C 499 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 427 | 16.2 | 67.5 | 347  | 9 | CL701965  | CL701965  | CL701965   | SP_Ba007    | C 500 | 16 | 66.7 | 422 | 8 | AQ467052 | AQ467052 |
| C 428 | 16.2 | 67.5 | 348  | 7 | CK586334  | CK586334  | CK586334   | IST_W15_2   |       |    |      |     |   |          |          |
| C 429 | 16.2 | 67.5 | 348  | 8 | BZ312680  | BZ312680  | BZ312680   | 128B01.5    |       |    |      |     |   |          |          |
| C 430 | 16.2 | 67.5 | 349  | 5 | BY310493  | BY310493  | BY310493   | BY310493    |       |    |      |     |   |          |          |
| C 431 | 16.2 | 67.5 | 352  | 8 | AQ250801  | AQ250801  | AQ250801   | T20D13-T7   |       |    |      |     |   |          |          |
| C 432 | 16.2 | 67.5 | 352  | 5 | BA469089  | BA469089  | BA469089   | BA469089    |       |    |      |     |   |          |          |
| C 433 | 16.2 | 67.5 | 357  | 2 | BF400229  | BF400229  | BF400229   | UI-R-CA1-   |       |    |      |     |   |          |          |
| C 434 | 16.2 | 67.5 | 357  | 1 | AV187868  | AV187868  | AV187868   | AV187868    |       |    |      |     |   |          |          |
| C 435 | 16.2 | 67.5 | 360  | 1 | AV193366  | AV193366  | AV193366   | AV193366    |       |    |      |     |   |          |          |
| C 436 | 16.2 | 67.5 | 360  | 6 | C40472    | C40472    | C40472     | C40472      |       |    |      |     |   |          |          |
| C 437 | 16.2 | 67.5 | 360  | 6 | C43390    | C43390    | C43390     | C43390      |       |    |      |     |   |          |          |
| C 438 | 16.2 | 67.5 | 360  | 6 | C45991    | C45991    | C45991     | C45991      |       |    |      |     |   |          |          |
| C 439 | 16.2 | 67.5 | 360  | 6 | C46626    | C46626    | C46626     | C46626      |       |    |      |     |   |          |          |
| C 440 | 16.2 | 67.5 | 365  | 4 | BM210268  | BM210268  | BM210268   | C0661G07-   |       |    |      |     |   |          |          |
| C 441 | 16.2 | 67.5 | 368  | 7 | CK577148  | CK577148  | CK577148   | IST_W15_1   |       |    |      |     |   |          |          |
| C 442 | 16.2 | 67.5 | 368  | 7 | CO154614  | CO154614  | CO154614   | CO154614    |       |    |      |     |   |          |          |
| C 443 | 16.2 | 67.5 | 370  | 1 | AV418550  | AV418550  | AV418550   | AV418550    |       |    |      |     |   |          |          |
| C 444 | 16.2 | 67.5 | 370  | 8 | B80155    | B80155    | B80155     | CIT-HSP-204 |       |    |      |     |   |          |          |
| C 445 | 16.2 | 67.5 | 372  | 6 | C70997    | C70997    | C70997     | C70997      |       |    |      |     |   |          |          |
| C 446 | 16.2 | 67.5 | 372  | 8 | BZ329995  | BZ329995  | BZ329995   | bv89c09-b   |       |    |      |     |   |          |          |
| C 447 | 16.2 | 67.5 | 373  | 6 | C43815    | C43815    | C43815     | C43815      |       |    |      |     |   |          |          |
| C 448 | 16.2 | 67.5 | 373  | 6 | C69610    | C69610    | C69610     | C69610      |       |    |      |     |   |          |          |
| C 449 | 16.2 | 67.5 | 375  | 6 | C69244    | C69244    | C69244     | C69244      |       |    |      |     |   |          |          |
| C 450 | 16.2 | 67.5 | 375  | 6 | C70287    | C70287    | C70287     | C70287      |       |    |      |     |   |          |          |
| C 451 | 16.2 | 67.5 | 375  | 6 | CD541782  | CD541782  | CD541782   | CD541782    |       |    |      |     |   |          |          |
| C 452 | 16.2 | 67.5 | 376  | 1 | AV186862  | AV186862  | AV186862   | AV186862    |       |    |      |     |   |          |          |
| C 453 | 16.2 | 67.5 | 376  | 6 | C42374    | C42374    | C42374     | C42374      |       |    |      |     |   |          |          |
| C 454 | 16.2 | 67.5 | 377  | 1 | AV192255  | AV192255  | AV192255   | AV192255    |       |    |      |     |   |          |          |
| C 455 | 16.2 | 67.5 | 377  | 6 | BY771923  | BY771923  | BY771923   | BY771923    |       |    |      |     |   |          |          |
| C 456 | 16.2 | 67.5 | 382  | 7 | CK577136  | CK577136  | CK577136   | IST_W15_1   |       |    |      |     |   |          |          |
| C 457 | 16.2 | 67.5 | 382  | 7 | CV203169  | CV203169  | CV203169   | EST862879   |       |    |      |     |   |          |          |
| C 458 | 16.2 | 67.5 | 383  | 7 | CK577142  | CK577142  | CK577142   | CK577142    |       |    |      |     |   |          |          |
| C 459 | 16.2 | 67.5 | 387  | 5 | BY404011  | BY404011  | BY404011   | BY404011    |       |    |      |     |   |          |          |
| C 460 | 16.2 | 67.5 | 389  | 7 | CR514345  | CR514345  | CR514345   | CR514345    |       |    |      |     |   |          |          |
| C 461 | 16.2 | 67.5 | 399  | 5 | BY006000  | BY006000  | BY006000   | BY006000    |       |    |      |     |   |          |          |
| C 462 | 16.2 | 67.5 | 400  | 7 | CK577143  | CK577143  | CK577143   | IST_W15_1   |       |    |      |     |   |          |          |

## ALIGNMENTS

BM718194 213 bp mRNA linear EST 01-MAR-2002  
UI-E-E30-ain-m-04-0-UI.r1 UI-E-E30 Homo sapiens cDNA clone  
UI-E-E30-ain-m-04-0-UI 5', mRNA sequence.

BM718194.1 GI:19036354  
EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Ronald, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research Genetics ([www.resgen.com](http://www.resgen.com)).  
The following repetitive elements were found in this cDNA sequence: 90-212, >LINE2 (matched complement)

**FEATURES**  
**source**

Location/Qualifiers  
1. .213

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJO-ain-m-04-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJO"
/notes="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJO is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGATCAAGA; lens, CGATTAGCGA; eye anterior segment,
AATGCCGCAI; optic nerve, CATTAAATG; retina, CGCCG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI)."

```

## ORIGIN

|                       |              |                    |               |             |
|-----------------------|--------------|--------------------|---------------|-------------|
| Query Match           | 75.8%        | Score 18.2;        | DB 4;         | Length 213; |
| Best Local Similarity | 87.0%;       | Pred. No. 6.6e+02; |               |             |
| Matches 20;           | Conservative | 0;                 | Mismatches 3; | Indels 0;   |
|                       |              |                    |               | Gaps 0;     |

Qy 2 CCGAGACGGTTCTGAGGGCTTAC 24  
|||  
80 CCGAGACGATTCTGGGGGCATAC 104  
Db

[illegible]

| REFERENCE<br>AUTHORS   | TITLE<br>JOURNAL<br>COMMENT   |
|--|---|
| 1 (bases 1 to 501)   |   |
| McCartar, J., Clifton, S., ChisPELLI, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theisinger, B., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagarisvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Sreptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, McCann, R., Waterston, R. and Wilson, R. | The Washington Univ. Nematode EST Project, 1999<br>Unpublished (1999)<br>Contact: McCarter JP   |
|  | The Washington Univ. Nematode EST Project, 1999<br>Washington University School of Medicine<br>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA<br>Tel: 314 286 1800<br>Fax: 314 286 1810 |

Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
The library was contributed by Dr. Geert Smant of the Laboratory of  
Nematology at Wageningen University, Wageningen,  
Netherlands ([geert.smant@nema.dpw.wau.nl](mailto:geert.smant@nema.dpw.wau.nl)). DNA Sequencing by:  
Washington University Genome Sequencing Center  
Seq primer: -40RP from Gibco  
High quality sequence stop: 479.

**FEATURES**  
**SOURCE**

Location/Qualifiers  
1. .501

```

/organism="Globodera rostochiensis"
/mol_type="mRNA"
/db_xref="taxon:31243"
/dev_stage="J2"
/lab_host="DH108"
/clone_lib="Globodera rostochiensis J2 pCDNAIL Snaunt v1"
/notes="Vector: pCDNAIL (Invitrogen); Site_1: BstXI; Site_2: EcoRI; The library was donated for sequencing by Geert Snaunt from Wageningen University, Laboratory of Nematology, The Netherlands."

```

## ORIGIN

|                          |        |                  |           |             |
|--------------------------|--------|------------------|-----------|-------------|
| Query Match              | 75.8%  | Score 18.2;      | DB 4;     | Length 501; |
| Best Local Similarity    | 87.0%; | Pred. No. 7e+02; |           |             |
| Matches 20: Conservative | 0;     | Mismatches 3;    | Indels 0; | Gaps 0;     |

QY 2 CCGAGACGGTTCCTGAGGGCTTAC 24  
DB 105 CCGAGACGGTTCCTGGTGGCTTC 83

|            |                  |            |                        |  |
|------------|------------------|------------|------------------------|--|
| RESULT 3   | AW569902         | 463 bp     | linear                 | EST 14-JUL-2004                                      |
| LOCUS      | si3a12.y1        | Gm-c1031   | Glycine max cDNA clone | GENOME SYSTEMS CLONE ID:                             |
| DEFINITION | Gm-c1031-1271 5' | similar to | TR:022616              | O22616 ORNITHINE DECARBOXYLASE. [1] ; mRNA sequence. |

Email: est@watson.wustl.edu  
When it was determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com) Insert Length: 634 Std Error: 0.00  
High quality sequence stop: 396.

FEATURES  
source

Location/Qualifiers  
1. .463

```
1. 403
source
/organism="Glycine max
/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
```



4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 421.

#### FEATURES

Location/Qualifiers

1. .538  
 /organism="Glycine soja"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3848"  
 /clone="SOYBEAN CLONE ID: Gm-c1059-3772"  
 /tissue\_type="Whole seedling, 2 week old, etiolated"  
 /lab\_host="DH10B"  
 /clone\_lib="Gm-c1059"  
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from 2 week old etiolated whole seedlings of PI468916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI- XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed in the laboratory of Dr. Randy Shoemaker at Iowa state university."

#### ORIGIN

Query Match 74.2%; Score 17.8; DB 4; Length 538;  
 Best Local Similarity 90.5%; Pred. No. 1.1e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGACGGTCTGAGGGCTTAC 24  
 |||||  
 Db 290 GATACGGTCTGAGGGATTAC 310

#### RESULT 6

CA853343  
 LOCUS B07B08.seq cDNA Peking library 12hr SCN3 linear EST 01-AUG-2003  
 DEFINITION B07B08 5', mRNA sequence.

ACCESSION CA853343  
 VERSION CA853343.1 GI:33390136  
 KEYWORDS EST.

#### SOURCE

Glycine max (soybean)  
 Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

#### REFERENCE

1 (bases 1 to 542)  
 Alkharouf, N.W., Khan, R. and Matthews, B.F.  
 Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode  
 Unpublished (2002)

#### JOURNAL

Comment: Alkharouf, N.W.  
 Soybean Genomics and Improvement Laboratory (SGIL)  
 US Department of Agriculture (USDA), ARS, PSI  
 Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA

Tel: 301 504 5750  
 Fax: 301 504 5728  
 Email: alkharouf@ba.ars.usda.gov.

#### FEATURES

Location/Qualifiers  
 1. .542  
 /organism="Glycine max"  
 /mol\_type="mRNA"

/cultivar="Peking"  
 /db\_xref="taxon:3847"  
 /clone="B07B08"

/tissue\_type="Roots"  
 /dev\_stage="Seedlings"

/clone\_lib="cDNA Peking library 12hr SCN3"  
 /notes="Vector: pBluescript SK-; cDNA clones from mRNA extracted from roots of soybean cv. Peking 12 hrs after infection by SCN race 3. These are cloned in pBluescript SK- phagemid."

#### ORIGIN

Query Match 74.2%; Score 17.8; DB 6; Length 542;  
 Best Local Similarity 90.5%; Pred. No. 1.1e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGACGGTCTGAGGGCTTAC 24  
 |||||  
 Db 405 GATACGGTCTGAGGGATTAC 425

#### RESULT 7

BMS20767  
 LOCUS sal30d08.y1 Gm-c1059 Glycine soja cDNA clone SOYBEAN CLONE ID: Gm-c1059-3639 5', similar to SW:DCOR\_DATST P50134 ORNITHINE DECARBOXYLASE ;, mRNA sequence.

#### ACCESSION

VERSION BMS20767  
 KEYWORDS BMS20767.1 GI:18691927  
 SOURCE EST.

#### ORGANISM

Glycine soja  
 Glycine soja  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

#### REFERENCE

1 (bases 1 to 544)  
 Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
 Public Soybean EST Project  
 Unpublished (1999)

#### TITLE

JOURNAL Public Soybean EST Project  
 COMMENT Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 428.

#### FEATURES

Location/Qualifiers

1. .544  
 /organism="Glycine soja"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3848"  
 /clone="SOYBEAN CLONE ID: Gm-c1059-3639"  
 /tissue\_type="Whole seedling, 2 week old, etiolated"  
 /lab\_host="DH10B"  
 /clone\_lib="Gm-c1059"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from 2 week old etiolated whole seedlings of PI468916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA"

fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI- XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed in the laboratory of Dr. Randy Shoemaker at Iowa state university."

## ORIGIN

Query Match 74.2%; Score 17.8; DB 4; Length 544;  
 Best Local Similarity 90.5%; Pred. No. 1.1e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 4 GAGACGGTCTCTGAGGGCTTAC 24  
 |||||  
 Db 290 GATACGGTCTCTGAGGGATTAC 310  
 |||||

## RESULT 8

BQ080425 545 bp mRNA linear EST 05-JUL-2004  
 LOCUS  
 DEFINITION  
 san33a10.y1 Gm-cl084 Glycine max cDNA clone SOYBEAN CLONE ID:  
 Gm-cl084-5420 5' similar to TR:022616 O22616 ORNITHINE  
 DECARBOXYLASE. [1] ; mRNA sequence.

## ACCESSION

BQ080425 GI:19935398

## VERSION

EST.

## KEYWORDS

Glycine max (soybean)

## SOURCE

Glycine max

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.

## REFERENCE

1 (bases 1 to 545)

## AUTHORS

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,  
 Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,  
 Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,  
 Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,  
 Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
 McCann, R., Waterston, R. and Wilson, R.

## TITLE

Public Soybean EST Project

## JOURNAL

Unpublished (1999)

## COMMENT

Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 When it has been determined, an EST from the other end of this  
 clone is listed in the 'Other ESTs on clone' field. This clone is  
 available through: Biogenetic Services, 801 32nd Ave. Brookings, SD  
 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 421.

## FEATURES

Location/Qualifiers

1..545

/organism="Glycine max"

/mol\_type="mRNA"

/cultivar="Williams 82"

/db\_xref="taxon:3847"

/clone="SOYBEAN CLONE ID: Gm-cl084-5420"

/tissue\_type="Etiolated hypocotyls (Williams 82)"

/lab\_host="DH10B"

/clone\_lib="Gm-cl084"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:

XhoI; The cDNA library was constructed by M. Bhattacharya

from mRNA isolated from etiolated hypocotyls from the

cultivar Williams 82. Tissue was inoculated with

Phytophthora soyae race 1 and tissues were harvested 2 and

4 hours following infection. The library is the pool of

these two time points. Complementary DNA was synthesized

from mRNA using a primer consisting of a poly(dT) sequence

with a XhoI restriction site. EcoRI adapters were ligated

## ORIGIN

Query Match 74.2%; Score 17.8; DB 5; Length 545;  
 Best Local Similarity 90.5%; Pred. No. 1.1e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 4 GAGACGGTCTCTGAGGGCTTAC 24  
 |||||  
 Db 151 GATACGGTCTCTGAGGGATTAC 171  
 |||||

## RESULT 9

BQ080423 553 bp mRNA linear EST 05-JUL-2004  
 LOCUS  
 DEFINITION  
 san33a08.y1 Gm-cl084 Glycine max cDNA clone SOYBEAN CLONE ID:  
 Gm-cl084-5416 5' similar to TR:022616 O22616 ORNITHINE  
 DECARBOXYLASE. [1] ; mRNA sequence.

## ACCESSION

BQ080423 GI:19935393

## VERSION

EST.

## KEYWORDS

Glycine max (soybean)

## SOURCE

Glycine max

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.  
 1 (bases 1 to 553)  
 Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,  
 Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,  
 Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,  
 Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,  
 Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
 McCann, R., Waterston, R. and Wilson, R.

## TITLE

Public Soybean EST Project

## JOURNAL

Unpublished (1999)

## COMMENT

Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 When it has been determined, an EST from the other end of this  
 clone is listed in the 'Other ESTs on clone' field. This clone is  
 available through: Biogenetic Services, 801 32nd Ave. Brookings, SD  
 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 422.

## FEATURES

Location/Qualifiers

1..553

/organism="Glycine max"

/mol\_type="mRNA"

/cultivar="Williams 82"

/db\_xref="taxon:3847"

/clone="SOYBEAN CLONE ID: Gm-cl084-5416"

/tissue\_type="Etiolated hypocotyls (Williams 82)"

/lab\_host="DH10B"

/clone\_lib="Gm-cl084"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:

XhoI; The cDNA library was constructed by M. Bhattacharya

from mRNA isolated from etiolated hypocotyls from the

cultivar Williams 82. Tissue was inoculated with

Phytophthora soyae race 1 and tissues were harvested 2 and

4 hours following infection. The library is the pool of

these two time points. Complementary DNA was synthesized

from mRNA using a primer consisting of a poly(dT) sequence

with a XhoI restriction site. EcoRI adapters were ligated

to the blunt-ended cDNA fragments followed by XhoI  
 digestion. The cDNA fragments were directionally cloned  
 into the EcoRI-XhoI restriction site of the pBluescript  
 vector. The ligated cDNA fragments were transformed into  
 DH10B host cells (Gibco BRL). This library was constructed  
 by M. Bhattacharya in the laboratory of Dr. Randy  
 Shoemaker at Iowa State University."

with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by M. Bhattacharya in the laboratory of Dr. Randy Shoemaker at Iowa State University."

## ORIGIN

Query Match 74.2%; Score 17.8; DB 5; Length 553;  
Best Local Similarity 90.5%; Pred. No. 1.1e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGACGGTCTGAGGGCTTAC 24  
|||||  
Db 151 GATACGGTCTGAGGGATTAC 171

## RESULT 10

BM954596 554 bp mRNA linear EST 05-JUL-2004  
LOCUS san08c04.y1 Gm-cl084 Glycine max cDNA clone SOYBEAN CLONE ID:  
DEFINITION Gm-cl084-3199 5' similar to TR:O22616 O22616 ORNITHINE  
DECARBOXYLASE. [1] ;, mRNA sequence.

## ACCESSION

BM954596 GI:19453186

## VERSION

EST.

## KEYWORDS

Glycine max (soybean)

## SOURCE

Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

## REFERENCE

1 (bases 1 to 554)  
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,  
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,  
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,  
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,  
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
McCann, R., Waterson, R. and Wilson, R.  
Public Soybean EST Project

## TITLE

Unpublished (1999)

## JOURNAL

COMMENT

Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)  
Seq primer: -40RP from Gibco  
High quality sequence stop: 421.

## FEATURES

source

1..554  
Location/Qualifiers  
/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="Williams 82"  
/db\_xref="taxon:3847"  
/clone="SOYBEAN CLONE ID: Gm-cl084-3199"  
/tissue\_type="Etiolated hypocotyls (Williams 82)"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl084"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed by M. Bhattacharya from mRNA isolated from etiolated hypocotyls from the cultivar Williams 82. Tissue was inoculated with Phytophthora soyae race 1 and tissues were harvested 2 and 4 hours following infection. The library is the pool of these two time points. Complementary DNA was synthesized

from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by M. Bhattacharya in the laboratory of Dr. Randy Shoemaker at Iowa State University."

## ORIGIN

Query Match 74.2%; Score 17.8; DB 5; Length 554;  
Best Local Similarity 90.5%; Pred. No. 1.1e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGACGGTCTGAGGGCTTAC 24  
|||||  
Db 141 GATACGGTCTGAGGGATTAC 161

## RESULT 11

BM093047 558 bp mRNA linear EST 08-JUL-2004  
LOCUS saj04d03.y1 Gm-cl065 Glycine max cDNA clone GENOME SYSTEMS CLONE  
DEFINITION ID: Gm-cl065-9389 5' similar to SW:DCOR\_DATST P50134 ORNITHINE  
DECARBOXYLASE ;, mRNA sequence.

## ACCESSION

BM093047 GI:17022013

## VERSION

EST.

## KEYWORDS

Glycine max (soybean)

## SOURCE

Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

## REFERENCE

1 (bases 1 to 558)  
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,  
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,  
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,  
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,  
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
McCann, R., Waterson, R. and Wilson, R.  
Public Soybean EST Project

## TITLE

Unpublished (1999)

## JOURNAL

COMMENT

Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)  
High quality sequence stop: 422.

## FEATURES

source

1..558  
Location/Qualifiers  
/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="Williams"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl065-9389"  
/tissue\_type="germinating shoots"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl065"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from germinating shoots of the cultivar Williams. The seeds were allowed to germinate for 24 hours prior to being cold stressed for 2 days at 4C. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI



adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

## ORIGIN

Query Match 74.2%; Score 17.8; DB 4; Length 559;  
Best Local Similarity 90.5%; Pred. No. 1.1e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGACGGTCTGAGGCGCTTAC 24  
|||||

Db 517 GATACGGTCTGAGGCGCTTAC 537  
|||||

## RESULT 12

AG239356/c

## LOCUS

AG239356 591 bp DNA linear GSS 19-JUL-2003  
Lotus corniculatus var. japonicus DNA, clone:UjT04e13\_not, genomic survey sequence.

## ACCESSION

AG239356

## VERSION

AG239356.1 GI:26550193

## KEYWORDS

GSS.

## SOURCE

Lotus corniculatus var. japonicus (Lotus japonicus)

## ORGANISM

Lotus corniculatus var. japonicus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Loteae;  
Lotus.

## REFERENCE

1 Sato, S., Nakamura, Y. and Tabata, S.

## AUTHORS

Lotus japonicus TAC End sequences

## TITLE

Published Only in Database (2002)

## JOURNAL

2 (bases 1 to 591)

## REFERENCE

Sato, S.  
Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,  
The First Laboratory for Plant Gene Research; 2-6-7  
Kazusa-kamata-ri, Kisarazu, Chiba 292-0818, Japan  
(E-mail: ssato@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/,  
Tel: 81-438-52-3935 (ex. 2336), Fax: 81-438-52-3934)

## FEATURES

Location/Qualifiers

1..591

/organism="Lotus corniculatus var. japonicus"

/mol\_type="genomic DNA"

/strain="Miyakojima MG-20"

/variety="japonicus"

/db\_xref="taxon:34305"

/clone="UjT04e13\_not"

/clone\_lib="genomic TAC library"

/notes="VECTOR:pLTTAC7-synonym: Lotus japonicus"

## ORIGIN

Query Match 74.2%; Score 17.8; DB 9; Length 591;  
Best Local Similarity 90.5%; Pred. No. 1.1e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGACGGTCTGAGGCGCTTAC 24  
|||||

Db 122 GAGATGGTCTGAGGCGCTAC 102  
|||||

## RESULT 13

AW309508/c

## LOCUS

AW309508 655 bp mRNA linear EST 16-JUL-2004  
sf20d06.x1 Gm-cl028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
Gm-cl028-516 3', similar to TR:022616 O22616 ORNITHINE  
DECARBOXYLASE. [1], mRNA sequence.

## ACCESSION

AW309508

## VERSION

AW309508.1 GI:6725109

## KEYWORDS

## SOURCE

## ORGANISM

Glycine max (soybean)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

## REFERENCE

## AUTHORS

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,  
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,  
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,  
Bowers, Y., Pearson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,  
Schurk, R., Ritter, E., Kohn, S., Shin, I., Jackson, Y., Cardenas, M.,  
McCann, R., Waterston, R. and Wilson, R.

## TITLE

## JOURNAL

## COMMENT

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this  
clone is listed in the 'Other ESTs on clone' field. This clone is  
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD  
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)  
Insert Length: 1561 Std Error: 0.00  
High quality sequence stop: 457.

## FEATURES

Location/Qualifiers

1..655

/organism="Glycine max"

/mol\_type="mRNA"

/cultivar="Supernod"

/db\_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl028-516"

/tissue\_type="roots of 'Supernod' plants"

/lab\_host="DH10B"

/clone\_lib="Gm-cl028"

/note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:

'Supernod' plants generously donated by Dr. Gary Stacey.

The seedlings were inoculated with Bradyrhizobium

japonicus, strain USDA110 prior to harvest. Stragene's

cDNA synthesis Kit (catalog number 200401) was used to

synthesize the cDNA. First-strand synthesis was performed

with 5-methyl dCTP, hence the ligated cDNA was

hemimethylated. A modification of Stragene's

first-strand synthesis primer was used. An 'anchor'

nucleotide (V=A,C, or G) was added to the 3' end of the

primer [GAGAGAGAGAGAGAGAGAGACTGCTCGAG(T)18V] to anchor

the primer at the 5' end of the poly(A) tract. After

second-strand synthesis, the cDNA ends were filled in with

cloned Pfu DNA polymerase, ligated to EcoRI adapters and

subsequently phosphorylated. The XhoI site within the

first-strand synthesis primer was then restricted by

digestion with XhoI; all XhoI sites in the cDNA would be

protected by their hemimethylated status. The cDNA

constructs were size-fractionated with a 500bp cutoff,

using GibcoBRL Life Technologies' cDNA Size Fractionation

column. The column eluent was then ligated into

Stragene's pBluescript II XR Predigested vector

(pBluescript II SK(+)) that has been digested with EcoRI

and XhoI, and phosphorylated by Stragene). Both the

white and blue colonies appear to contain recombinant

plasmids with cDNA inserts, based on size (n=25). This

library was constructed by Dr. Paul Keim and Dr. Virginia

Coryell."

## ORIGIN

Query Match 74.2%; Score 17.8; DB 2; Length 655;  
Best Local Similarity 90.5%; Pred. No. 1.1e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



detailed information on the source library for each clone can also be obtained by referring to the Incyte Genomics clone ID of the original cDNA library that is also listed under 'OTHER EST'."

**ORIGIN**

Query Match 74.2%; Score 17.8; DB 4; Length 660;  
 Best Local Similarity 90.5%; Pred. No. 1.1e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGACGGTTCTGAGGGCTTAC 24  
 |||||  
 Db 412 GATACGGTTCTGAGGGATTAC 392

**RESULT 14**  
 BI971255/c  
 LOCUS  
 DEFINITION  
 Gm830012B21F02 Gm-r1083 Glycine max cDNA clone Gm-r1083-4492 3', mRNA linear EST 23-OCT-2001  
 mRNA sequence.

ACCESSION  
 VERSION  
 BI971255.1 GI:16345660  
 EST.

KEYWORDS  
 SOURCE  
 ORGANISM  
 Glycine max (soybean)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE  
 1 (bases 1 to 660)  
 Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Coryell, V., Erpelting, J., Raph, C., Shoop, E., Pardini, J., Liu, L. and Lewin, H. A Functional Genomics Program for Soybean (NSF 9872565) Unpublished (1999)

TITLE  
 JOURNAL  
 COMMENT  
 Other ESTs: BE021647 corresponding to Gm-c1028-8322 (5')  
 Contact: Vodkin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)  
 Lewin, H. A., Director, Keck Center for Comparative and Functional Genomics  
 University of Illinois  
 Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA  
 Tel: (217) 244-6147  
 Fax: (217) 333-4582  
 Email: l-vodkin@uiuc.edu

This clone is available through: Incyte Genomics, 4633 World Parkway Circle St. Louis, Missouri 63134. Phone (800) 430-0030 or (314) 427-3222 FAX: (314) 427-3324. Web site: <http://www.incyte.com/reagents/catalog.jsp?page=clones/collaboration/index>

Seq primer: 5'-TTTTTTTTTTTTTTTTT(A/C/G)-3'.

**FEATURES**  
 source  
 Location/Qualifiers  
 1..660  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3847"  
 /clone="Gm-r1083-4492"  
 /clone\_lib="Gm-r1083"  
 /note="The library Gm-r1083 is a sequence-driven, reracked set of 4,992 clones selected from cDNA libraries from various tissues and stages of development of soybean. It represents 1117 sequences from the progenitor library Gm-c1009 (from mature roots of 2 month old greenhouse grown 'Williams' soybean plants); 820 sequences from the progenitor library Gm-c1013 (from 2 to 3 week old whole plants of Williams); and 3055 sequences from library Gm-c1028 (from 'Supernod' plants whose seedlings were inoculated with Bradyrhizobium japonicum, courtesy of Dr. Gary Stacey). The 5' ESTs of the source clones from the different progenitor libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm-r1083. The cDNA clones of the reracked Gm-r1083 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, <http://web.ahc.umn.edu/biodata/nsfsoy/>.  
 Reracking was performed by Incyte Genomics, St. Louis, <http://www.incyte.com>, and 3' sequencing by the Keck Center for Comparative and Functional Genomics, University of Illinois, <http://www.lie.uiuc.edu/biotech/keck.html>.  
 Note: The corresponding 5' EST from each clone in the Gm-r1083 library is listed in the 'OTHER EST' field. The

**ORIGIN**

Query Match 74.2%; Score 17.8; DB 7; Length 715;  
 Best Local Similarity 90.5%; Pred. No. 1.1e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCT 21  
 |||||  
 Db 27 TCCGAGACGGTTCTGAGGGGT 7

**RESULT 16**  
 BI971148/c  
 LOCUS  
 DEFINITION  
 Gm830012B10F02 Gm-r1083 Glycine max cDNA clone Gm-r1083-4491 3', mRNA linear EST 23-OCT-2001  
 mRNA sequence.

ACCESSION  
 VERSION  
 BI971148.1 GI:16345553  
 EST.

**FEATURES**  
 source  
 Location/Qualifiers  
 1..715  
 /organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9823"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 4PIG"  
 /note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI; Library made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."

SOURCE Glycine max (soybean)  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 REFERENCE 1 (bases 1 to 761)  
 AUTHORS Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Coryell, V., Erpelind, J., Raph, C., Shoop, E., Pardini, J., Liu, L. and Lewin, H. A Functional Genomics Program for Soybean (NSF 9872565)  
 TITLE Unpublished (1999)  
 JOURNAL Other ESTs: BE057453 corresponding to Gm-cl028-8092 (5')  
 COMMENT Contact: Vodkin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)  
 Lewin, H. A., Director, Keck Center for Comparative and Functional Genomics  
 University of Illinois  
 Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA  
 Tel: (217) 244-6147  
 Fax: (217) 333-4582  
 Email: l-vodkin@uiuc.edu  
 This clone is available through: Incyte Genomics, 4633 World Parkway Circle St. Louis, Missouri 63134. Phone (800) 430-0030 or (314) 427-3222 FAX: (314) 427-3324. Web site: http://www.incyte.com/reagents/catalog.jsp?page=clones/collaboration/index  
 Seq primer: 5'-TTTTTTTTTTTTTTTTTTT(A/C/G)-3'.  
 Location/Qualifiers  
 1..761  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3847"  
 /clone="Gm-r1083-4491"  
 /clone\_lib="Gm-r1083"  
 /note="The library Gm-r1083 is a sequence-driven, reracked set of 4,992 clones selected from cDNA libraries from various tissues and stages of development of soybean. It represents 1117 sequences from the progenitor library Gm-cl009 (from mature roots of 2 month old greenhouse grown 'Williams' soybean plants); 820 sequences from the progenitor library Gm-cl013 (from 2 to 3 week old whole plants of Williams); and 3055 sequences from library Gm-cl028 (from 'Supernod' plants whose seedlings were inoculated with Bradyrhizobium japonicum, courtesy of Dr. Gary Stacey). The 5' ESTs of the source clones from the different progenitor libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm-r1083. The cDNA clones of the reracked Gm-r1083 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://web.ahc.umn.edu/biodata/nsfsoy/. Reracking was performed by Incyte Genomics, St. Louis, Center for Comparative and Functional Genomics, University of Illinois, http://www.lie.uiuc.edu/biotech/keck.html. Note: The corresponding 5' EST from each clone in the Gm-r1083 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Incyte Genomics clone ID of the original cDNA library that is also listed under 'OTHER EST'."

FEATURES  
source

1..796  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="breed: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_45603"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 74.2%; Score 17.8; DB 4; Length 761;  
 Best Local Similarity 90.5%; Pred. No. 1.1e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 GAGACGGTTCGAGGGCTTAC 24  
 |||  
 Db 373 GATACGGTTCGAGGGATTC 353  
 |||

RESULT 17  
CC577625  
LOCUS

## DEFINITION

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISMREFERENCE  
AUTHORSTITLE  
JOURNAL  
COMMENTFEATURES  
source

1..796  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="breed: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_45603"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 74.2%; Score 17.8; DB 9; Length 796;  
 Best Local Similarity 90.5%; Pred. No. 1.1e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 CGAGACGGTTCGAGGGCTTA 23  
 |||  
 Db 621 CGGACGGTTCGAGGGTTTA 641  
 |||

RESULT 18  
AW349137/c

## LOCUS

## DEFINITION

ACCESSION  
VERSION  
KEYWORDS

CC577625 796 bp DNA linear GSS 18-JUN-2003  
 CH240\_45603.TARBAC13P2 CHORI-240 Bos taurus genomic clone  
 CH240\_45603, genomic survey sequence.  
 CC577625 1 GI:31921484  
 CC577625 Bos taurus (cow)  
 GSS.  
 Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 796)  
 Holt, R., Stott, J., Yang, G., Barber, S., Smaluis, D., Prabhu, A.-L., Tsai, M., Cloutier, A., Lee, D., Girm, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., de Jong, P., Keele, J.W. and Kappes, S.M.  
 Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478  
 Unpublished (2003)  
 Other GSSs: CH240\_45603.T7  
 Contact: Rob Holt  
 Sequencing  
 The British Columbia Cancer Agency Genome Science Centre  
 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6  
 Tel: 604-877-6085  
 Fax: 604-877-6276  
 Email: rholt@bcgsc.ca  
 Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering/information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.  
 Plate: 456 row: O column: 3  
 Seq primer: SP6  
 Class: BAC ends.  
 Location/Qualifiers  
 1..796  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="breed: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_45603"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

Query Match 74.2%; Score 17.8; DB 9; Length 796;  
 Best Local Similarity 90.5%; Pred. No. 1.1e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 CGAGACGGTTCGAGGGCTTA 23  
 |||  
 Db 621 CGGACGGTTCGAGGGTTTA 641  
 |||



Email: szhao@tigr.org  
 Clones are derived from the rat BAC library CHORI-230  
 (http://www.chori.org/bacpac/rat230.htm). For BAC library  
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/or\_ering\_information.htm). BAC end  
 page: http://www.tigr.org/tdb/bac\_ends/rat/bac\_end\_intro.html  
 Plate: 348 row: J column: 2  
 Seq primer: T7  
 Class: BAC ends.

**FEATURES**  
 source  
 Location/Qualifiers  
 1..1028  
 /organism="Rattus norvegicus"  
 /mol\_type="genomic DNA"  
 /strain="BN/SENHsd/MCW"  
 /db\_xref="taxon:10116"  
 /clone="CH230-348J2"  
 /sex="Female"  
 /cell\_type="Brain"  
 /clone\_lib="CHORI-230 Segment 2"  
 /note="Vector: pTARBAC1.3; Site\_1: MboI; Site\_2: MboI;  
 CHORI-230 Rat (BN/SENHsd/MCW) BAC library produced by  
 Pieter de Jong"

**ORIGIN**

Query Match 74.2%; Score 17.8; DB 8; Length 1028;  
 Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GAGACGGTTCTGAGGGCTTAC 24  
 ||||| ||||| ||||| ||||| |||||  
 Db 207 GAGACAGATCTGAGGGCTTAC 187

**RESULT 21**

CNS03040  
 LOCUS  
 DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone  
 183122 of library G from Tetraodon nigroviridis, genomic survey  
 sequence.

ACCESSION AL221793.1 GI:7880612  
 VERSION GSS; genome survey sequence.  
 KEYWORDS Tetraodon nigroviridis  
 SOURCE Tetraodon nigroviridis  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 Tetraodontidae; Tetraodontidae; Tetraodon.

**REFERENCE**

1 Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,  
 Bernot, A., Fzames, C., Wincker, P., Brottier, P., Quetier, F.,  
 Saurin, W., and Weissenbach, J.  
 Estimate of human gene number provided by genome-wide analysis  
 using Tetraodon nigroviridis DNA sequence  
 Nat. Genet. 25 (2), 235-238 (2000)

**JOURNAL**

MEDLINE 20296633  
 PUBMED 10835645

**REFERENCE**

2 Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,  
 Fzames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,  
 Saurin, W., Bernot, A., and Weissenbach, J.  
 Characterization and repeat analysis of the compact genome of the  
 freshwater pufferfish Tetraodon nigroviridis  
 Genome Res. 10 (7), 939-949 (2000)

**JOURNAL**

MEDLINE 20329837  
 PUBMED 10899143

**REFERENCE**

3 (bases 1 to 1058)  
 Genoscope.  
 Direct Submission  
 Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)

**COMMENT**

This sequence is a single read and was generated as part of a large  
 scale clone-end sequencing project of the Tetraodon nigroviridis  
 genome. For more information, please take a look at  
 http://www.genoscope.cns.fr/Tetraodon.

**FEATURES**

## source

Location/Qualifiers  
 1..1058  
 /organism="Tetraodon nigroviridis"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:99883"  
 /clone="183L22"  
 /clone\_lib="G"  
 /note="Genoscope sequence ID : COAG183DF11LP1-end : T7"

**ORIGIN**

Query Match 74.2%; Score 17.8; DB 9; Length 1058;  
 Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TCCGACGCGTTCGTGAGGCT 21  
 ||||| ||||| ||||| ||||| |||||  
 Db 271 TCCGACACAGTTCTGAGGCT 291

**RESULT 22**

CL199305  
 LOCUS  
 DEFINITION ZMMBBc007101lr ZMMBBc (EcoRI) Zea mays genomic clone ZMMBBc007101l  
 3', genomic survey sequence.

ACCESSION CL199305  
 VERSION CL199305.1 GI:40711831  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 257)

AUTHORS Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,  
 Zohovetz, V., Fuks, G., Yu, Y., Wing, R., and Messing, J.  
 Sequencing of the maize genome at PGIR (2003c)  
 Unpublished (2003)  
 Contact: Bharti, A.K.  
 Dr. Joachim Messing's lab  
 The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
 University  
 190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
 Tel: 732 445 3801  
 Fax: 732 445 5735  
 Email: bharti@waksman.rutgers.edu

Seq primer: SP6  
 Class: BAC ends

High quality sequence start: 155.

Location/Qualifiers

1..257

/organism="Zea mays"

/mol\_type="genomic DNA"

/cultivar="B73"

/db\_xref="taxon:4577"

/clone="ZMMBBc007101l"

/lab\_host="E. coli DH10B"

/clone\_lib="ZMMBBc (EcoRI)"

/note="Vector: pTARBAC2.1; Site\_1: EcoRI; Site\_2: EcoRI"

**FEATURES**

## source

Location/Qualifiers

1..257

/organism="Zea mays"

/mol\_type="genomic DNA"

/cultivar="B73"

/db\_xref="taxon:4577"

/clone="ZMMBBc007101l"

/lab\_host="E. coli DH10B"

/clone\_lib="ZMMBBc (EcoRI)"

/note="Vector: pTARBAC2.1; Site\_1: EcoRI; Site\_2: EcoRI"

Query Match 73.3%; Score 17.6; DB 9; Length 257;  
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TCCGACGCGTTCGTGAGGCTTAC 24  
 ||||| ||||| ||||| ||||| |||||  
 Db 23 TACGTGACGCTTCGTGGGGCGTAC 46

```

RESULT 23
AA193764/c
LOCUS
DEFINITION
r802f12.r1 Sommer Pristionchus Pristionchus pacificus cDNA clone
456 5' similar to WP:C06A1.1 CE02114 PROTEIN P97 ;, mRNA sequence.
ACCESSION
AA193764
VERSION
AA193764.1 GI:11783443
KEYWORDS
EST.
SOURCE
Pristionchus pacificus
ORGANISM
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 311)
AUTHORS
McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tsagarisvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
CONTACT: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estowatson.wustl.edu
Contact Dr. Ralf Sommer (sorra@mail.mpiib-tuebingen.mpg.de) for
information about this clone.
High quality sequence stop: 293.
FEATURES
source
1..311
/organism="Pristionchus pacificus"
/mol_type="mRNA"
/strain="PS 312"
/db_xref="taxon:54126"
/clonetype="456"
/sex="predominantly hermaphroditic"
/dev_stage="mixed stages (embryo to adult)"
/lab_host="not applicable (host cell line)"
/clone_lib="Sommer Pristionchus"
/notes="Vector: Uni-ZAP XR Vector (Stratagene); Site 1: 5'
EcoRI; Site 2: 3' XhoI; 1st strand cDNA was primed with a
XhoI - oligo(dT) primer. Double-stranded cDNA was ligated
to EcoRI adaptors digested with XhoI and cloned into XhoI
and EcoRI sites. Primary complexity of the library was 10
in the 7th. The library went through one round of
amplification."
ORIGIN
Query Match 73.3%; Score 17.6; DB 1; Length 311;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TCCGAGACGGTCTGAGGCGCTTAC 24
|||||
Db 44 TCCGAGACGGATCTGCGGCAAC 21

RESULT 24
AI986900/c
LOCUS
DEFINITION
AI986900 380 bp mRNA linear EST 10-MAY-2001
r819a09.y1 Sommer Pristionchus Pristionchus pacificus cDNA 5'
similar to WP:C06A1.1 CE02114 TRANSITIONAL ENDOPLASMIC RETICULUM
ATPASE HOMOLOG 1 ;, mRNA sequence.
ACCESSION
AI986900
VERSION
AI986900.1 GI:5815984
KEYWORDS
EST.
SOURCE
Pristionchus pacificus
ORGANISM
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

```

```

Neodiplogasteridae; Pristionchus.
1 (bases 1 to 380)
AUTHORS
McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tsagarisvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
CONTACT: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estowatson.wustl.edu
The library was constructed by Dr. Ralf Sommer DNA Sequencing by:
Washington University Genome Sequencing Center
Contact Dr. Ralf Sommer (ralf.sommer@tuebingen.mpg.de) for
information about this clone.
Seq primer: -40RP from Gibco
High quality sequence stop: 373.
FEATURES
source
1..380
/organism="Pristionchus pacificus"
/mol_type="mRNA"
/strain="PS 312"
/db_xref="taxon:54126"
/sex="predominantly hermaphroditic"
/dev_stage="mixed stages (embryo to adult)"
/lab_host="not applicable (host cell line)"
/clone_lib="Sommer Pristionchus"
/notes="Vector: Uni-ZAP XR Vector (Stratagene); Site 1: 5'
EcoRI; Site 2: 3' XhoI; 1st strand cDNA was primed with a
XhoI - oligo(dT) primer. Double-stranded cDNA was ligated
to EcoRI adaptors digested with XhoI and cloned into XhoI
and EcoRI sites. Primary complexity of the library was 10
in the 7th. The library went through one round of
amplification."
ORIGIN
Query Match 73.3%; Score 17.6; DB 1; Length 380;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TCCGAGACGGTCTGAGGCGCTTAC 24
|||||
Db 155 TCCGAGACGGATCTGCGGCAAC 132

RESULT 25
B26775/c
LOCUS
DEFINITION
B26775 TAMU Arabidopsis thaliana genomic clone TIC12, genomic
survey sequence.
ACCESSION
B26775
VERSION
B26775.1 GI:2512741
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 403)
REFERENCE
1 (bases 1 to 403)
AUTHORS
Rounsley, S.D., Kelley, J.M., Field, C.E., Craven, M.B., Adams, M.D. and
Venter, J.C.
Use of a BAC End Sequence Database To Identify Minimal Overlaps for
Arabidopsis Genomic Sequencing
Unpublished (1997)
Other GSSs: TIC12TF
CONTACT: Steve Rounsley

```

Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: rounseley@tigr.org  
Seq primer: M13 Reverse  
Class: BAC ends  
High quality sequence stop: 403.

FEATURES  
source  
1. .403  
Location/Qualifiers

/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Columbia"  
/db\_xref="taxon:3702"  
/clone="T1C12"  
/sex="hermaphrodite"  
/clone\_lib="TAMU"  
/notes="Vector: BelOBACII; Site 1: HindIII; Site 2:  
HindIII; Produced by Rod Wing"

## ORIGIN

Query Match 73.3%; Score 17.6; DB 8; Length 403;  
Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 TCCGACGCGTCTGAGGCTTAC 24  
Db 162 TCCAGTCGCTTGTGAGGCTAC 139

## RESULT 26

BQ292360  
LOCUS BQ292360 435 bp mRNA linear EST 15-MAY-2002  
DEFINITION PM2-AN0089-021200-012-b09 AN0089 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BQ292360  
VERSION BQ292360.1 GI:20801310  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 435)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20020663  
10737800  
PUBMED  
CONTACT: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM2&t2=PM2-AN0089-  
021200-012-b09&t3=2000-12-02&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 5  
High quality sequence stop: 45.

## FEATURES

source  
1. .435  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"

## ORIGIN

Query Match 73.3%; Score 17.6; DB 5; Length 435;  
Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 TCCGACGCGTCTGAGGCTTAC 24  
Db 341 TTCGAGCGCTTGTGAGGCTTAC 364

## RESULT 27

AW097360/c  
LOCUS AW097360 465 bp mRNA linear EST 10-MAY-2001  
DEFINITION rs4207.y1 Sommer Pristionchus Pristionchus pacificus CDNA 5'  
similar to WP:C41C4.8 CE05402 TRANSITIONAL ENDOPLASMIC RETICULUM  
ATPASE HOMOLOG 2 ;, mRNA sequence.

ACCESSION AW097360  
VERSION AW097360.1 GI:6067671  
KEYWORDS EST.  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.

## REFERENCE

AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,  
Wyllie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,  
Tsagarisshvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,  
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
McCann,R., Waterston,R. and Wilson,R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)  
CONTACT: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

## TITLE

JOURNAL  
COMMENT  
The library was constructed by Dr. Ralf Sommer DNA Sequencing by:  
Washington University Genome Sequencing Center  
Contact Dr. Ralf Sommer (ralf.sommer@uebingen.mpg.de) for  
information about this clone.  
Seq primer: -40RP from Gibco  
High quality sequence stop: 395.

## FEATURES

source  
1. .465  
Location/Qualifiers  
/organism="Pristionchus pacificus"  
/mol\_type="mRNA"  
/strain="PS 312"  
/db\_xref="taxon:54126"  
/sex="predominantly hermaphroditic"  
/dev\_stages="mixed stages (embryo to adult)"  
/lab\_host="not applicable (host cell line)"  
/clone\_lib="Sommer Pristionchus"  
/note="Vector: Uni-Zap XR Vector (Stratagene); Site 1: 5'  
EcoRI; Site 2: 3' XhoI; 1st strand cDNA was primed with a  
XhoI - oligo(dT) primer. Double-stranded cDNA was ligated  
to EcoRI adaptors digested with XhoI and cloned into XhoI  
and EcoRI sites. Primary complexity of the library was 10  
in the 7th. The library went through one round of

/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="AN0089"  
/note="Organ: amnion\_normal; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## amplification."

## ORIGIN

Query Match 73.3%; Score 17.6; DB 2; Length 465;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTAC 24  
 |||||  
 DB 436 TCCGAGACGGATCTGCGGCAAC 413

## RESULT 28

BU467230

## LOCUS

DEFINITION 603372043F1 CSQRBN20 Gallus gallus cdna clone CHEST280e12 5', mRNA

## ACCESSION

BU467230

## VERSION

EST.

## KEYWORDS

Gallus gallus (chicken)

## SOURCE

Gallus gallus

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 517)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,

Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)

22335534

12445392

COMMENT

Contact: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

1. .517

/organism="Gallus gallus"

/mol\_type="mRNA"

/strain="Layer and broiler"

/db\_xref="taxon:9031"

/clone="CHEST280e12"

/sex="Male and female"

/tissue\_type="Chondrocytes isolated from growth plate

cartilage"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="CSQRBN20"

/notes="Vector: pBluescript II KS(+); Site\_1: EcoRI;

Site\_2: NotI; this normalized library was constructed from

1 million independent clones. cDNA synthesis was initiated

using an oligo(dT) primer, using methylated C in the first

strand synthesis reaction. Following this first strand

reaction, double-stranded cDNA was blunted, ligated to

NotI adapters, digested with EcoRI, size-selected, and

cloned into the NotI and EcoRI compatible sites of a

custom modified MCS of the pBluescript (KS+) vector. The

library was normalized in 2 rounds using conditions

adapted from Soares et al., PNAS (1994) 91: 9228-9232 and

Bonald et al., Genome Research 6 (1996): 791, except that

a significantly longer reannealing hybridization was

used."

## ORIGIN

Query Match

Best Local Similarity

Matches

20; Conservative

0; Mismatches

4; Indels

0; Gaps

0;

## QY

BU468159

## LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

1. .517

/organism="Gallus gallus"

/mol\_type="mRNA"

/strain="Layer and broiler"

/db\_xref="taxon:9031"

/clone="CHEST284e24"

/sex="Male and female"

/tissue\_type="Chondrocytes isolated from growth plate

cartilage"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="CSQRBN20"

/notes="Vector: pBluescript II KS(+); Site\_1: EcoRI;

Site\_2: NotI; this normalized library was constructed from

1 million independent clones. cDNA synthesis was initiated

using an oligo(dT) primer, using methylated C in the first

strand synthesis reaction. Following this first strand

reaction, double-stranded cDNA was blunted, ligated to

NotI adapters, digested with EcoRI, size-selected, and

cloned into the NotI and EcoRI compatible sites of a

custom modified MCS of the pBluescript (KS+) vector. The

library was normalized in 2 rounds using conditions

adapted from Soares et al., PNAS (1994) 91: 9228-9232 and

Bonald et al., Genome Research 6 (1996): 791, except that

a significantly longer reannealing hybridization was

used."

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used."



```

/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL418120ex"
/tissue_type="anterior neuroectoderm"
/dev_stage="late gastrula (stage 12.5)"
/clone_lib="Osada Taira anterior neuroectoderm (ANE)
PC3105 cDNA library".

```



## ORIGIN

Query Match 73.3%; Score 17.6; DB 5; Length 586;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCTGAGGGCTTAC 24  
 |||||  
 Db 578 TCCGAGACGGTTCTGCGGGGTGAC 555

## RESULT 33

AQ979046  
 LOCUS  
 DEFINITION AQ979046 601 bp DNA linear GSS 29-JAN-2000  
 genomic survey sequence.  
 ACCESSION AQ979046  
 VERSION  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 601)  
 AUTHORS Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,  
 Akinret,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de  
 Jong,P. and Fraser,C.M.  
 Mouse BAC End Sequences from Library RPCI-23  
 Other\_GSSs: RPCI-23-341H6.TJ  
 Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: szhao@tigr.org  
 Clones are derived from the mouse BAC library RPCI-23. For BAC  
 library availability, please contact Pieter de Jong  
 (pieterdejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)  
 or from Resea ch Genetics (info@resgen.com). BAC end page:  
[http://www.tigr.org/tdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html)  
 Plate: 341 row: H column: 6  
 Seq primer: T7  
 Class: BAC ends.

## FEATURES

source  
 Location/Qualifiers  
 1..601  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="RPCI-23-341H6"  
 /sex="Female"  
 /lab\_host="DH10B"  
 /clone\_lib="RPCI-23"  
 /notes="Organ: Kidney/Brain; Vector: pBACE3.6; Site 1:  
 EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney\_and/or  
 brain genomic DNA was isolated and partially digested  
 with a combination of EcoRI and EcoRI Methyase. Site  
 selected DNA was cloned into the pBACE3.6 vector at the  
 EcoRI sites. The ligation products were transformed into  
 DH10B electrocompetent cells (BRL Life Technologies)."

## ORIGIN

Query Match 73.3%; Score 17.6; DB 8; Length 601;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCTGAGGGCTTAC 24  
 |||||  
 Db 288 TCAGAGACTGTTCTGAGGGCAGAC 311

## RESULT 34

CD734101  
 LOCUS  
 DEFINITION CD734101 612 bp mRNA linear EST 26-JUN-2003  
 clone lGAL\_19123 5', mRNA sequence.  
 ACCESSION CD734101  
 VERSION  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 612)  
 AUTHORS Min,W., Lillehoj,H.S., Ashwell,C.M., Matukumalli,L.K., van  
 Tassel,C. and Han,J.Y.  
 Chicken intestinal lymphocyte EST database as a resource for the  
 analysis of mucosal immune function  
 Unpublished (2003)  
 JOURNAL Contact: Hyun S. Lillehoj  
 COMMENT Animal Parasite Diseases Laboratory  
 Animal and Natural Resources Institute, USDA  
 Bldg-1043, BARC-East, Beltsville, MD 20705, USA  
 Tel: 3015048771  
 Fax: 3015045103  
 Email: hlilleho@anri.barc.usda.gov  
 Single pass sequencing. Bases called and trimmed with phred  
 0.000925 using options -trim\_alt -trim\_fasta. Vector identified  
 by cross\_match using options -minmatch 12 -minscore 18  
 Plate: 19 row: I column: 23  
 Seq primer: ATTTAGTGACACTATAG  
 High quality sequence stop: 612.

## FEATURES

source  
 Location/Qualifiers  
 1..612  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="white leghorn SC"  
 /db\_xref="taxon:9031"  
 /clone="lGAL\_19123"  
 /sex="mixed"  
 /tissue\_type="Gut"  
 /cell\_type="Lymphocyte"  
 /dev\_stage="Adult"  
 /lab\_host="EMDH10B"  
 /clone\_lib="lGAL - Chicken Intestinal Lymphocyte"  
 /note="Organ: Intestine; Vector: pCMV-SPORT6; Site 1:  
 SalI; Site 2: NotI; Normalized library from chicken gut  
 infected with coccidia duodenum and middle gut."

## ORIGIN

Query Match 73.3%; Score 17.6; DB 6; Length 612;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCTGAGGGCTTAC 24  
 |||||  
 Db 516 TCCAGAGTGTCTGAGGGCTTTC 539

## RESULT 35

BU290274  
 LOCUS  
 DEFINITION BU290274 642 bp mRNA linear EST 27-NOV-2002  
 604166906F1 CSEQCHN55 Gallus gallus cdna clone Chest102712 5', mRNA  
 sequence.  
 ACCESSION BU290274  
 VERSION BU290274.1 GI:25739730  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.

1 (bases 1 to 642)  
Boardman, P. B., Sanz-Esquerro, J., Overton, I. M., Burt, D. W., Bosch, E.,  
Fong, W. T., Tickle, C., Brown, W. R. A., Wilson, S. A. and Hubbard, S. J.  
A Comprehensive Collection of Chicken CDNA's  
Curr Biol. 12 (22), 1965-1969 (2002)  
22335534  
MEDLINE  
12445392  
PUBMED  
Contact: Simon Hubbard

Department of Promotional Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)

FEATURES  
Location/Qualifiers  
1 542  
Email: SIMON.HUBBARD@umist.ac.uk.

| ORIGIN                               |        |                    |            |             |    |        |    |      |    |
|--------------------------------------|--------|--------------------|------------|-------------|----|--------|----|------|----|
| reannealing hybridization was used." |        |                    |            |             |    |        |    |      |    |
| Query Match                          | 73.3%  | Score 17.6;        | DB 5;      | Length 642; |    |        |    |      |    |
| Best Local Similarity                | 83.3%; | Pred. No. 1.4e+03; |            |             |    |        |    |      |    |
| Matches                              | 20;    | Conservative       | 0;         | Mismatches  | 4; | Indels | 0; | Gaps | 0; |
| OY                                   | 1      | TCCGAGACGGTTC      | TGAGGCTTAC | 24          |    |        |    |      |    |
|                                      |        |                    |            |             |    |        |    |      |    |
| Db                                   | 492    | TCCCAGGTGTTCT      | GAGGCTTTC  | 515         |    |        |    |      |    |

RESULT 36  
 BU360919  
 LOCUS  
 DEFINITION  
 BU360919  
 ACCESSION  
 BU360919  
 VERSION  
 BU360919.1  
 GI:25868920  
 EST  
 Gallus gallus (chicken)  
 SOURCE  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

REFERENCE  
1. Hubbard, S.J., and Burt, D.W. (1964)  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
PUBLISHED  
12445392  
CONTACT: Simon Hubbard  
Department of Biomolecular Sciences  
University of Cambridge  
1. and Burt, D.W. (1964)  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
PUBLISHED  
12445392  
CONTACT: Simon Hubbard  
Department of Biomolecular Sciences  
University of Cambridge

University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

**FEATURES**  
**SOURCE**

## ORIGIN

```

Query Match      73.3%; Score 17.6; DB 5; Length 664;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGCGTTAC 24
Db 415 TCCGAGGTGGTTCTGAGGCGTTTC 438

```

|            |   |
|------------|---|
| RESULT     | 37  |
| BU455179   |   |
| LOCUS      |   |
| DEFINITION |   |
| ACCESSION  | BU455179  |
| VERSION    | BU455179  |
| KEYWORDS   | EST.  |
| SOURCE     | Gallus gallus (chicken)   |
| ORGANISM   | Gallus gallus   |
|            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
|            | Archosauia; Aves; Neognathae; Galliformes; Phasianidae;           |
|            | Phasianinae; Gallus.  |
| REFERENCE  | 1 (bases 1 to 674)  |

1. *Thalassidroma*, *Caprimulgus*,  
Boardman, P. E. Szlez, Ezquerro J., Overton, I. M., Burt, D. W., Bosch, E.,  
Pong, W. T., Tickle, C., Brown, R. A., Wilson, S. A. and Hubbard, S. J.  
A Comprehensive Collection of Chicken cDNAs  
*Curr. Biol.* 12 (22), 1965-1969 (2002)  
22335534  
JOURNAL MEDLINE  
PUBMED  
Contact: Simon Hubbard

|     | FEATURES    | SOURCE |
|-----|-------------|--------|
| 1   | 100% Cotton | 100%   |
| 2   | 100% Cotton | 100%   |
| 3   | 100% Cotton | 100%   |
| 4   | 100% Cotton | 100%   |
| 5   | 100% Cotton | 100%   |
| 6   | 100% Cotton | 100%   |
| 7   | 100% Cotton | 100%   |
| 8   | 100% Cotton | 100%   |
| 9   | 100% Cotton | 100%   |
| 10  | 100% Cotton | 100%   |
| 11  | 100% Cotton | 100%   |
| 12  | 100% Cotton | 100%   |
| 13  | 100% Cotton | 100%   |
| 14  | 100% Cotton | 100%   |
| 15  | 100% Cotton | 100%   |
| 16  | 100% Cotton | 100%   |
| 17  | 100% Cotton | 100%   |
| 18  | 100% Cotton | 100%   |
| 19  | 100% Cotton | 100%   |
| 20  | 100% Cotton | 100%   |
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| 23  | 100% Cotton | 100%   |
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| 27  | 100% Cotton | 100%   |
| 28  | 100% Cotton | 100%   |
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| 30  | 100% Cotton | 100%   |
| 31  | 100% Cotton | 100%   |
| 32  | 100% Cotton | 100%   |
| 33  | 100% Cotton | 100%   |
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| 35  | 100% Cotton | 100%   |
| 36  | 100% Cotton | 100%   |
| 37  | 100% Cotton | 100%   |
| 38  | 100% Cotton | 100%   |
| 39  | 100% Cotton | 100%   |
| 40  | 100% Cotton | 100%   |
| 41  | 100% Cotton | 100%   |
| 42  | 100% Cotton | 100%   |
| 43  | 100% Cotton | 100%   |
| 44  | 100% Cotton | 100%   |
| 45  | 100% Cotton | 100%   |
| 46  | 100% Cotton | 100%   |
| 47  | 100% Cotton | 100%   |
| 48  | 100% Cotton | 100%   |
| 49  | 100% Cotton | 100%   |
| 50  | 100% Cotton | 100%   |
| 51  | 100% Cotton | 100%   |
| 52  | 100% Cotton | 100%   |
| 53  | 100% Cotton | 100%   |
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| 55  | 100% Cotton | 100%   |
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| 59  | 100% Cotton | 100%   |
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| 61  | 100% Cotton | 100%   |
| 62  | 100% Cotton | 100%   |
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| 69  | 100% Cotton | 100%   |
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| 72  | 100% Cotton | 100%   |
| 73  | 100% Cotton | 100%   |
| 74  | 100% Cotton | 100%   |
| 75  | 100% Cotton | 100%   |
| 76  | 100% Cotton | 100%   |
| 77  | 100% Cotton | 100%   |
| 78  | 100% Cotton | 100%   |
| 79  | 100% Cotton | 100%   |
| 80  | 100% Cotton | 100%   |
| 81  | 100% Cotton | 100%   |
| 82  | 100% Cotton | 100%   |
| 83  | 100% Cotton | 100%   |
| 84  | 100% Cotton | 100%   |
| 85  | 100% Cotton | 100%   |
| 86  | 100% Cotton | 100%   |
| 87  | 100% Cotton | 100%   |
| 88  | 100% Cotton | 100%   |
| 89  | 100% Cotton | 100%   |
| 90  | 100% Cotton | 100%   |
| 91  | 100% Cotton | 100%   |
| 92  | 100% Cotton | 100%   |
| 93  | 100% Cotton | 100%   |
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| 95  | 100% Cotton | 100%   |
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| 97  | 100% Cotton | 100%   |
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| 100 | 100% Cotton | 100%   |



reannealing hybridization was used."

## ORIGIN

Query Match 73.3%; Score 17.6; DB 5; Length 710;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGCGTTAC 24  
 |||||  
 Db 277 TCCAGGTGGTCTGAGGCGTTTC 300

RESULT 40  
 BU233904  
 LOCUS  
 DEFINITION 603410086F1 CSEQCHN24 Gallus gallus mRNA linear EST 26-NOV-2002  
 sequence.  
 ACCESSION BU233904  
 VERSION BU233904.1 GI:25477968  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus

REFERENCE  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 743)  
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
 A Comprehensive Collection of Chicken cDNAs  
 Curr. Biol. 12 (22), 1965-1969 (2002)  
 22335534  
 PUBMED 12445392

COMMENT  
 Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

source

1. 743  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn, Hisex"  
 /db\_xref="taxon:9031"  
 /clone="CHEST325121"  
 /dev\_stage="22"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQCHN24"  
 /note="Organ: heads; Vector: pBluescript II KS(+); Site\_1:  
 EcoRI; Site\_2: NotI; This normalized library was  
 constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dT) primer, using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand reaction, double-stranded cDNA  
 was blunted, ligated to NotI adapters, digested with  
 EcoRI, size-selected, and cloned into the NotI and EcoRI  
 compatible sites of a custom modified MCS of the  
 pBluescript (KS+) vector. The library was normalized in 2  
 rounds using conditions adapted from Soares et al., PNAS  
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
 (1996): 791, except that a significantly longer  
 reannealing hybridization was used."

## ORIGIN

Query Match 73.3%; Score 17.6; DB 5; Length 743;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGCGTTAC 24  
 |||||  
 Db 315 TCCAGGTGGTCTGAGGCGTTTC 338

RESULT 41  
 BU307797

LOCUS  
 DEFINITION 60339776F1 CSEQCHN60 Gallus gallus mRNA linear EST 28-NOV-2002  
 sequence.  
 ACCESSION BU307797  
 VERSION BU307797  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus

## REFERENCE

1 (bases 1 to 770)  
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
 A Comprehensive Collection of Chicken cDNAs  
 Curr. Biol. 12 (22), 1965-1969 (2002)  
 22335534  
 PUBMED 12445392

## AUTHORS

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

## TITLE

A Comprehensive Collection of Chicken cDNAs

## JOURNAL

Curr. Biol. 12 (22), 1965-1969 (2002)

## MEDLINE

22335534

## PUBMED

12445392

## COMMENT

Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

source

1. 770  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Compton Line 151"  
 /db\_xref="taxon:9031"  
 /clone="CHEST507919"  
 /sex="Female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQCHN60"  
 /note="Organ: heart; Vector: pBluescript II KS(+); Site\_1:  
 EcoRI; Site\_2: NotI; This normalized library was  
 constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dT) primer, using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand reaction, double-stranded cDNA  
 was blunted, ligated to NotI adapters, digested with  
 EcoRI, size-selected, and cloned into the NotI and EcoRI  
 compatible sites of a custom modified MCS of the  
 pBluescript (KS+) vector. The library was normalized in 2  
 rounds using conditions adapted from Soares et al., PNAS  
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
 (1996): 791, except that a significantly longer  
 reannealing hybridization was used."

## ORIGIN

Query Match 73.3%; Score 17.6; DB 5; Length 770;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGCGTTAC 24  
 |||||  
 Db 337 TCCAGGTGGTCTGAGGCGTTTC 360

RESULT 42

BU456386

LOCUS

DEFINITION 603217494F1 CSEQCHN14 Gallus gallus mRNA linear EST 29-NOV-2002

sequence.

ACCESSION BU456386

VERSION BU456386.1 GI:25945697

# KEYWORDS SOURCE ORGANISM

EST.  
Gallus gallus (chicken)  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

## REFERENCE

AUTHORS  
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr Biol. 12 (22), 1965-1969 (2002)

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

### source

1..781  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Layer"  
/db\_xref="taxon:9031"  
/clone="CHEST206K24"  
/sex="Female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQRN14"  
/notes="Organ: ovary; Vector: pBluescript II KS(+); Site\_1:  
EcoRI; Site\_2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was bluntended, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

## ORIGIN

Query Match 73.3%; Score 17.6; DB 5; Length 781;  
Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGAGCGGTTCTGAGGCTTAC 24

Db 379 TCCGAGGTGTTCTGAGGCTTTC 402

## RESULT 43

## CA217713

## LOCUS

CA217713 786 bp mRNA linear EST 25-SEP-2003  
SCRUAD1133E05.b AD1 Saccharum officinarum cDNA clone SCRUAD1133E05  
3', mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Saccharum officinarum  
Saccharum officinarum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD  
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum  
complex.

## REFERENCE

## AUTHORS

Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

# TITLE JOURNAL COMMENT

The libraries that made SUCEST  
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br  
Clone distribution: clone distribution information can be found  
through the Brazilian Clone Collection Center (BCCC) at  
http://www.bcccenter.fcav.unesp.br  
Plate: 133 row: E column: 05  
Seq primer: SP6 Promoter primer.

## FEATURES

### source

1..786  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"  
/clone="SCRUAD1133E05"  
/lab\_host="DH10B"  
/clone\_lib="AD1"  
/notes="Organ: seedlings inoculated with Gluconacetobacter  
diazotrophicans; Vector: pSport1; Site\_1: SalI; Site\_2:  
NotI; An unidirectional cDNA library generated from  
seedlings inoculated with Gluconacetobacter  
diazotrophicans. cDNA was prepared from polyA+ mRNA using  
SuperScript Plasmid System Kit (Invitrogen). The  
double-strand cDNAs were fractionated in a sepharose  
CL-2B 40cm-columns and fragments sizing between 0.8 and  
1.5 Kb were directionally cloned into the vector. Details  
of each source of RNA and library construction can be  
obtained at http://sucest.lad.ic.unicamp.br/public"

## ORIGIN

Query Match 73.3%; Score 17.6; DB 6; Length 786;  
Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGAGCGGTTCTGAGGCTTAC 24

Db 638 TCCGGACGGTACTCGAGGCTTAC 661

## RESULT 44

## BU268001

## LOCUS

603817361F1 CSEQCHN52 Gallus gallus cDNA clone CHEST81316 5', mRNA  
sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Gallus gallus (chicken)  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

## REFERENCE

## AUTHORS

Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)

## MEDLINE

## PUBMED

## COMMENT

Contact: Simon Hubbard  
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University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

Location/Qualifiers

## source

1. .789  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn, Hisex"  
 /db\_xref="taxon:9031"  
 /clone="CHEST813116"  
 /dev\_stage="22"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQCHN52"  
 /note="Organ: limbs; Vector: pBluescript II KS(+); Site\_1: EcoRI; Site\_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 73.3%; Score 17.6; DB 5; Length 789;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 TCCGAGACGGTCTTGAGGGCTTAC 24  
 |||||  
 Db 407 TCCAGAGGTCTTGAGGGCTTTC 430

## RESULT 45

BH503335/c  
 LOCUS  
 DEFINITION BH503335 801 bp DNA linear GSS 13-DRG-2001 BOHG11TR BOHG Brassica oleracea genomic clone BOHG11, genomic survey sequence.  
 ACCESSION BH503335  
 VERSION BH503335.1 GI:17711432  
 KEYWORDS GSS.  
 SOURCE Brassica oleracea  
 ORGANISM Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 801)  
 Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.  
 Whole genome shotgun sequencing of Brassica oleracea  
 Other GSSs: BOHG11TF  
 Contact: Chris Town  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@igr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TR  
 Class: sheared ends.

## FEATURES

## source

1. .801  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /strain="TO1000DH3"  
 /db\_xref="taxon:3712"  
 /clone="BOHG11"  
 /note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"

## ORIGIN

Query Match 73.3%; Score 17.6; DB 8; Length 801;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 TCCGAGACGGTCTTGAGGGCTTAC 24  
 |||||  
 Db 762 TCCGAGAGGTATTGAGGGCTTGAC 739

RESULT 46  
 BU356670  
 LOCUS  
 DEFINITION BU356670 806 bp mRNA linear EST 28-NOV-2002 603473324F1 CSEQCHN70 Gallus gallus cDNA clone CHEST35305 5', mRNA sequence.  
 ACCESSION BU356670  
 VERSION BU356670.1 GI:25864671  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
 1 (bases 1 to 806)  
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
 A Comprehensive Collection of Chicken cDNAs  
 Curr. Biol. 12 (22), 1965-1969 (2002)  
 22335534  
 12445392  
 Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers  
 1. .806  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn, Hisex"  
 /db\_xref="taxon:9031"  
 /clone="CHEST35305"  
 /dev\_stage="36"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQCHN70"  
 /note="Organ: hearts; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

FEATURES  
source

## ORIGIN

Query Match 73.3%; Score 17.6; DB 5; Length 806;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 TCCGAGACGGTCTTGAGGGCTTAC 24  
 |||||  
 Db 451 TCCAGAGGTCTTGAGGGCTTTC 474

## RESULT 47

CL747554 894 bp DNA linear GSS 27-JUL-2004  
 LOCUS OR\_BBa0112K21.f OR\_BBa Oryza rufipogon genomic clone OR\_BBa0112K21  
 DEFINITION 5', genomic survey sequence.  
 ACCESSION CL747554  
 VERSION CL747554.1 GI:50690865  
 SOURCE GSS.  
 ORGANISM Oryza rufipogon  
 Oryza rufipogon  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.  
 REFERENCE 1. (bases 1 to 894)  
 AUTHORS Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,  
 Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.  
 TITLE ONAP Project  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Rod A. Wing  
 Arizona Genomics Institute  
 University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9595  
 Fax: 520 621 1259  
 Email: http://genome.arizona.edu  
 PCR Primers  
 FORWARD: TAA TAC GAC TCA CTA TAG GG  
 BACKWARD: CAC TCA TTA GGC ACC CCA  
 Insert Length: 161 Std Error: 0.00  
 Plate: 0112 row: K column: 21  
 Seq primer: TAA TAC GAC TCA CTA TAG GG  
 Class: BAC ends.

FEATURES  
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 1. .894  
 Location/Qualifiers  
 /organism="Oryza rufipogon"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:4529"  
 /clone="OR\_BBa0112K21"  
 /tissue\_type="young leaves"  
 /lab\_host="DH10B-T1 phage resistant"  
 /clone\_lib="OR\_BBa"  
 /note="Vector: pAGIBAC1; Site\_1: HindIII; Site\_2: HindIII"

ORIGIN  
 Query Match 73.3%; Score 17.6; DB 9; Length 894;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGTTCTGAGGCTTAC 24  
 |||||  
 DB 501 TCCGTGACGAATCTGAGGCTTGC 524

RESULT 48  
 BI2912/c 896 bp DNA linear GSS 14-MAY-1997  
 LOCUS TIC12-Sp6.1 TAMU Arabidopsis thaliana genomic clone TIC12, genomic  
 DEFINITION survey sequence.  
 ACCESSION BI2912  
 VERSION BI2912.1 GI:2094044  
 SOURCE GSS.  
 ORGANISM Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.  
 REFERENCE 1. (bases 1 to 896)  
 AUTHORS Peng,J., Dewar,K., Buehler,E., Kim,C., Li,Y., Shinn,P., Sun,H. and  
 Ecker,J.  
 TITLE BAC End Sequences at ATGC  
 JOURNAL Unpublished (1997)  
 COMMENT Other\_GSSs: TIC12-T7, TIC12-Sp6  
 Contact: Ecker J.  
 Arabidopsis Thaliana Genome Center

FEATURES  
 source  
 1. .896  
 Location/Qualifiers  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /ecotype="Columbia"  
 /db\_xref="taxon:3702"  
 /clone="TIC12"  
 /sex="hermaphrodite"  
 /clone\_lib="TAMU"  
 /note="Vector: BelOBACII; Site\_1: HindIII; Site\_2:  
 HindIII; Produced by Rod Wing"

ORIGIN  
 Query Match 73.3%; Score 17.6; DB 6; Length 915;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGTTCTGAGGCTTAC 24  
 |||||  
 DB 687 TCAGAGCGTTCTGAGGCTTAC 710

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 Dept. of Biology, University of Pennsylvania, Philadelphia, PA  
 19104  
 Tel: 215-898-9384  
 Fax: 215-898-8780  
 Email: jecker@atgenome.bio.upenn.edu  
 Seq primer: Sp6  
 Class: BAC ends  
 High quality sequence start: 98  
 High quality sequence stop: 290.  
 Location/Qualifiers  
 1. .896  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /ecotype="Columbia"  
 /db\_xref="taxon:3702"  
 /clone="TIC12"  
 /sex="hermaphrodite"  
 /clone\_lib="TAMU"  
 /note="Vector: BelOBACII; Site\_1: HindIII; Site\_2:  
 HindIII; Produced by Rod Wing"

ORIGIN  
 Query Match 73.3%; Score 17.6; DB 8; Length 896;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGTTCTGAGGCTTAC 24  
 |||||  
 DB 247 TCCAGTCGGTTCTGATGGCTAC 224

RESULT 49  
 CB556234 915 bp mRNA linear EST 02-APR-2003  
 LOCUS AMGNNUC:NRHY4-00132-H1-A W Rat hypothalamus (10464) Rattus  
 DEFINITION norvegicus cDNA clone nrhy4-00132-h1 5', mRNA sequence.  
 ACCESSION CB556234  
 VERSION CB556234.1 GI:29495634  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 REFERENCE 1. (bases 1 to 915)  
 AUTHORS Amgen EST Program.  
 TITLE Amgen Rat EST Program  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Dan Fitzpatrick  
 Amgen, Inc  
 One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
 Tel: 805 447-4881  
 Plate: 00132 row: h column: 1.

FEATURES  
 source  
 1. .915  
 Location/Qualifiers  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10116"  
 /clone="nrhy4-00132-h1"  
 /clone\_lib="W Rat hypothalamus (10464)"  
 /note="Vector: pSPORT1; Site\_1: SalI; Site\_2: NotI; W Rat  
 hypothalamus adult female Wistar rat avg. Insert size 2.3  
 kb fraction 6 and 7"

ORIGIN  
 Query Match 73.3%; Score 17.6; DB 6; Length 915;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGTTCTGAGGCTTAC 24  
 |||||  
 DB 687 TCAGAGCGTTCTGAGGCTTAC 710

Search completed: March 25, 2005, 12:33:59  
Job time : 1850 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 10:59:21 ; Search time 78.2857 Seconds  
(without alignments)  
501.632 Million cell updates/sec

Title: US-10-688-489-75

Perfect score: 24

Sequence: 1 tcgcagcgggttcgagggcttac 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Lieting first 500 summaries

Database :

Issued Patents NA:\*

1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*

2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*

3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*

4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*

5: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq.\*

6: /cgn2\_6/ptodata/1/ina/backfileseq1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length  | ID | Description          |
|------------|-------|-------------|---------|----|----------------------|
| 1          | 16.8  | 70.0        | 2799    | 3  | US-08-368-752B-5     |
| 2          | 16.8  | 70.0        | 2799    | 3  | US-09-536-224-5      |
| 3          | 16.6  | 69.2        | 601     | 4  | US-09-949-016-157466 |
| 4          | 16.6  | 69.2        | 601     | 4  | US-09-949-016-157573 |
| 5          | 16.6  | 69.2        | 601     | 4  | US-09-949-016-157573 |
| 6          | 16.6  | 69.2        | 126176  | 4  | US-09-949-016-16137  |
| 7          | 16.6  | 69.2        | 126176  | 4  | US-09-949-016-16137  |
| 8          | 16.6  | 69.2        | 138866  | 4  | US-09-949-016-16919  |
| 9          | 16.6  | 69.2        | 166698  | 4  | US-09-949-016-16038  |
| 10         | 16.6  | 69.2        | 767677  | 4  | US-09-949-016-12147  |
| 11         | 16.6  | 69.2        | 767677  | 4  | US-09-949-016-17361  |
| 12         | 16.6  | 69.2        | 4403765 | 3  | US-09-103-840A-2     |
| 13         | 16.6  | 69.2        | 4411529 | 3  | US-09-103-840A-1     |
| 14         | 16.2  | 67.5        | 921     | 4  | US-09-107-532A-2264  |
| 15         | 16.2  | 67.5        | 1815    | 4  | US-09-832-496-1      |
| 16         | 16.2  | 67.5        | 1815    | 4  | US-09-832-616-1      |
| 17         | 16.2  | 67.5        | 21721   | 4  | US-09-369-939A-41    |
| 18         | 16.2  | 67.5        | 22976   | 4  | US-09-369-939A-19    |
| 19         | 16.2  | 67.5        | 23187   | 4  | US-09-499-522-1      |
| 20         | 16    | 66.7        | 522     | 4  | US-09-252-991A-8519  |
| 21         | 16    | 66.7        | 579     | 4  | US-09-270-767-12997  |
| 22         | 16    | 66.7        | 1113    | 4  | US-09-352-991A-8445  |
| 23         | 16    | 66.7        | 1850    | 4  | US-09-739-451-367    |
| 24         | 16    | 66.7        | 2409    | 4  | US-09-252-991A-8479  |
| 25         | 16    | 66.7        | 7240    | 4  | US-09-695-795A-1     |
| 26         | 15.8  | 65.8        | 37      | 1  | US-08-199-507B-21    |
| 27         | 15.8  | 65.8        | 37      | 1  | US-08-441-828-21     |

|     |      |        |        |   |                      |                    |
|-----|------|--------|--------|---|----------------------|--------------------|
| 28  | 15.8 | 65.8   | 601    | 4 | US-09-949-016-192257 | Sequence 192257,   |
| 29  | 15.8 | 65.8   | 1621   | 1 | US-08-292-688A-10    | Sequence 10, Appl  |
| 30  | 15.8 | 1795   | 1795   | 2 | US-08-791-849A-12    | Sequence 12, Appl  |
| 31  | 15.8 | 55031  | 55031  | 4 | US-09-949-016-17389  | Sequence 17389, A  |
| 32  | 15.8 | 90776  | 90776  | 4 | US-09-949-016-17230  | Sequence 17230, A  |
| 33  | 15.8 | 122772 | 122772 | 4 | US-09-949-016-14132  | Sequence 14132, A  |
| 34  | 15.8 | 767677 | 767677 | 4 | US-09-949-016-12147  | Sequence 12147, A  |
| 35  | 15.8 | 65.8   | 767677 | 4 | US-09-949-016-17361  | Sequence 17361, A  |
| 36  | 15.6 | 601    | 601    | 4 | US-09-949-016-45837  | Sequence 45837, A  |
| 37  | 15.6 | 65.0   | 601    | 4 | US-09-949-016-45859  | Sequence 45859, A  |
| 38  | 15.6 | 65.0   | 948    | 4 | US-09-489-039A-1034  | Sequence 1034, Ap  |
| 39  | 15.6 | 1341   | 1341   | 4 | US-09-248-796A-6062  | Sequence 6062, Ap  |
| 40  | 15.6 | 2121   | 2121   | 4 | US-09-902-540-8806   | Sequence 8806, Ap  |
| 41  | 15.6 | 2332   | 2332   | 4 | US-09-949-016-253    | Sequence 253, App  |
| 42  | 15.6 | 65.0   | 2332   | 4 | US-09-949-016-5522   | Sequence 5522, App |
| 43  | 15.6 | 65.0   | 3595   | 4 | US-09-949-016-408    | Sequence 408, App  |
| 44  | 15.6 | 65.0   | 3607   | 4 | US-09-563-269-17     | Sequence 17, Appl  |
| 45  | 15.6 | 65.0   | 3943   | 3 | US-08-506-296B-27    | Sequence 27, Appl  |
| 46  | 15.6 | 65.0   | 4041   | 4 | US-09-949-016-1305   | Sequence 1305, Ap  |
| 47  | 15.6 | 65.0   | 4041   | 4 | US-09-949-016-1306   | Sequence 1306, Ap  |
| 48  | 15.6 | 65.0   | 4078   | 4 | US-09-016-434-1152   | Sequence 1152, Ap  |
| 49  | 15.6 | 65.0   | 4546   | 4 | US-09-949-016-4140   | Sequence 4140, Ap  |
| 50  | 15.6 | 65.0   | 4553   | 4 | US-09-023-655-975    | Sequence 975, App  |
| 51  | 15.6 | 65.0   | 4553   | 4 | US-09-949-016-726    | Sequence 726, App  |
| 52  | 15.6 | 65.0   | 5319   | 2 | US-08-861-464-7      | Sequence 7, Appli  |
| 53  | 15.6 | 65.0   | 5319   | 2 | US-08-396-001-7      | Sequence 7, Appli  |
| 54  | 15.6 | 65.0   | 5319   | 3 | US-09-323-433A-7     | Sequence 7, Appli  |
| 55  | 15.6 | 65.0   | 5319   | 4 | US-09-826-752-7      | Sequence 7, Appli  |
| 56  | 15.6 | 65.0   | 10096  | 4 | US-09-902-540-935    | Sequence 935, App  |
| 57  | 15.6 | 65.0   | 15659  | 4 | US-09-949-016-16053  | Sequence 16053, A  |
| 58  | 15.6 | 65.0   | 16924  | 4 | US-09-949-016-13720  | Sequence 13720, A  |
| 59  | 15.6 | 65.0   | 18318  | 1 | US-08-414-926A-6     | Sequence 6, Appli  |
| 60  | 15.6 | 65.0   | 18318  | 2 | US-08-926-922-6      | Sequence 6, Appli  |
| 61  | 15.6 | 65.0   | 18318  | 3 | US-09-253-682-6      | Sequence 6, Appli  |
| 62  | 15.6 | 65.0   | 18318  | 3 | US-09-527-657-6      | Sequence 6, Appli  |
| 63  | 15.6 | 65.0   | 18318  | 4 | US-09-892-100-6      | Sequence 6, Appli  |
| 64  | 15.6 | 65.0   | 60304  | 4 | US-09-949-016-11995  | Sequence 11995, A  |
| 65  | 15.6 | 65.0   | 60304  | 4 | US-09-949-016-17264  | Sequence 17264, A  |
| 66  | 15.6 | 65.0   | 63183  | 4 | US-09-949-016-13047  | Sequence 13047, A  |
| 67  | 15.6 | 65.0   | 63183  | 4 | US-09-949-016-13048  | Sequence 13048, A  |
| 68  | 15.6 | 65.0   | 229354 | 4 | US-09-705-400-64     | Sequence 64, Appl  |
| 69  | 15.6 | 65.0   | 325034 | 4 | US-09-949-016-14957  | Sequence 14957, A  |
| 70  | 15.6 | 65.0   | 389504 | 4 | US-09-949-016-11774  | Sequence 11774, A  |
| 71  | 15.4 | 64.2   | 73853  | 4 | US-09-949-016-12029  | Sequence 12029, A  |
| 72  | 15.4 | 64.2   | 134987 | 4 | US-09-949-016-15348  | Sequence 15348, A  |
| 73  | 15.4 | 64.2   | 134987 | 4 | US-09-949-016-15349  | Sequence 15349, A  |
| 74  | 15.4 | 64.2   | 134987 | 4 | US-09-949-016-15350  | Sequence 15350, A  |
| 75  | 15.4 | 64.2   | 134987 | 4 | US-09-949-016-15507  | Sequence 15507, A  |
| 76  | 15.4 | 64.2   | 134987 | 4 | US-09-949-016-15508  | Sequence 15508, A  |
| 77  | 15.4 | 64.2   | 134987 | 4 | US-09-949-016-15509  | Sequence 15509, A  |
| 78  | 15.2 | 63.3   | 147    | 4 | US-09-513-999C-22084 | Sequence 22084, A  |
| 79  | 15.2 | 63.3   | 221    | 4 | US-09-513-999C-22084 | Sequence 22084, A  |
| 80  | 15.2 | 63.3   | 601    | 4 | US-09-949-016-21395  | Sequence 21395, A  |
| 81  | 15.2 | 63.3   | 601    | 4 | US-09-949-016-21396  | Sequence 21396, A  |
| 82  | 15.2 | 63.3   | 601    | 4 | US-09-949-016-26139  | Sequence 26139, A  |
| 83  | 15.2 | 63.3   | 601    | 4 | US-09-949-016-128275 | Sequence 128275,   |
| 84  | 15.2 | 63.3   | 601    | 4 | US-09-949-016-190884 | Sequence 190884,   |
| 85  | 15.2 | 63.3   | 601    | 4 | US-09-949-016-190885 | Sequence 190885,   |
| 86  | 15.2 | 63.3   | 1035   | 4 | US-09-540-236-1142   | Sequence 1142, Ap  |
| 87  | 15.2 | 63.3   | 1368   | 4 | US-09-489-039A-5652  | Sequence 5652, Ap  |
| 88  | 15.2 | 63.3   | 1492   | 4 | US-09-369-247-23     | Sequence 23, Appl  |
| 89  | 15.2 | 63.3   | 1611   | 4 | US-09-808-701A-13    | Sequence 13, Appl  |
| 90  | 15.2 | 63.3   | 2213   | 4 | US-09-620-312D-1038  | Sequence 1038, Ap  |
| 91  | 15.2 | 63.3   | 2478   | 3 | US-08-485-355B-47    | Sequence 47, Appl  |
| 92  | 15.2 | 63.3   | 2478   | 3 | US-08-485-355B-49    | Sequence 49, Appl  |
| 93  | 15.2 | 63.3   | 2478   | 3 | US-09-194-613-1      | Sequence 1, Appli  |
| 94  | 15.2 | 63.3   | 2782   | 4 | US-08-485-355B-51    | Sequence 51, Appl  |
| 95  | 15.2 | 63.3   | 2782   | 4 | US-09-949-016-5457   | Sequence 5457, Ap  |
| 96  | 15.2 | 63.3   | 2797   | 3 | US-09-240-639-3      | Sequence 3, Appli  |
| 97  | 15.2 | 63.3   | 2797   | 3 | US-09-908-510A-3     | Sequence 3, Appli  |
| 98  | 15.2 | 63.3   | 2797   | 4 | US-09-905-744B-3     | Sequence 3, Appli  |
| 99  | 15.2 | 63.3   | 2797   | 4 | US-10-107-660-3      | Sequence 3, Appli  |
| 100 | 15.2 | 63.3   | 2797   | 4 | US-10-107-576-3      | Sequence 3, Appli  |

|       |      |      |         |   |                      |                    |     |      |      |        |   |                      |                    |
|-------|------|------|---------|---|----------------------|--------------------|-----|------|------|--------|---|----------------------|--------------------|
| C 101 | 15.2 | 63.3 | 2797    | 4 | US-09-905-732B-3     | Sequence 3, Appli  | 174 | 14.8 | 61.7 | 601    | 4 | US-09-949-016-156680 | Sequence 156680,   |
| C 102 | 15.2 | 63.3 | 2797    | 4 | US-09-923-304-3      | Sequence 3, Appli  | 175 | 14.8 | 61.7 | 758    | 4 | US-09-976-594-101    | Sequence 101, App  |
| C 103 | 15.2 | 63.3 | 2797    | 4 | US-09-949-016-178    | Sequence 178, App  | 176 | 14.8 | 61.7 | 1437   | 4 | US-09-894-844-90     | Sequence 90, Appl  |
| C 104 | 15.2 | 63.3 | 2797    | 4 | US-09-905-743B-3     | Sequence 3, Appli  | 177 | 14.8 | 61.7 | 1693   | 1 | US-08-292-688A-13    | Sequence 13, Appl  |
| C 105 | 15.2 | 63.3 | 3424    | 3 | US-09-336-643A-9     | Sequence 9, Appli  | 178 | 14.8 | 61.7 | 1693   | 1 | US-08-292-688A-14    | Sequence 14, Appl  |
| C 106 | 15.2 | 63.3 | 3611    | 4 | US-09-949-016-3632   | Sequence 3632, Ap  | 179 | 14.8 | 61.7 | 1729   | 4 | US-09-620-312D-1016  | Sequence 1016, Ap  |
| C 107 | 15.2 | 63.3 | 13782   | 4 | US-09-949-016-14992  | Sequence 14992, A  | 180 | 14.8 | 61.7 | 12460  | 4 | US-09-949-016-13009  | Sequence 13009, A  |
| C 108 | 15.2 | 63.3 | 13854   | 4 | US-09-811-825A-3     | Sequence 3, Appli  | 181 | 14.8 | 61.7 | 38961  | 4 | US-09-949-016-12143  | Sequence 12143, A  |
| C 109 | 15.2 | 63.3 | 20444   | 4 | US-09-596-002-16     | Sequence 16, Appl  | 182 | 14.8 | 61.7 | 38961  | 4 | US-09-949-016-14474  | Sequence 14474, A  |
| C 110 | 15.2 | 63.3 | 22407   | 4 | US-09-949-016-1750   | Sequence 1750, A   | 183 | 14.8 | 61.7 | 73818  | 4 | US-09-949-016-16822  | Sequence 16822, A  |
| C 111 | 15.2 | 63.3 | 45539   | 4 | US-09-949-016-11920  | Sequence 11920, A  | 184 | 14.8 | 61.7 | 194889 | 4 | US-09-949-016-15654  | Sequence 15654, A  |
| C 112 | 15.2 | 63.3 | 45540   | 4 | US-09-949-016-17199  | Sequence 17199, A  | 185 | 14.8 | 61.7 | 231129 | 4 | US-09-949-016-16110  | Sequence 16110, A  |
| C 113 | 15.2 | 63.3 | 54463   | 4 | US-09-949-016-14781  | Sequence 14781, A  | 186 | 14.8 | 61.7 | 266293 | 4 | US-09-949-016-11934  | Sequence 11934, A  |
| C 114 | 15.2 | 63.3 | 52522   | 4 | US-09-949-016-12150  | Sequence 12150, A  | 187 | 14.6 | 60.8 | 71     | 1 | US-08-148-910-10     | Sequence 10, Appl  |
| C 115 | 15.2 | 63.3 | 52522   | 4 | US-09-949-016-12150  | Sequence 12150, A  | 187 | 14.6 | 60.8 | 71     | 1 | US-08-148-910-10     | Sequence 10, Appl  |
| C 116 | 15.2 | 63.3 | 276687  | 4 | US-09-949-016-13374  | Sequence 13374, A  | 188 | 14.6 | 60.8 | 71     | 1 | US-08-148-910-10     | Sequence 10, Appl  |
| C 117 | 15   | 62.5 | 258     | 4 | US-09-949-016-13840  | Sequence 13840, A  | 189 | 14.6 | 60.8 | 235    | 4 | US-09-513-999C-12048 | Sequence 12048, A  |
| C 118 | 15   | 62.5 | 524     | 4 | US-09-313-294A-2060  | Sequence 2060, Ap  | 190 | 14.6 | 60.8 | 341    | 4 | US-09-513-999C-3453  | Sequence 3453, Ap  |
| C 119 | 15   | 62.5 | 524     | 4 | US-09-270-767-4427   | Sequence 4427, Ap  | 191 | 14.6 | 60.8 | 349    | 4 | US-09-621-976-7870   | Sequence 7870, Ap  |
| C 120 | 15   | 62.5 | 601     | 4 | US-09-270-767-19709  | Sequence 19709, A  | 192 | 14.6 | 60.8 | 366    | 4 | US-09-424-840B-29    | Sequence 29, Appl  |
| C 121 | 15   | 62.5 | 601     | 4 | US-09-949-016-46408  | Sequence 46408, A  | 193 | 14.6 | 60.8 | 464    | 4 | US-09-949-016-90142  | Sequence 90142, A  |
| C 122 | 15   | 62.5 | 601     | 4 | US-09-949-016-63051  | Sequence 63051, A  | 194 | 14.6 | 60.8 | 464    | 4 | US-09-949-016-90168  | Sequence 90168, A  |
| C 123 | 15   | 62.5 | 601     | 4 | US-09-949-016-63052  | Sequence 63052, A  | 195 | 14.6 | 60.8 | 465    | 4 | US-09-949-016-90141  | Sequence 90141, A  |
| C 124 | 15   | 62.5 | 601     | 4 | US-09-949-016-168647 | Sequence 168647, A | 196 | 14.6 | 60.8 | 465    | 4 | US-09-949-016-90167  | Sequence 90167, A  |
| C 125 | 15   | 62.5 | 744     | 4 | US-09-489-039A-4338  | Sequence 4338, Ap  | 197 | 14.6 | 60.8 | 486    | 4 | US-09-702-705-877    | Sequence 877, App  |
| C 126 | 15   | 62.5 | 747     | 4 | US-09-543-681A-156   | Sequence 156, App  | 198 | 14.6 | 60.8 | 486    | 4 | US-09-736-457-877    | Sequence 877, App  |
| C 127 | 15   | 62.5 | 897     | 3 | US-09-058-389A-17    | Sequence 17, Appl  | 199 | 14.6 | 60.8 | 486    | 4 | US-09-614-124B-877   | Sequence 877, App  |
| C 128 | 15   | 62.5 | 897     | 3 | US-09-611-781-17     | Sequence 17, Appl  | 200 | 14.6 | 60.8 | 486    | 4 | US-09-671-325-877    | Sequence 877, App  |
| C 129 | 15   | 62.5 | 1035    | 4 | US-09-489-039A-4287  | Sequence 4287, Ap  | 201 | 14.6 | 60.8 | 486    | 4 | US-09-658-824-877    | Sequence 877, App  |
| C 130 | 15   | 62.5 | 1272    | 3 | US-09-058-389A-7     | Sequence 7, Appli  | 202 | 14.6 | 60.8 | 491    | 4 | US-09-513-999C-23735 | Sequence 23735, A  |
| C 131 | 15   | 62.5 | 1272    | 3 | US-09-611-781-7      | Sequence 7, Appli  | 203 | 14.6 | 60.8 | 503    | 4 | US-09-621-976-10616  | Sequence 10616, A  |
| C 132 | 15   | 62.5 | 1738    | 2 | US-08-932-376A-1     | Sequence 1, Appli  | 204 | 14.6 | 60.8 | 512    | 4 | US-09-621-976-10625  | Sequence 10625, A  |
| C 133 | 15   | 62.5 | 1847    | 3 | US-09-058-389A-9     | Sequence 9, Appli  | 205 | 14.6 | 60.8 | 518    | 4 | US-09-621-976-2942   | Sequence 2942, Ap  |
| C 134 | 15   | 62.5 | 1847    | 3 | US-09-611-781-9      | Sequence 9, Appli  | 206 | 14.6 | 60.8 | 519    | 4 | US-09-640-211A-1714  | Sequence 1714, Ap  |
| C 135 | 15   | 62.5 | 1963    | 4 | US-09-620-312D-596   | Sequence 596, App  | 207 | 14.6 | 60.8 | 535    | 4 | US-09-242-999-23     | Sequence 23, Appl  |
| C 136 | 15   | 62.5 | 2220    | 2 | US-08-932-376A-3     | Sequence 3, Appli  | 208 | 14.6 | 60.8 | 588    | 3 | US-09-227-357-114    | Sequence 114, App  |
| C 137 | 15   | 62.5 | 6101    | 4 | US-09-949-016-1376   | Sequence 1376, Ap  | 209 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-27228  | Sequence 27228, A  |
| C 138 | 15   | 62.5 | 6354    | 3 | US-09-058-389A-5     | Sequence 5, Appli  | 210 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-30639  | Sequence 30639, A  |
| C 139 | 15   | 62.5 | 6354    | 3 | US-09-611-781-5      | Sequence 5, Appli  | 211 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-50453  | Sequence 50453, A  |
| C 140 | 15   | 62.5 | 6384    | 4 | US-09-949-016-12165  | Sequence 12165, A  | 212 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-73142  | Sequence 73142, A  |
| C 141 | 15   | 62.5 | 7077    | 4 | US-09-949-016-13581  | Sequence 13581, A  | 213 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-81278  | Sequence 81278, A  |
| C 142 | 15   | 62.5 | 7077    | 4 | US-09-949-016-67     | Sequence 67, Appl  | 214 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-90139  | Sequence 90139, A  |
| C 143 | 15   | 62.5 | 9990    | 4 | US-09-949-016-15542  | Sequence 15542, A  | 215 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-90140  | Sequence 90140, A  |
| C 144 | 15   | 62.5 | 12023   | 4 | US-09-634-238-405    | Sequence 405, App  | 216 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-90165  | Sequence 90165, A  |
| C 145 | 15   | 62.5 | 12359   | 4 | US-09-949-016-13082  | Sequence 13082, A  | 217 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-90165  | Sequence 90165, A  |
| C 146 | 15   | 62.5 | 12366   | 4 | US-09-949-016-13082  | Sequence 13082, A  | 218 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-90165  | Sequence 90165, A  |
| C 147 | 15   | 62.5 | 22131   | 4 | US-09-949-016-15391  | Sequence 15391, A  | 219 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-102925 | Sequence 102925, A |
| C 148 | 15   | 62.5 | 22131   | 4 | US-09-949-016-15391  | Sequence 15391, A  | 220 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-102925 | Sequence 102925, A |
| C 149 | 15   | 62.5 | 27180   | 4 | US-09-949-016-15392  | Sequence 15392, A  | 221 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-105796 | Sequence 105796, A |
| C 150 | 15   | 62.5 | 27180   | 4 | US-09-949-016-15392  | Sequence 15392, A  | 222 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-105797 | Sequence 105797, A |
| C 151 | 15   | 62.5 | 30364   | 4 | US-09-949-016-14587  | Sequence 14587, A  | 223 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-145130 | Sequence 145130, A |
| C 152 | 15   | 62.5 | 30364   | 4 | US-09-949-016-15620  | Sequence 15620, A  | 224 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-145131 | Sequence 145131, A |
| C 153 | 15   | 62.5 | 32155   | 4 | US-09-949-016-16497  | Sequence 16497, A  | 225 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-178559 | Sequence 178559, A |
| C 154 | 15   | 62.5 | 32155   | 4 | US-08-311-731A-1     | Sequence 1, Appli  | 226 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-186488 | Sequence 186488, A |
| C 155 | 15   | 62.5 | 41617   | 4 | US-09-949-016-14356  | Sequence 14356, A  | 227 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-203565 | Sequence 203565, A |
| C 156 | 15   | 62.5 | 47498   | 4 | US-09-949-016-14681  | Sequence 14681, A  | 228 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-203566 | Sequence 203566, A |
| C 157 | 15   | 62.5 | 47498   | 4 | US-09-949-016-13241  | Sequence 13241, A  | 229 | 14.6 | 60.8 | 601    | 4 | US-09-949-016-203567 | Sequence 203567, A |
| C 158 | 15   | 62.5 | 58439   | 4 | US-09-949-016-13565  | Sequence 13565, A  | 230 | 14.6 | 60.8 | 615    | 4 | US-09-949-001-452    | Sequence 452, App  |
| C 159 | 15   | 62.5 | 98439   | 4 | US-09-949-016-13597  | Sequence 13597, A  | 231 | 14.6 | 60.8 | 615    | 4 | US-09-461-325-122    | Sequence 122, App  |
| C 160 | 15   | 62.5 | 107800  | 4 | US-09-949-016-13118  | Sequence 13118, A  | 232 | 14.6 | 60.8 | 615    | 4 | US-10-012-542-122    | Sequence 122, App  |
| C 161 | 15   | 62.5 | 116425  | 4 | US-09-949-016-13118  | Sequence 13118, A  | 233 | 14.6 | 60.8 | 918    | 4 | US-10-115-123-122    | Sequence 122, App  |
| C 162 | 15   | 62.5 | 176373  | 3 | US-09-128-153-17     | Sequence 17, Appl  | 234 | 14.6 | 60.8 | 1200   | 4 | US-09-949-016-4373   | Sequence 4373, Ap  |
| C 163 | 15   | 62.5 | 264358  | 4 | US-09-949-016-15725  | Sequence 15725, A  | 235 | 14.6 | 60.8 | 1635   | 3 | US-09-807-802A-8     | Sequence 8, Appli  |
| C 164 | 15   | 62.5 | 373182  | 4 | US-09-949-016-17371  | Sequence 17371, A  | 236 | 14.6 | 60.8 | 1635   | 3 | US-09-234-332-4      | Sequence 4, Appli  |
| C 165 | 15   | 62.5 | 373694  | 4 | US-09-949-016-12062  | Sequence 12062, A  | 237 | 14.6 | 60.8 | 1635   | 4 | US-09-702-305-1798   | Sequence 1798, Ap  |
| C 166 | 15   | 62.5 | 462589  | 4 | US-09-949-016-12900  | Sequence 12900, A  | 238 | 14.6 | 60.8 | 1635   | 4 | US-09-736-457-1798   | Sequence 1798, Ap  |
| C 167 | 15   | 62.5 | 476044  | 4 | US-09-949-016-12900  | Sequence 12900, A  | 239 | 14.6 | 60.8 | 1647   | 3 | US-09-671-325-1798   | Sequence 44, Appl  |
| C 168 | 15   | 62.5 | 1230025 | 4 | US-09-198-482A-1     | Sequence 12412, A  | 240 | 14.6 | 60.8 | 1716   | 4 | US-09-674-677-6      | Sequence 6, Appli  |
| C 169 | 15   | 62.5 | 1230230 | 4 | US-09-438-185A-1     | Sequence 1, Appli  | 241 | 14.6 | 60.8 | 1872   | 4 | US-09-807-802A-4     | Sequence 4, Appli  |
| C 170 | 15   | 62.5 | 4403765 | 3 | US-09-103-840A-2     | Sequence 2, Appli  | 242 | 14.6 | 60.8 | 2130   | 3 | US-09-552-322-1      | Sequence 1, Appli  |
| C 171 | 14.8 | 61.7 | 207     | 4 | US-09-513-999C-10938 | Sequence 10938, A  | 243 | 14.6 | 60.8 | 2150   | 4 | US-09-461-325-76     | Sequence 76, Appl  |
| C 172 | 14.8 | 61.7 | 593     | 4 | US-09-517-431E-10    | Sequence 10, Appl  | 244 | 14.6 | 60.8 | 2150   | 4 | US-10-012-542-76     | Sequence 76, Appl  |
| C 173 | 14.8 | 61.7 | 601     | 4 | US-09-949-016-138761 | Sequence 138761, A | 245 | 14.6 | 60.8 | 3116   | 1 | US-10-115-123-76     | Sequence 76, Appl  |
|       |      |      |         |   |                      |                    | 246 | 14.6 | 60.8 | 3116   | 1 | US-08-149-103-2      | Sequence 2, Appli  |



|       |      |      |        |   |                     |                   |       |      |      |     |   |                      |                    |
|-------|------|------|--------|---|---------------------|-------------------|-------|------|------|-----|---|----------------------|--------------------|
| 393   | 14.4 | 60.0 | 18650  | 4 | US-09-949-016-14366 | Sequence 14366, A | 466   | 14.2 | 59.2 | 601 | 4 | US-09-949-016-152579 | Sequence 152579, A |
| C 394 | 14.4 | 60.0 | 22010  | 4 | US-09-949-016-15960 | Sequence 15960, A | 467   | 14.2 | 59.2 | 601 | 4 | US-09-949-016-152580 | Sequence 152580, A |
| C 395 | 14.4 | 60.0 | 22121  | 4 | US-09-949-016-14309 | Sequence 14309, A | 468   | 14.2 | 59.2 | 601 | 4 | US-09-949-016-152581 | Sequence 152581, A |
| C 396 | 14.4 | 60.0 | 22121  | 4 | US-09-949-016-14309 | Sequence 14309, A | C 469 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-174616 | Sequence 174616, A |
| C 397 | 14.4 | 60.0 | 26116  | 4 | US-09-949-016-16852 | Sequence 16852, A | C 470 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-174617 | Sequence 174617, A |
| C 398 | 14.4 | 60.0 | 27663  | 4 | US-09-949-016-16160 | Sequence 16160, A | C 471 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 399 | 14.4 | 60.0 | 34011  | 4 | US-09-949-016-12485 | Sequence 12485, A | C 472 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 400 | 14.4 | 60.0 | 34011  | 4 | US-09-949-016-12485 | Sequence 12485, A | C 473 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 401 | 14.4 | 60.0 | 34223  | 4 | US-09-949-016-14417 | Sequence 14417, A | C 474 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 402 | 14.4 | 60.0 | 37875  | 4 | US-09-949-016-13182 | Sequence 13182, A | C 475 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 403 | 14.4 | 60.0 | 40624  | 4 | US-09-949-016-11904 | Sequence 11904, A | C 476 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 404 | 14.4 | 60.0 | 42348  | 4 | US-09-949-016-17157 | Sequence 17157, A | C 477 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 405 | 14.4 | 60.0 | 42989  | 4 | US-09-949-016-17157 | Sequence 17157, A | C 478 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 406 | 14.4 | 60.0 | 42992  | 4 | US-09-949-016-12231 | Sequence 12231, A | C 479 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 407 | 14.4 | 60.0 | 42992  | 4 | US-09-949-016-12231 | Sequence 12231, A | C 480 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 408 | 14.4 | 60.0 | 44120  | 4 | US-09-949-016-15428 | Sequence 15428, A | C 481 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 409 | 14.4 | 60.0 | 44120  | 4 | US-09-949-016-14902 | Sequence 14902, A | C 482 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 410 | 14.4 | 60.0 | 44120  | 4 | US-09-949-016-14151 | Sequence 14151, A | C 483 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 411 | 14.4 | 60.0 | 44120  | 4 | US-09-949-016-14152 | Sequence 14152, A | C 484 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 412 | 14.4 | 60.0 | 44120  | 4 | US-09-949-016-14153 | Sequence 14153, A | C 485 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 413 | 14.4 | 60.0 | 44120  | 4 | US-09-949-016-14154 | Sequence 14154, A | C 486 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 414 | 14.4 | 60.0 | 44120  | 4 | US-09-949-016-14155 | Sequence 14155, A | C 487 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 415 | 14.4 | 60.0 | 44120  | 4 | US-09-949-016-14156 | Sequence 14156, A | C 488 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 416 | 14.4 | 60.0 | 45427  | 4 | US-09-949-016-16243 | Sequence 16243, A | C 489 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 417 | 14.4 | 60.0 | 50725  | 4 | US-09-902-540-1271  | Sequence 1271, A  | C 490 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 418 | 14.4 | 60.0 | 66788  | 4 | US-09-949-001-37    | Sequence 37, A    | C 491 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 419 | 14.4 | 60.0 | 67629  | 4 | US-09-949-016-12254 | Sequence 12254, A | C 492 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 420 | 14.4 | 60.0 | 87629  | 4 | US-09-949-016-15262 | Sequence 15262, A | C 493 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 421 | 14.4 | 60.0 | 87629  | 4 | US-09-949-016-15263 | Sequence 15263, A | C 494 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 422 | 14.4 | 60.0 | 87629  | 4 | US-09-949-016-15264 | Sequence 15264, A | C 495 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 423 | 14.4 | 60.0 | 87734  | 4 | US-09-949-016-15265 | Sequence 15265, A | C 496 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 424 | 14.4 | 60.0 | 87870  | 4 | US-09-949-016-17521 | Sequence 17521, A | C 497 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 425 | 14.4 | 60.0 | 112239 | 4 | US-09-949-016-14461 | Sequence 14461, A | C 498 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 426 | 14.4 | 60.0 | 124480 | 4 | US-09-949-016-13144 | Sequence 13144, A | C 499 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 427 | 14.4 | 60.0 | 124480 | 4 | US-09-949-016-13144 | Sequence 13144, A | C 500 | 14.2 | 59.2 | 601 | 4 | US-09-949-016-205599 | Sequence 205599, A |
| C 428 | 14.4 | 60.0 | 184061 | 4 | US-09-128-155-16    | Sequence 155, A   |       |      |      |     |   |                      |                    |
| C 429 | 14.4 | 60.0 | 173992 | 4 | US-09-949-016-17422 | Sequence 17422, A |       |      |      |     |   |                      |                    |
| C 430 | 14.4 | 60.0 | 223934 | 4 | US-09-949-016-13379 | Sequence 13379, A |       |      |      |     |   |                      |                    |
| C 431 | 14.4 | 60.0 | 223934 | 4 | US-09-949-016-13379 | Sequence 13379, A |       |      |      |     |   |                      |                    |
| C 432 | 14.4 | 60.0 | 264206 | 4 | US-09-705-400-64    | Sequence 64, A    |       |      |      |     |   |                      |                    |
| C 433 | 14.4 | 60.0 | 264304 | 4 | US-09-949-016-12731 | Sequence 12731, A |       |      |      |     |   |                      |                    |
| C 434 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 435 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 436 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 437 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 438 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 439 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 440 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 441 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 442 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 443 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 444 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 445 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 446 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 447 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 448 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 449 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 450 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 451 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 452 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 453 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 454 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 455 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 456 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 457 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 458 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 459 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 460 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 461 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 462 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 463 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 464 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |
| C 465 | 14.4 | 60.0 | 340380 | 4 | US-09-949-016-13249 | Sequence 13249, A |       |      |      |     |   |                      |                    |

## ALIGNMENTS

## RESULT 1

US-08-968-752B-5  
; Sequence 5, Application US/08968752B  
; Patent No. 6043073  
; GENERAL INFORMATION:  
; APPLICANT: Frohman, Michael A.  
; APPLICANT: Morris, Andrew  
; TITLE OF INVENTION: No. 6043073el Phospholipase D Polypeptide and  
; TITLE OF INVENTION: DNA Sequences  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ONYX Pharmaceuticals, Inc.  
; STREET: 3031 Research Drive  
; CITY: Richmond  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94806  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/968,752B  
; FILING DATE: 13-AUG-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/025,469  
; FILING DATE: 05-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Giotta, Gregory J.  
; REGISTRATION NUMBER: 32, 028  
; REFERENCE/DOCKET NUMBER: ONYX2004

TELECOMMUNICATION INFORMATION:

TELEPHONE: 510-222-9700  
TELEFAX: 510-222-9758  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2799 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2799  
US-08-968-752B-5

Query Match 70.0%; Score 16.8; DB 3; Length 2799;  
Best Local Similarity 90.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTCTCTGAGGGCT 21  
||||| ||||| ||||| ||||| |||||  
Db 444 CCGAGGAGGTTCTGAGGGCT 463

RESULT 2

US-09-536-224-5  
Sequence 5, Application US/09536224  
Patent No. 6379665

GENERAL INFORMATION:  
APPLICANT: Frohman, Michael A.  
APPLICANT: Morris, Andrew  
TITLE OF INVENTION: No. 6379665el Phospholipase D Polypeptide and  
TITLE OF INVENTION: DNA Sequences  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ONYX Pharmaceuticals, Inc.  
STREET: 3031 Research Drive  
CITY: Richmond  
STATE: California  
COUNTRY: USA  
ZIP: 94806

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/536,224  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/968,752  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Giotta, Gregory J.  
REGISTRATION NUMBER: 32,028  
REFERENCE/DOCKET NUMBER: ONYX2004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-222-9700  
TELEFAX: 510-222-9758  
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
LENGTH: 2799 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS

LOCATION: 1..2799  
US-09-536-224-5

Query Match 70.0%; Score 16.8; DB 3; Length 2799;  
Best Local Similarity 90.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTCTCTGAGGGCT 21  
||||| ||||| ||||| ||||| |||||  
Db 444 CCGAGGAGGTTCTGAGGGCT 463

RESULT 3

US-09-949-016-157466  
Sequence 157466, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 157466  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-157466

Query Match 69.2%; Score 16.6; DB 4; Length 601;  
Best Local Similarity 82.6%; Pred. No. 1.2e+02;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTA 23  
||||| ||||| ||||| ||||| |||||  
Db 273 TCAGAGATGATTTTGAGGGCTTA 295

RESULT 4

US-09-949-016-157573  
Sequence 157573, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 157573  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-157573

Query Match 69.2%; Score 16.6; DB 4; Length 601;  
Best Local Similarity 82.6%; Pred. No. 1.2e+02;







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RESULT 13
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      69.2%; Score 16.6; DB 3; Length 4411529;
Best Local Similarity 82.6%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGGCTTA 23
Db 2394408 TCCGAGACGGTTCGAGGGCGGATA 2394386

RESULT 14
US-09-107-532A-2264
; Sequence 2284, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 2264:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: Double
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; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...921
; SEQUENCE DESCRIPTION: SEQ ID NO: 2264:
US-09-107-532A-2264

Query Match      67.5%; Score 16.2; DB 4; Length 921;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GAGACGGTTCGAGGGCTTAC 24
Db 533 GAGACGGTTCGAGGGCTTCC 553

RESULT 15
US-09-832-496-1
; Sequence 1, Application US/09832496
; Patent No. 6503508
; GENERAL INFORMATION:
; APPLICANT: Danielisen, Steffen
; APPLICANT: Schneider, Pallo
; TITLE OF INVENTION: Polypeptides having haloperoxidase activity
; FILE REFERENCE: 10042.200-US
; CURRENT APPLICATION NUMBER: US/09/832,496
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1815
; TYPE: DNA
; ORGANISM: Dreschlera hartleibii
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1815)
US-09-832-496-1

Query Match      67.5%; Score 16.2; DB 4; Length 1815;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGAGACGGTTCGAGGGCTTA 23
Db 1606 CGTGAGGGTTGTGAGGGCTTA 1626

RESULT 16
US-09-832-616-1
; Sequence 1, Application US/09832616
; Patent No. 6506586
; GENERAL INFORMATION:
; APPLICANT: Danielisen, Steffen
; APPLICANT: Schneider, Pallo
; TITLE OF INVENTION: Nucleic acids encoding polypeptides having haloperoxidase activity
; FILE REFERENCE: 10175.200-US
; CURRENT APPLICATION NUMBER: US/09/832,616
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1815
; TYPE: DNA
; ORGANISM: Dreschlera hartleibii
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1815)
US-09-832-616-1
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Query Match      67.5%; Score 16.2; DB 4; Length 1815;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGAGACGGTCTTGAGGGCTTA 23
    |||||
Db 1606 CGTGAGGGTTGTGAGGGCTTA 1626

RESULT 17
US-09-269-939A-41/c
; Sequence 41, Application US/09269939A
; Patent No. 6635431
; GENERAL INFORMATION:
; APPLICANT: Bihain, Bernard
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Yen-Potin, Frances
; TITLE OF INVENTION: LSR Receptor, Its Activity, Its Cloning and Its Application To
; TITLE OF INVENTION: The Diagnosis Prevention And/or Treatment of Obesity and
; TITLE OF INVENTION: Related Risks or Complications
; FILE REFERENCE: GENSET-035APC
; CURRENT APPLICATION NUMBER: US/09/269,939A
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: FR 97/40088
; PRIOR FILING DATE: 1997-08-06
; PRIOR APPLICATION NUMBER: FR 98/05032
; PRIOR FILING DATE: 1998-04-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent.pm
; SEQ ID NO 41
; LENGTH: 21721
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1898..2253
; NAME/KEY: exon
; LOCATION: 3438..3782
; NAME/KEY: exon
; LOCATION: 12064..12183
; NAME/KEY: exon
; LOCATION: 15049..15105
; NAME/KEY: exon
; LOCATION: 15670..15816
; NAME/KEY: exon
; LOCATION: 19486..19659
; NAME/KEY: exon
; LOCATION: 19806..19865
; NAME/KEY: exon
; LOCATION: 19963..20094
; NAME/KEY: exon
; LOCATION: 20236..20864
; NAME/KEY: exon
; LOCATION: 20954..21094
; NAME/KEY: Misc_Feature
; LOCATION: 715
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AC002128
; NAME/KEY: Misc_Feature
; LOCATION: 1229
; OTHER INFORMATION: diverging insertion, G in ref genbank:AC002128
; NAME/KEY: Misc_Feature
; LOCATION: 3676
; OTHER INFORMATION: diverging nucleotide, T in ref genbank:AC002128
; NAME/KEY: Misc_Feature
; LOCATION: 5039
; OTHER INFORMATION: diverging deletion, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 5118
; OTHER INFORMATION: diverging nucleotide, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 7337
; OTHER INFORMATION: diverging deletion, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 8294
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 8604
; OTHER INFORMATION: diverging nucleotide, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 8928
; OTHER INFORMATION: diverging nucleotide, A in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 9021
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 9851
; OTHER INFORMATION: diverging insertion, GAATGAAA in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 9878
; OTHER INFORMATION: diverging nucleotide, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 11478
; OTHER INFORMATION: diverging nucleotide, T in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 11577
; OTHER INFORMATION: diverging deletion, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 11779
; OTHER INFORMATION: diverging nucleotide, T in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 13411
; OTHER INFORMATION: diverging deletion, T in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 13538
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 13896
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 14912
; OTHER INFORMATION: diverging nucleotide, A in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 16732
; OTHER INFORMATION: diverging nucleotide, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 17169
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 18946
; OTHER INFORMATION: diverging deletion, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 19474
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 20500
; OTHER INFORMATION: diverging deletion, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 20501
; OTHER INFORMATION: diverging deletion, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 20502
; OTHER INFORMATION: diverging deletion, A in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 21270
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 21356
; OTHER INFORMATION: diverging insertion, T in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 21476
; OTHER INFORMATION: diverging nucleotide, A in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 21588
; OTHER INFORMATION: diverging insertion, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
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; LOCATION: 21601  
 ; OTHER INFORMATION: diverging deletion, T in ref genbank:AD000684  
 ; NAME/KEY: Misc.Feature  
 ; LOCATION: 21635  
 ; OTHER INFORMATION: diverging insertion, G in ref genbank:AD000684  
 ; NAME/KEY: Misc.Feature  
 ; LOCATION: 19963..19965  
 ; OTHER INFORMATION: Potential variant splicing site AAG  
 ; NAME/KEY: Misc.Feature  
 ; LOCATION: 1..21721  
 ; OTHER INFORMATION: n= a,g,c or t  
 ; US-09-269-939A-41

Query Match 67.5%; Score 16.2; DB 4; Length 21721;  
 Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTCTGAGGGCT 21  
 Db 14809 TCCAGGGGGTCTCTGAGGGCT 14789

RESULT 18  
 US-09-269-939A-19/c  
 ; Sequence 19, Application US/09269939A  
 ; Patent No. 6635431  
 ; GENERAL INFORMATION:

; APPLICANT: Bihain, Bernard  
 ; APPLICANT: Bougueleret, Lydie  
 ; APPLICANT: Yen-Potin, Frances  
 ; TITLE OF INVENTION: LSR Receptor, Its Activity, Its Cloning and Its Application To  
 ; TITLE OF INVENTION: The Diagnosis Prevention And/or Treatment of Obesity and  
 ; TITLE OF INVENTION: Related Risks or Complications  
 ; FILE REFERENCE: GENSET.035APC  
 ; CURRENT APPLICATION NUMBER: US/09/269,939A  
 ; PRIOR FILING DATE: 1999-05-28  
 ; PRIOR APPLICATION NUMBER: FR 97/10088  
 ; PRIOR FILING DATE: 1997-08-06  
 ; PRIOR APPLICATION NUMBER: FR 98/05032  
 ; PRIOR FILING DATE: 1998-04-22  
 ; NUMBER OF SEQ ID NOS: 41  
 ; SOFTWARE: Patent.pm

SEQ ID NO 19  
 LENGTH: 22976

TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: 1898..2253  
 NAME/KEY: exon  
 LOCATION: 3437..3781  
 NAME/KEY: exon  
 LOCATION: 12065..12184  
 NAME/KEY: exon  
 LOCATION: 15045..15101  
 NAME/KEY: exon  
 LOCATION: 15666..15812  
 NAME/KEY: exon  
 LOCATION: 19479..19652  
 NAME/KEY: exon  
 LOCATION: 19799..19858  
 NAME/KEY: exon  
 LOCATION: 19956..20087  
 NAME/KEY: exon  
 LOCATION: 20229..20854  
 NAME/KEY: exon  
 LOCATION: 20944..21094  
 NAME/KEY: Misc.Feature  
 LOCATION: 19956..19958  
 ; OTHER INFORMATION: Potential variant splicing site AAG  
 ; US-09-269-939A-19

Query Match

67.5%; Score 16.2; DB 4; Length 22976;

Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 TCCGAGACGGTCTCTGAGGGCT 21  
 Db 14805 TCCAGGGGGTCTCTGAGGGCT 14785

RESULT 19

US-09-499-522-1/c  
 ; Sequence 1, Application US/09499522  
 ; Patent No. 6479238  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Blumenfeld, Marta  
 ; APPLICANT: Bougueleret, Lydie  
 ; APPLICANT: Bihain, Bernard  
 ; TITLE OF INVENTION: POLYMORPHIC MARKERS OF THE LSR GENE  
 ; FILE REFERENCE: GENSET.053AUS  
 ; CURRENT APPLICATION NUMBER: US/09/499,522  
 ; CURRENT FILING DATE: 2000-02-10  
 ; EARLIER APPLICATION NUMBER: US 60/119,592  
 ; EARLIER FILING DATE: 1999-02-10  
 ; EARLIER APPLICATION NUMBER: US 60/144,784  
 ; EARLIER FILING DATE: 1999-07-20  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 1  
 ; LENGTH: 23187  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 NAME/KEY: exon  
 LOCATION: 2001..2356  
 ; OTHER INFORMATION: exon1  
 ; FEATURE:  
 NAME/KEY: exon  
 LOCATION: 3540..3884  
 ; OTHER INFORMATION: exon2  
 ; FEATURE:  
 NAME/KEY: exon  
 LOCATION: 12163..12282  
 ; OTHER INFORMATION: exon3  
 ; FEATURE:  
 NAME/KEY: exon  
 LOCATION: 15144..15200  
 ; OTHER INFORMATION: exon4  
 ; FEATURE:  
 NAME/KEY: exon  
 LOCATION: 15765..15911  
 ; OTHER INFORMATION: exon5  
 ; FEATURE:  
 NAME/KEY: exon  
 LOCATION: 19579..19752  
 ; OTHER INFORMATION: exon6  
 ; FEATURE:  
 NAME/KEY: exon  
 LOCATION: 19899..19958  
 ; OTHER INFORMATION: exon7  
 ; FEATURE:  
 NAME/KEY: exon  
 LOCATION: 20056..20187  
 ; OTHER INFORMATION: exon8  
 ; FEATURE:  
 NAME/KEY: exon  
 LOCATION: 20329..20957  
 ; OTHER INFORMATION: exon9  
 ; FEATURE:  
 NAME/KEY: exon  
 LOCATION: 21047..21187  
 ; OTHER INFORMATION: exon10  
 ; FEATURE:  
 NAME/KEY: polyA signal  
 LOCATION: 21168..21173

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; OTHER INFORMATION: AATAAA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..2000
; OTHER INFORMATION: potential 5'regulatory region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 22324..23187
; OTHER INFORMATION: homology with USF2 gene in ref: emb1 Y07661
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 523..544
; OTHER INFORMATION: upstream amplification primer 17-2
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 1047..1068
; OTHER INFORMATION: downstream amplification primer 17-2, complement
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 946..963
; OTHER INFORMATION: upstream amplification primer 99-4576
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 1385..1402
; OTHER INFORMATION: downstream amplification primer 99-4576, complement
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 1096..1115
; OTHER INFORMATION: upstream amplification primer 9-19
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 1616..1635
; OTHER INFORMATION: downstream amplification primer 9-19, complement
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 1602..1621
; OTHER INFORMATION: upstream amplification primer 9-20
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 2074..2093
; OTHER INFORMATION: downstream amplification primer 9-20, complement
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 2036..2053
; OTHER INFORMATION: upstream amplification primer 99-4557
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 2563..2580
; OTHER INFORMATION: downstream amplification primer 99-4557, complement
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 2084..2102
; OTHER INFORMATION: upstream amplification primer 9-1
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 2483..2500
; OTHER INFORMATION: downstream amplification primer 9-1, complement
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 2470..2489
; OTHER INFORMATION: upstream amplification primer 9-21, complement
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 2062..2081
; OTHER INFORMATION: downstream amplification primer 9-21
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 3455..3474
; OTHER INFORMATION: upstream amplification primer 9-3
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 3882..3901
; OTHER INFORMATION: downstream amplification primer 9-3, complement

```

```

; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 3775..3792
; OTHER INFORMATION: upstream amplification primer 99-4558
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 4336..4356
; OTHER INFORMATION: downstream amplification primer 99-4558, complement
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 4902..4920
; OTHER INFORMATION: upstream amplification primer 99-14419, complement
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 4444..4463
; OTHER INFORMATION: downstream amplification primer 99-14419
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 6638..6655
; OTHER INFORMATION: upstream amplification primer 99-4577
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 7072..7089
; OTHER INFORMATION: downstream amplification primer 99-4577, complement
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 7995..8012
; OTHER INFORMATION: upstream amplification primer 99-4559
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 8576..8593
; OTHER INFORMATION: downstream amplification primer 99-4559, complement
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 9622..9639
; OTHER INFORMATION: upstream amplification primer 99-3148
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 10023..10040
; OTHER INFORMATION: downstream amplification primer 99-3148, complement
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 9964..9981
; OTHER INFORMATION: upstream amplification primer 99-4560
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 10546..10563
; OTHER INFORMATION: downstream amplification primer 99-4560, complement
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 10996..11015
; OTHER INFORMATION: upstream amplification primer 99-14411, complement
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 10492..10512
; OTHER INFORMATION: downstream amplification primer 99-14411
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 11972..11990
; OTHER INFORMATION: upstream amplification primer 99-4561
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 12481..12501
; OTHER INFORMATION: downstream amplification primer 99-4561, complement

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Query Match 67.5%; Score 16.2; DB 4; Length 23187;  
 Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTGAGGCT 21  
 ||||| ||||| ||||| |||||

Db 14904 TCCAGGGGGTCTGAGGCT 14884

```
RESULT 20
US-09-252-991A-8519
; Sequence 8519, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8519
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8519

Query Match      66.7%; Score 16; DB 4; Length 522;
Best Local Similarity 79.2%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGGCTTAC 24
Db 425 TCCGAGACGGTTCGAGGGCTTGC 448

RESULT 21
US-09-270-767-12997
; Sequence 12997, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12997
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12997

Query Match      66.7%; Score 16; DB 4; Length 579;
Best Local Similarity 79.2%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGGCTTAC 24
Db 195 TCCGAGACGGTTCGAGGGCTTTC 218

RESULT 22
US-09-252-991A-8445
; Sequence 8445, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
```

```
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8445
; LENGTH: 1113
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8445

Query Match      66.7%; Score 16; DB 4; Length 1113;
Best Local Similarity 79.2%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGGCTTAC 24
Db 103 TCCGAGACGGTTCGAGGGCTTGC 126

RESULT 23
US-09-799-451-367
; Sequence 367, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Kyle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yungqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 367
; LENGTH: 1850
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (274)..(1236)
US-09-799-451-367

Query Match      66.7%; Score 16; DB 4; Length 1850;
Best Local Similarity 79.2%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGGCTTAC 24
Db 587 TCCGAGCCTTTCGAGGGCTTTC 610

RESULT 24
US-09-252-991A-8479
; Sequence 8479, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
```

```

; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/199,507B
; FILING DATE: 22 FEBRUARY 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
;
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-199-507B-21
;
; Query Match 65.8%; Score 15.8; DB 1; Length 37;
; Best Local Similarity 89.5%; Pred. No. 2.2e+02;
; Matches 17; Conservative 0; Mismatches 2; Indels
;
;
; QY 2 CCAGACGGTCTCAGGGC 20
; DB 20 CCAGACGGTCTCAGGGC 2
;
;
; RESULT 27
; US-08-441-828-21/c
; Sequence 21, Application US/08441828
; Patent No. 5734034
; GENERAL INFORMATION:
; APPLICANT: JAVASENA, S. AND GOLD, L.
; TITLE OF INVENTION: NUCLEIC ACID LIGAND INHIBITORS
; TITLE OF INVENTION: OF HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB
; MEDIUM TYPE: storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,828
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/199,507

```

```
/ FILING DATE: 22 FEBRUARY 1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/714,131
/ FILING DATE: 10-JUNE-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/536,428
/ FILING DATE: 11-JUNE-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Barry J. Swanson
/ REGISTRATION NUMBER: 33,215
/ REFERENCE/DOCKET NUMBER: NEX13
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (303) 793-3333
/ TELEFAX: (303) 793-3433
/ INFORMATION FOR SEQ ID NO: 21:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 37 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-441-828-21

Query Match 65.8%; Score 15.8; DB 1; Length 37;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTTCGAGGC 20
Db 20 CCGAGACGGTTCGAGGC 2

RESULT 28
US-09-949-016-192257
/ Sequence 192257, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 192257
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
/ US-09-949-016-192257

Query Match 65.8%; Score 15.8; DB 4; Length 601;
Best Local Similarity 89.5%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGACGGTTCGAGGCCTTA 23
Db 126 AGACGGCTCTGAGGCCTA 144

RESULT 29
US-08-292-688A-10
/ Sequence 10, Application US/08292688A
/ Patent No. 5814493
/ GENERAL INFORMATION:
/ APPLICANT: ROBERTSON, Donald L.
/ APPLICANT: FISHER, Kuhia L.
/ TITLE OF INVENTION: VIRUSES AND EXPRESSION VECTORS
```

```
/ TITLE OF INVENTION: CONTAINING LTR SIZE VARIANTS
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
/ STREET: P.O. Box 1404
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: United States
/ ZIP: 22313-1404
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/292,688A
/ FILING DATE: 18-AUG-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Radio, Susan M.
/ REGISTRATION NUMBER: 40,373
/ REFERENCE/DOCKET NUMBER: 004535-001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 836-6620
/ TELEFAX: (703) 836-2021
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1621 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-292-688A-10

Query Match 65.8%; Score 15.8; DB 1; Length 1621;
Best Local Similarity 89.5%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGACGGTTCGAGGCCTTA 23
Db 980 AGACGGTTCGAGGCCTTA 998

RESULT 30
US-08-791-849A-12
/ Sequence 12, Application US/08791849A
/ Patent No. 5914449
/ GENERAL INFORMATION:
/ APPLICANT: Makoto MURASE et al.
/ TITLE OF INVENTION: Method for Increasing Storage
/ Capacity in Plant Seed
/ NUMBER OF SEQUENCES: 15
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Wenderoth, Lind & Ponack
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: Wordperfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/791,849A
/ FILING DATE: January 30, 1997
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warren M. Cheek, Jr.
```

REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1795 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: soybean (Glycine max)  
US-08-791-849A-12

Query Match 65.8%; Score 15.8; DB 2; Length 1795;  
Best Local Similarity 89.5%; Pred. No. 3.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCGAGCGTCTCTGAGGC 20  
Db 177 CCGAGAGCTCTGAGGC 195

RESULT 31  
US-09-949-016-17389/c  
Sequence 17389, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17389  
LENGTH: 55031  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)...((55031)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-17389

Query Match 65.8%; Score 15.8; DB 4; Length 55031;  
Best Local Similarity 89.5%; Pred. No. 5.1e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGACGGTCTCTGAGGCTT 22  
Db 52159 GAGACGCTCTGAGGCTT 52141

RESULT 32  
US-09-949-016-17230/c  
Sequence 17230, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17230  
LENGTH: 90776  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-17230

Query Match 65.8%; Score 15.8; DB 4; Length 90776;  
Best Local Similarity 89.5%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGACGGTCTCTGAGGCTTA 23  
Db 45462 AGACGCTCTGAGGCTTA 45444

RESULT 33  
US-09-949-016-14132  
Sequence 14132, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14132  
LENGTH: 122772  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-14132

Query Match 65.8%; Score 15.8; DB 4; Length 122772;  
Best Local Similarity 89.5%; Pred. No. 5.5e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAGACGGTCTCTGAGGCT 21  
Db 76088 CGAGACGTTCTGAGGCT 76106

RESULT 34  
US-09-949-016-12147  
Sequence 12147, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20

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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12147
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12147

Query Match          65.8%; Score 15.8; DB 4; Length 767677;
Best Local Similarity 89.5%; Pred. No. 6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTCTCGAGGC 20
Db 240204 CCGAGATGGTCTGAGTGC 240222

RESULT 35
US-09-949-016-17361
; Sequence 17361, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17361
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17361

Query Match          65.8%; Score 15.8; DB 4; Length 767677;
Best Local Similarity 89.5%; Pred. No. 6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTCTCGAGGC 20
Db 240204 CCGAGATGGTCTGAGTGC 240222

RESULT 36
US-09-949-016-45837
; Sequence 45837, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
```

```
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45837
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-45837
```

```
Query Match          65.0%; Score 15.6; DB 4; Length 601;
Best Local Similarity 81.8%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 TCCGAGACGGTCTCGAGGCTT 22
Db 96 TCCGAGAGGGGCTCGAGGCTT 117
```

```
RESULT 37
US-09-949-016-45859
; Sequence 45859, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45859
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-45859
```

```
Query Match          65.0%; Score 15.6; DB 4; Length 601;
Best Local Similarity 81.8%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 TCCGAGACGGTCTCGAGGCTT 22
Db 96 TCCGAGAGGGGCTCGAGGCTT 117
```

```
RESULT 38
US-09-489-039A-1034
; Sequence 1034, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 1034
```



```

; LENGTH: 948
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1034

Query Match      65.0%; Score 15.6; DB 4; Length 948;
Best Local Similarity 81.8%; Pred. No. 4.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 CGAGACGGTCTCAGGCGCTTAC 24
||||| ||||| ||||| ||||| |||||
Db 780 CGAGCGCGTCTCAGGCGCTTAC 801

RESULT 39
US-09-248-796A-6062
; Sequence 6062, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 6062
; LENGTH: 1341
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-6062

Query Match      65.0%; Score 15.6; DB 4; Length 1341;
Best Local Similarity 81.8%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 CGAGACGGTCTCAGGCGCTTAC 24
||||| ||||| ||||| ||||| |||||
Db 669 CCAGCGCGTCTCAGACGCTTAC 690

RESULT 40
US-09-902-540-8806/c
; Sequence 8806, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8806
; LENGTH: 2121
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8806

Query Match      65.0%; Score 15.6; DB 4; Length 2121;
Best Local Similarity 81.8%; Pred. No. 4.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCAGGCGCTT 22
||||| ||||| ||||| ||||| |||||

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Db 737 TCCGGGCCGGTCTGTGAGGCCT 716

RESULT 41
US-09-949-016-253/c
; Sequence 253, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 253
; LENGTH: 2332
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-253

Query Match      65.0%; Score 15.6; DB 4; Length 2332;
Best Local Similarity 81.8%; Pred. No. 4.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CCGAGACGGTCTGTGAGGCCTTA 23
||||| ||||| ||||| ||||| |||||
Db 1016 CCAGGACGGTCTTCCGGGCTTA 995

RESULT 42
US-09-949-016-5522/c
; Sequence 5522, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5522
; LENGTH: 2332
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5522

Query Match      65.0%; Score 15.6; DB 4; Length 2332;
Best Local Similarity 81.8%; Pred. No. 4.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CCGAGACGGTCTGTGAGGCCTTA 23
||||| ||||| ||||| ||||| |||||
Db 1016 CCAGGACGGTCTTCCGGGCTTA 995

RESULT 43
US-09-949-016-408/c

```

; Sequence 408, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 408  
; LENGTH: 3595  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-408

Query Match 65.0%; Score 15.6; DB 4; Length 3595;  
Best Local Similarity 81.8%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CGAGACGGTCTGAGGCGCTTAC 24  
Db 2924 CAAGAGCGCTCTGAGGCGCTTAC 2903

## RESULT 44

US-09-563-269-17/c  
; Sequence 17, Application US/09563269  
; Patent No. 6555655  
; GENERAL INFORMATION:  
; APPLICANT: RUPAR, MARK J.  
; APPLICANT: DONOVAN, WILLIAM P.  
; APPLICANT: CHU, CHIH-REI  
; APPLICANT: PEASE, ELIZABETH  
; APPLICANT: TAN, YUPING  
; APPLICANT: SLANEY, ANNETTE C.  
; APPLICANT: BAUM, JAMES A.  
; APPLICANT: MALVAR, THOMAS M.  
; TITLE OF INVENTION: COLEOPTERAN-TOXIC POLYPEPTIDE COMPOSITIONS AND INSECT  
; FILE REFERENCE: MEC0164  
; CURRENT APPLICATION NUMBER: US/09/563,269  
; CURRENT FILING DATE: 2000-05-03  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 3607  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis  
US-09-563-269-17

Query Match 65.0%; Score 15.6; DB 4; Length 3607;  
Best Local Similarity 81.8%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTGAGGCGCTT 22  
Db 3547 TTCTAGACGCTTCTGAGGCGATT 3526

## RESULT 45

US-08-506-296B-27  
; Sequence 27, Application US/08506296B  
; Patent No. 6313265  
; GENERAL INFORMATION:  
; APPLICANT: Phillips, Greg

; APPLICANT: Cunningham, Bruce A.  
; APPLICANT: Crossin, Kathryn L.  
; TITLE OF INVENTION: NEURITE OUTGROWTH-PROMOTING POLYPEPTIDES  
; TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute  
; STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8  
; CITY: La Jolla  
; STATE: California  
; COUNTRY: U.S.  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/506,296B  
; FILING DATE: 24-JUL-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: TSRI 488.0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 554-2937  
; TELEFAX: (619) 554-6312  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3943 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 33..3839  
US-08-506-296B-27

Query Match 65.0%; Score 15.6; DB 3; Length 3943;  
Best Local Similarity 81.8%; Pred. No. 4.7e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTGAGGCGCTT 22  
Db 3325 TCCGAGTGTGCTGAGGCGCT 3346

## RESULT 46

US-09-949-016-1305  
; Sequence 1305, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1305  
; LENGTH: 4041  
; TYPE: DNA

```

; ORGANISM: Human
US-09-949-016-1305

Query Match      65.0%; Score 15.6; DB 4; Length 4041;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTT 22
| ||||| || ||||| ||||| |||||
Db 1768 TCCGAGAGGGCCTCTGAGGGCTT 1789

RESULT 47
US-09-949-016-1306
; Sequence 1306, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1306
; LENGTH: 4041
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1306

Query Match      65.0%; Score 15.6; DB 4; Length 4041;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTT 22
| ||||| || ||||| ||||| |||||
Db 1768 TCCGAGAGGGCCTCTGAGGGCTT 1789

RESULT 48
US-09-016-434-1152/c
; Sequence 1152, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1152:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4078 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1524091
US-09-016-434-1152

Query Match      65.0%; Score 15.6; DB 4; Length 4078;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTT 22
| ||||| || ||||| ||||| |||||
Db 2759 TCCGAGACGCTGTTGAGGGCAT 2738

RESULT 49
US-09-949-016-4140/c
; Sequence 4140, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4140
; LENGTH: 4546
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4140

Query Match      65.0%; Score 15.6; DB 4; Length 4546;
Best Local Similarity 81.8%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTT 22
| ||||| || ||||| ||||| |||||
Db 2752 TCCGAGACGCTGTTGAGGGCAT 2731

RESULT 50
US-09-023-655-975/c
; Sequence 975, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

```

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/ TITLE OF INVENTION: EXPRESSION
/ NUMBER OF SEQUENCES: 1508
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WordPerfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/023,655
/ FILING DATE: HEREMITH
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0001 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 975:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4553 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: g1524091
/
US-09-023-655-975

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Query Match      65.0%; Score 15.6; DB 4; Length 4553;
Best Local Similarity 81.8%; Pred. NO. 4.8e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy      1 TCCGACGCGTCTGTGAGGCTT 22
      |||||
Db      2759 TCCGACGCGTGTGAGGCGAT 2738

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Search completed: March 25, 2005, 12:35:23  
Job time : 119.786 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 11:41:26 ; Search time 277.714 Seconds  
(without alignments)  
515.004 Million cell updates/sec

Title: US-10-688-489-75  
Perfect score: 24  
Sequence: 1 tcgcagcggtcttgagggttacc 24

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5552208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters: 11104416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : Published Applications\_NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1          | 24    | 100.0       | 24     | 18 | US-10-688-489-74  |
| 2          | 24    | 100.0       | 24     | 18 | US-10-688-489-75  |
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| 4          | 24    | 100.0       | 25     | 18 | US-10-815-480-2   |
| 5          | 24    | 100.0       | 25     | 18 | US-10-815-480-7   |
| 6          | 24    | 100.0       | 25     | 18 | US-10-815-480-8   |
| 7          | 24    | 100.0       | 48     | 18 | US-10-688-489-73  |
| 8          | 24    | 100.0       | 51     | 18 | US-10-688-489-84  |
| 9          | 24    | 100.0       | 70     | 18 | US-10-688-489-72  |
| 10         | 24    | 100.0       | 98     | 18 | US-10-815-480-71  |
| 11         | 24    | 100.0       | 10945  | 18 | US-10-361-002-5   |
|            |       |             |        |    | Sequence 74, Appl |
|            |       |             |        |    | Sequence 75, Appl |
|            |       |             |        |    | Sequence 1, Appl  |
|            |       |             |        |    | Sequence 2, Appl  |
|            |       |             |        |    | Sequence 7, Appl  |
|            |       |             |        |    | Sequence 8, Appl  |
|            |       |             |        |    | Sequence 73, Appl |
|            |       |             |        |    | Sequence 74, Appl |
|            |       |             |        |    | Sequence 84, Appl |
|            |       |             |        |    | Sequence 72, Appl |
|            |       |             |        |    | Sequence 71, Appl |
|            |       |             |        |    | Sequence 5, Appl  |

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| 24 | 100.0 | 11029  | 19 | US-10-679-520A-66    | Sequence 66, Appl                  |
| 24 | 100.0 | 11029  | 19 | US-10-706-892-1      | Sequence 1, Appl                   |
| 23 | 95.8  | 23     | 18 | US-10-706-892-76     | Sequence 76, Appl                  |
| 23 | 95.8  | 50     | 18 | US-10-688-489-85     | Sequence 85, Appl                  |
| 22 | 91.7  | 22     | 18 | US-10-688-489-77     | Sequence 2, Appl                   |
| 22 | 91.7  | 22     | 18 | US-10-688-489-86     | Sequence 77, Appl                  |
| 21 | 87.5  | 49     | 18 | US-10-688-489-87     | Sequence 86, Appl                  |
| 21 | 87.5  | 23     | 18 | US-10-688-489-149    | Sequence 149, Appl                 |
| 19 | 79.2  | 19     | 18 | US-10-688-489-116    | Sequence 116, Appl                 |
| 18 | 79.2  | 87     | 18 | US-10-688-489-101    | Sequence 101, Appl                 |
| 17 | 74.2  | 434    | 17 | US-10-425-114-6462   | Sequence 6462, Ap                  |
| 17 | 74.2  | 1831   | 17 | US-10-424-599-28488  | Sequence 28488, A                  |
| 17 | 73.3  | 1661   | 17 | US-10-225-066A-1045  | Sequence 1045, Ap                  |
| 17 | 73.3  | 1661   | 17 | US-10-302-267-29     | Sequence 29, Appl                  |
| 17 | 73.3  | 1661   | 17 | US-10-374-780A-2387  | Sequence 2387, Ap                  |
| 17 | 73.3  | 1661   | 17 | US-10-412-699B-411   | Sequence 411, Appl                 |
| 17 | 73.3  | 1661   | 17 | US-10-425-114-12992  | Sequence 12992, A                  |
| 17 | 71.7  | 2060   | 17 | US-10-424-599-83676  | Sequence 83676, A                  |
| 17 | 71.7  | 26     | 18 | US-10-815-480-4      | Sequence 4, Appl                   |
| 17 | 70.0  | 487    | 10 | US-09-918-995-5377   | Sequence 5377, Ap                  |
| 17 | 70.0  | 704    | 18 | US-10-437-963-80309  | Sequence 80309, A                  |
| 17 | 70.0  | 1416   | 18 | US-10-437-963-21906  | Sequence 21906, A                  |
| 17 | 70.0  | 2802   | 17 | US-10-261-175A-3     | Sequence 3, Appl                   |
| 17 | 70.0  | 33488  | 17 | US-10-085-117-235    | Sequence 235, Appl                 |
| 17 | 70.0  | 135827 | 18 | US-10-322-281-232    | Sequence 232, Appl                 |
| 17 | 69.2  | 597    | 18 | US-10-357-930-55914  | Sequence 55914, A                  |
| 17 | 69.2  | 723    | 9  | US-09-919-580-6      | Sequence 6, Appl                   |
| 17 | 69.2  | 1671   | 17 | US-10-369-493-24654  | Sequence 24654, A                  |
| 17 | 68.3  | 26     | 18 | US-10-815-480-5      | Sequence 5, Appl                   |
| 17 | 68.3  | 1929   | 9  | US-09-938-842A-1241  | Sequence 1241, Ap                  |
| 17 | 68.3  | 1929   | 11 | US-09-938-842A-1241  | Sequence 1241, Ap                  |
| 17 | 67.5  | 616    | 17 | US-10-449-857A-67    | Sequence 67, Appl                  |
| 17 | 67.5  | 1055   | 17 | US-10-425-114-6252   | Sequence 6252, Ap                  |
| 17 | 67.5  | 1122   | 17 | US-10-424-599-35449  | Sequence 35449, A                  |
| 17 | 67.5  | 1275   | 17 | US-10-424-599-73661  | Sequence 73661, A                  |
| 17 | 67.5  | 1685   | 18 | US-10-437-963-83700  | Sequence 83700, A                  |
| 17 | 67.5  | 1815   | 9  | US-09-832-616-1      | Sequence 1, Appl                   |
| 17 | 67.5  | 1815   | 9  | US-09-832-496-1      | Sequence 1, Appl                   |
| 17 | 67.5  | 1836   | 17 | US-10-152-319A-1999  | Sequence 1999, Ap                  |
| 17 | 67.5  | 1929   | 13 | US-10-027-632-257296 | Sequence 257296, Sequence 257296,  |
| 17 | 67.5  | 1929   | 17 | US-10-027-632-257296 | Sequence 83697, A                  |
| 17 | 67.5  | 5082   | 18 | US-10-437-963-83697  | Sequence 37, Appl                  |
| 17 | 67.5  | 5561   | 17 | US-10-429-802-37     | Sequence 28, Appl                  |
| 17 | 67.5  | 5561   | 17 | US-10-430-503-28     | Sequence 7543, Ap                  |
| 17 | 67.5  | 6734   | 10 | US-09-764-891-7543   | Sequence 43, Appl                  |
| 17 | 67.5  | 6752   | 18 | US-10-688-845-43     | Sequence 7544, Ap                  |
| 17 | 67.5  | 6756   | 10 | US-09-764-891-7544   | Sequence 41, Appl                  |
| 17 | 67.5  | 21721  | 17 | US-10-650-507-41     | Sequence 19, Appl                  |
| 17 | 67.5  | 22976  | 17 | US-10-650-507-19     | Sequence 1, Appl                   |
| 17 | 67.5  | 23187  | 16 | US-10-214-68A-1      | Sequence 116, Appl                 |
| 17 | 67.5  | 41936  | 9  | US-09-967-768A-116   | Sequence 31, Appl                  |
| 17 | 67.5  | 47098  | 17 | US-10-052-482-31     | Sequence 1789, Ap                  |
| 17 | 67.5  | 80077  | 13 | US-10-087-192-1789   | Sequence 5, Appl                   |
| 17 | 67.5  | 207433 | 17 | US-10-277-216-5      | Sequence 5, Appl                   |
| 17 | 67.5  | 207433 | 17 | US-10-126-022-5      | Sequence 841899, Sequence 4030, Ap |
| 17 | 66.7  | 25     | 19 | US-10-719-900-841899 | Sequence 34756, A                  |
| 17 | 66.7  | 364    | 17 | US-10-424-599-4030   | Sequence 106, App                  |
| 17 | 66.7  | 636    | 18 | US-10-425-115-34756  | Sequence 29600, A                  |
| 17 | 66.7  | 671    | 9  | US-09-764-853-106    | Sequence 1, Appl                   |
| 17 | 66.7  | 682    | 17 | US-10-369-493-29600  | Sequence 45, Appl                  |
| 17 | 66.7  | 872    | 17 | US-10-080-334-1      | Sequence 26978, A                  |
| 17 | 66.7  | 1458   | 15 | US-10-160-274-45     | Sequence 121, Appl                 |
| 17 | 66.7  | 1606   | 17 | US-10-425-114-25978  | Sequence 14, Appl                  |
| 17 | 66.7  | 1667   | 17 | US-10-094-749-121    | Sequence 19992, A                  |
| 17 | 66.7  | 1673   | 17 | US-10-296-606-14     | Sequence 367, Appl                 |
| 17 | 66.7  | 1822   | 18 | US-10-425-115-19992  | Sequence 39, Appl                  |
| 17 | 66.7  | 1850   | 17 | US-10-302-172-367    | Sequence 899, App                  |
| 17 | 66.7  | 2259   | 17 | US-10-291-265-39     | Sequence 6827, Ap                  |
| 17 | 66.7  | 11950  | 9  | US-09-764-853-899    |                                    |
| 17 | 66.7  | 160556 | 18 | US-10-719-993-6827   |                                    |

|     |      |      |         |    |                      |                        |       |      |      |      |    |                      |                      |
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| 85  | 16   | 66.7 | 2731748 | 18 | US-10-297-465A-1     | Sequence 1, Appli      | c 158 | 15.6 | 65.0 | 1849 | 18 | US-10-619-189-59     | Sequence 59, Appli   |
| 86  | 15.8 | 65.8 | 193     | 17 | US-10-424-599-232    | Sequence 232, App      | c 159 | 15.6 | 65.0 | 1951 | 17 | US-10-275-287-7      | Sequence 7, Appli    |
| 87  | 15.8 | 65.8 | 456     | 13 | US-10-027-632-285260 | Sequence 285260, Appli | c 160 | 15.6 | 65.0 | 1977 | 18 | US-10-619-189-33     | Sequence 33, Appli   |
| 88  | 15.8 | 65.8 | 456     | 13 | US-10-027-632-285261 | Sequence 285261, Appli | c 161 | 15.6 | 65.0 | 1977 | 18 | US-10-619-189-54     | Sequence 54, Appli   |
| 89  | 15.8 | 65.8 | 456     | 17 | US-10-027-632-285260 | Sequence 285260, Appli | c 162 | 15.6 | 65.0 | 1977 | 18 | US-10-619-189-58     | Sequence 58, Appli   |
| 90  | 15.8 | 65.8 | 456     | 17 | US-10-027-632-285261 | Sequence 285261, Appli | c 163 | 15.6 | 65.0 | 1977 | 18 | US-10-619-189-74     | Sequence 74, Appli   |
| 91  | 15.8 | 65.8 | 598     | 18 | US-10-021-323-9648   | Sequence 9648, App     | c 164 | 15.6 | 65.0 | 2000 | 9  | US-10-619-189-74     | Sequence 74, Appli   |
| 92  | 15.8 | 65.8 | 607     | 18 | US-10-357-930-57246  | Sequence 57246, App    | c 165 | 15.6 | 65.0 | 2000 | 11 | US-09-938-842A-5244  | Sequence 5244, App   |
| 93  | 15.8 | 65.8 | 637     | 17 | US-10-021-323-1197   | Sequence 1197, App     | c 166 | 15.6 | 65.0 | 2000 | 11 | US-09-938-842A-5244  | Sequence 5244, App   |
| 94  | 15.8 | 65.8 | 687     | 17 | US-10-424-599-95037  | Sequence 95037, App    | c 167 | 15.6 | 65.0 | 2068 | 9  | US-09-925-301-65     | Sequence 65, Appli   |
| 95  | 15.8 | 65.8 | 731     | 13 | US-10-027-632-147018 | Sequence 147018, App   | c 168 | 15.6 | 65.0 | 2167 | 17 | US-10-094-749-1611   | Sequence 1611, App   |
| 96  | 15.8 | 65.8 | 731     | 17 | US-10-027-632-147018 | Sequence 147018, App   | c 169 | 15.6 | 65.0 | 2303 | 18 | US-10-437-963-87573  | Sequence 87573, App  |
| 97  | 15.8 | 65.8 | 809     | 13 | US-10-027-632-143963 | Sequence 143963, App   | c 170 | 15.6 | 65.0 | 2332 | 18 | US-10-370-715B-575   | Sequence 575, App    |
| 98  | 15.8 | 65.8 | 809     | 17 | US-10-027-632-143963 | Sequence 143963, App   | c 171 | 15.6 | 65.0 | 2335 | 15 | US-10-119-926-50     | Sequence 50, Appli   |
| 99  | 15.8 | 65.8 | 1224    | 18 | US-10-767-795-4226   | Sequence 4226, App     | c 172 | 15.6 | 65.0 | 2335 | 17 | US-10-291-172-94     | Sequence 94, Appli   |
| 100 | 15.8 | 65.8 | 1282    | 17 | US-10-424-599-56333  | Sequence 56333, App    | c 173 | 15.6 | 65.0 | 2335 | 17 | US-10-221-278-94     | Sequence 94, Appli   |
| 101 | 15.8 | 65.8 | 1380    | 17 | US-10-424-599-56322  | Sequence 56322, App    | c 174 | 15.6 | 65.0 | 2555 | 17 | US-10-291-172-470    | Sequence 470, App    |
| 102 | 15.8 | 65.8 | 1380    | 17 | US-10-425-114-13692  | Sequence 13692, App    | c 175 | 15.6 | 65.0 | 2555 | 17 | US-10-221-278-470    | Sequence 470, App    |
| 103 | 15.8 | 65.8 | 3671    | 15 | US-10-128-714-4559   | Sequence 4559, App     | c 176 | 15.6 | 65.0 | 2574 | 17 | US-10-369-493-32402  | Sequence 32402, App  |
| 104 | 15.8 | 65.8 | 3812    | 15 | US-10-128-714-4559   | Sequence 4559, App     | c 177 | 15.6 | 65.0 | 2625 | 19 | US-10-741-849-6043   | Sequence 6043, App   |
| 105 | 15.8 | 65.8 | 96593   | 11 | US-09-997-722-16     | Sequence 16, Appli     | c 178 | 15.6 | 65.0 | 2672 | 17 | US-10-369-493-27194  | Sequence 27194, App  |
| 106 | 15.8 | 65.8 | 33381   | 19 | US-10-741-600-17681  | Sequence 17681, App    | c 179 | 15.6 | 65.0 | 2711 | 18 | US-10-357-930-22210  | Sequence 22210, App  |
| 107 | 15.6 | 65.0 | 206     | 17 | US-10-242-535A-23159 | Sequence 23159, App    | c 180 | 15.6 | 65.0 | 3004 | 17 | US-10-307-817-219    | Sequence 219, App    |
| 108 | 15.6 | 65.0 | 206     | 17 | US-10-085-783A-23159 | Sequence 23159, App    | c 181 | 15.6 | 65.0 | 3005 | 17 | US-10-307-817-219    | Sequence 219, App    |
| 109 | 15.6 | 65.0 | 402     | 10 | US-09-918-995-33100  | Sequence 33100, App    | c 182 | 15.6 | 65.0 | 3112 | 17 | US-10-369-493-27038  | Sequence 27038, App  |
| 110 | 15.6 | 65.0 | 410     | 18 | US-10-619-189-23     | Sequence 23, Appli     | c 183 | 15.6 | 65.0 | 3147 | 17 | US-10-307-817-215    | Sequence 215, App    |
| 111 | 15.6 | 65.0 | 431     | 17 | US-10-424-599-16296  | Sequence 16296, App    | c 184 | 15.6 | 65.0 | 3147 | 17 | US-10-307-817-215    | Sequence 215, App    |
| 112 | 15.6 | 65.0 | 442     | 10 | US-09-918-995-6236   | Sequence 6236, App     | c 185 | 15.6 | 65.0 | 3398 | 14 | US-10-198-846-10944  | Sequence 10944, App  |
| 113 | 15.6 | 65.0 | 442     | 18 | US-10-767-701-20827  | Sequence 20827, App    | c 186 | 15.6 | 65.0 | 3416 | 17 | US-10-424-599-141263 | Sequence 141263, App |
| 114 | 15.6 | 65.0 | 461     | 19 | US-10-696-633-2452   | Sequence 2452, App     | c 187 | 15.6 | 65.0 | 3607 | 17 | US-10-408-692-17     | Sequence 17, Appli   |
| 115 | 15.6 | 65.0 | 470     | 17 | US-10-242-535A-15857 | Sequence 15857, App    | c 188 | 15.6 | 65.0 | 3877 | 9  | US-09-764-847-1521   | Sequence 1521, App   |
| 116 | 15.6 | 65.0 | 470     | 17 | US-10-085-783A-15857 | Sequence 15857, App    | c 189 | 15.6 | 65.0 | 3877 | 14 | US-10-093-154-1521   | Sequence 1521, App   |
| 117 | 15.6 | 65.0 | 472     | 10 | US-09-918-995-21134  | Sequence 21134, App    | c 190 | 15.6 | 65.0 | 3879 | 9  | US-09-764-847-1519   | Sequence 1519, App   |
| 118 | 15.6 | 65.0 | 472     | 13 | US-10-027-632-286576 | Sequence 286576, App   | c 191 | 15.6 | 65.0 | 3879 | 14 | US-10-092-154-1519   | Sequence 1519, App   |
| 119 | 15.6 | 65.0 | 492     | 17 | US-10-027-632-286576 | Sequence 286576, App   | c 192 | 15.6 | 65.0 | 4017 | 9  | US-09-880-107-3029   | Sequence 3029, App   |
| 120 | 15.6 | 65.0 | 516     | 18 | US-10-619-189-22     | Sequence 22, Appli     | c 193 | 15.6 | 65.0 | 4021 | 14 | US-10-197-666A-137   | Sequence 137, App    |
| 121 | 15.6 | 65.0 | 516     | 18 | US-10-619-189-24     | Sequence 24, Appli     | c 194 | 15.6 | 65.0 | 4021 | 14 | US-10-305-720-1152   | Sequence 1152, App   |
| 122 | 15.6 | 65.0 | 544     | 13 | US-10-027-632-50478  | Sequence 50478, App    | c 195 | 15.6 | 65.0 | 4526 | 17 | US-10-379-632-63     | Sequence 63, Appli   |
| 123 | 15.6 | 65.0 | 544     | 13 | US-10-027-632-50479  | Sequence 50479, App    | c 196 | 15.6 | 65.0 | 4535 | 13 | US-10-087-192-1733   | Sequence 1733, App   |
| 124 | 15.6 | 65.0 | 544     | 17 | US-10-027-632-50478  | Sequence 50478, App    | c 197 | 15.6 | 65.0 | 4535 | 10 | US-09-960-706-1122   | Sequence 1122, App   |
| 125 | 15.6 | 65.0 | 544     | 17 | US-10-027-632-50479  | Sequence 50479, App    | c 198 | 15.6 | 65.0 | 4535 | 10 | US-09-873-319-744    | Sequence 744, App    |
| 126 | 15.6 | 65.0 | 582     | 18 | US-10-021-323-9209   | Sequence 9209, App     | c 199 | 15.6 | 65.0 | 4553 | 10 | US-09-873-367C-330   | Sequence 330, App    |
| 127 | 15.6 | 65.0 | 628     | 13 | US-10-027-632-136460 | Sequence 136460, App   | c 200 | 15.6 | 65.0 | 4553 | 17 | US-10-307-817-221    | Sequence 221, App    |
| 128 | 15.6 | 65.0 | 628     | 13 | US-10-027-632-136460 | Sequence 136460, App   | c 201 | 15.6 | 65.0 | 4553 | 17 | US-10-641-643-975    | Sequence 975, App    |
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| 130 | 15.6 | 65.0 | 639     | 13 | US-10-027-632-133837 | Sequence 133837, App   | c 203 | 15.6 | 65.0 | 4607 | 17 | US-10-379-632-66     | Sequence 66, Appli   |
| 131 | 15.6 | 65.0 | 639     | 13 | US-10-027-632-133838 | Sequence 133838, App   | c 204 | 15.6 | 65.0 | 4628 | 17 | US-10-379-632-66     | Sequence 66, Appli   |
| 132 | 15.6 | 65.0 | 639     | 13 | US-10-027-632-133839 | Sequence 133839, App   | c 205 | 15.6 | 65.0 | 4638 | 17 | US-10-379-632-9      | Sequence 9, Appli    |
| 133 | 15.6 | 65.0 | 639     | 17 | US-10-027-632-133837 | Sequence 133837, App   | c 206 | 15.6 | 65.0 | 4709 | 17 | US-10-379-632-62     | Sequence 62, Appli   |
| 134 | 15.6 | 65.0 | 639     | 17 | US-10-027-632-133838 | Sequence 133838, App   | c 207 | 15.6 | 65.0 | 4728 | 17 | US-10-379-632-62     | Sequence 62, Appli   |
| 135 | 15.6 | 65.0 | 639     | 17 | US-10-027-632-133839 | Sequence 133839, App   | c 208 | 15.6 | 65.0 | 4774 | 17 | US-10-379-632-22     | Sequence 22, Appli   |
| 136 | 15.6 | 65.0 | 639     | 17 | US-10-027-632-133840 | Sequence 133840, App   | c 209 | 15.6 | 65.0 | 4777 | 17 | US-10-379-632-38     | Sequence 38, Appli   |
| 137 | 15.6 | 65.0 | 639     | 17 | US-10-027-632-133840 | Sequence 133840, App   | c 210 | 15.6 | 65.0 | 4795 | 17 | US-10-379-632-6      | Sequence 6, Appli    |
| 138 | 15.6 | 65.0 | 712     | 13 | US-10-027-632-158494 | Sequence 158494, App   | c 211 | 15.6 | 65.0 | 4809 | 17 | US-10-379-632-65     | Sequence 65, Appli   |
| 139 | 15.6 | 65.0 | 725     | 13 | US-10-027-632-14209  | Sequence 14209, App    | c 212 | 15.6 | 65.0 | 4825 | 17 | US-10-379-632-35     | Sequence 35, Appli   |
| 140 | 15.6 | 65.0 | 725     | 13 | US-10-027-632-14209  | Sequence 14209, App    | c 213 | 15.6 | 65.0 | 4830 | 17 | US-10-379-632-40     | Sequence 40, Appli   |
| 141 | 15.6 | 65.0 | 757     | 13 | US-10-027-632-169459 | Sequence 169459, App   | c 214 | 15.6 | 65.0 | 4876 | 17 | US-10-379-632-71     | Sequence 71, Appli   |
| 142 | 15.6 | 65.0 | 757     | 13 | US-10-027-632-169459 | Sequence 169459, App   | c 215 | 15.6 | 65.0 | 4886 | 17 | US-10-379-632-44     | Sequence 44, Appli   |
| 143 | 15.6 | 65.0 | 757     | 17 | US-10-027-632-169459 | Sequence 169459, App   | c 216 | 15.6 | 65.0 | 4895 | 17 | US-10-379-632-8      | Sequence 8, Appli    |
| 144 | 15.6 | 65.0 | 757     | 17 | US-10-027-632-169459 | Sequence 169459, App   | c 217 | 15.6 | 65.0 | 4906 | 17 | US-10-379-632-64     | Sequence 64, Appli   |
| 145 | 15.6 | 65.0 | 896     | 13 | US-10-027-632-126347 | Sequence 126347, App   | c 218 | 15.6 | 65.0 | 4911 | 17 | US-10-379-632-34     | Sequence 34, Appli   |
| 146 | 15.6 | 65.0 | 896     | 13 | US-10-027-632-126348 | Sequence 126348, App   | c 219 | 15.6 | 65.0 | 4927 | 17 | US-10-379-632-39     | Sequence 39, Appli   |
| 147 | 15.6 | 65.0 | 896     | 17 | US-10-027-632-126347 | Sequence 126347, App   | c 220 | 15.6 | 65.0 | 4944 | 17 | US-10-379-632-3      | Sequence 3, Appli    |
| 148 | 15.6 | 65.0 | 896     | 17 | US-10-027-632-126348 | Sequence 126348, App   | c 221 | 15.6 | 65.0 | 4967 | 17 | US-10-379-632-49     | Sequence 49, Appli   |
| 149 | 15.6 | 65.0 | 938     | 9  | US-09-867-550-1629   | Sequence 1629, App     | c 222 | 15.6 | 65.0 | 4976 | 17 | US-10-379-632-21     | Sequence 21, Appli   |
| 150 | 15.6 | 65.0 | 1077    | 17 | US-10-243-552-701    | Sequence 701, App      | c 223 | 15.6 | 65.0 | 4979 | 17 | US-10-379-632-37     | Sequence 37, Appli   |
| 151 | 15.6 | 65.0 | 1287    | 18 | US-10-411-910A-190   | Sequence 190, App      | c 224 | 15.6 | 65.0 | 4981 | 17 | US-10-379-632-81     | Sequence 81, Appli   |
| 152 | 15.6 | 65.0 | 1335    | 18 | US-10-437-963-26436  | Sequence 26436, App    | c 225 | 15.6 | 65.0 | 4988 | 17 | US-10-379-632-41     | Sequence 41, Appli   |
| 153 | 15.6 | 65.0 | 1569    | 17 | US-10-424-599-18161  | Sequence 18161, App    | c 226 | 15.6 | 65.0 | 4992 | 17 | US-10-379-632-7      | Sequence 7, Appli    |
| 154 | 15.6 | 65.0 | 1620    | 18 | US-10-619-189-75     | Sequence 75, Appli     | c 227 | 15.6 | 65.0 | 4997 | 17 | US-10-379-632-5      | Sequence 5, Appli    |
| 155 | 15.6 | 65.0 | 1624    | 18 | US-10-437-963-2228   | Sequence 2228, App     | c 228 | 15.6 | 65.0 | 5008 | 17 | US-10-379-632-33     | Sequence 33, Appli   |
| 156 | 15.6 | 65.0 | 1778    | 18 | US-10-275-287-15     | Sequence 15, Appli     | c 229 | 15.6 | 65.0 | 5062 | 17 | US-10-379-632-78     | Sequence 78, Appli   |
| 157 | 15.6 | 65.0 | 1814    | 17 | US-10-275-287-6      | Sequence 6, Appli      | c 230 | 15.6 | 65.0 | 5069 | 17 | US-10-379-632-25     | Sequence 25, Appli   |
|     |      |      |         |    |                      |                        |       |      |      | 5073 | 17 | US-10-379-632-10     | Sequence 10, Appli   |

|     |      |      |        |    |                      |                    |       |      |      |       |    |                      |                   |
|-----|------|------|--------|----|----------------------|--------------------|-------|------|------|-------|----|----------------------|-------------------|
| 231 | 15.6 | 65.0 | 5076   | 17 | US-10-379-632-36     | Sequence 36, Appl  | 304   | 15.4 | 64.2 | 3015  | 18 | US-10-437-963-41677  | Sequence 41677, A |
| 232 | 15.6 | 65.0 | 5078   | 17 | US-10-379-632-69     | Sequence 69, Appl  | c 305 | 15.4 | 64.2 | 92076 | 18 | US-10-322-281-465    | Sequence 465, App |
| 233 | 15.6 | 65.0 | 5083   | 17 | US-10-379-632-75     | Sequence 75, Appl  | 306   | 15.2 | 63.3 | 60    | 10 | US-09-908-973-15491  | Sequence 15491, A |
| 234 | 15.6 | 65.0 | 5088   | 17 | US-10-379-632-43     | Sequence 43, Appl  | 307   | 15.2 | 63.3 | 201   | 18 | US-10-719-993-3740   | Sequence 3740, Ap |
| 235 | 15.6 | 65.0 | 5094   | 17 | US-10-379-632-4      | Sequence 4, Appl   | 308   | 15.2 | 63.3 | 201   | 18 | US-10-719-993-3742   | Sequence 3742, Ap |
| 236 | 15.6 | 65.0 | 5137   | 17 | US-10-379-632-28     | Sequence 28, Appl  | 309   | 15.2 | 63.3 | 201   | 18 | US-10-719-993-3744   | Sequence 3744, Ap |
| 237 | 15.6 | 65.0 | 5146   | 17 | US-10-379-632-2      | Sequence 2, Appl   | c 310 | 15.2 | 63.3 | 226   | 18 | US-10-425-115-1487   | Sequence 1487, Ap |
| 238 | 15.6 | 65.0 | 5164   | 17 | US-10-379-632-72     | Sequence 72, Appl  | 311   | 15.2 | 63.3 | 221   | 16 | US-10-029-386-19036  | Sequence 19036, A |
| 239 | 15.6 | 65.0 | 5169   | 17 | US-10-379-632-47     | Sequence 47, Appl  | 312   | 15.2 | 63.3 | 343   | 17 | US-10-424-599-116755 | Sequence 116755,  |
| 240 | 15.6 | 65.0 | 5175   | 17 | US-10-379-632-68     | Sequence 68, Appl  | 313   | 15.2 | 63.3 | 344   | 9  | US-09-878-134-220    | Sequence 220, App |
| 241 | 15.6 | 65.0 | 5183   | 17 | US-10-379-632-80     | Sequence 80, Appl  | 314   | 15.2 | 63.3 | 375   | 13 | US-10-040-739-1462   | Sequence 1462, Ap |
| 242 | 15.6 | 65.0 | 5185   | 17 | US-10-379-632-42     | Sequence 42, Appl  | c 315 | 15.2 | 63.3 | 441   | 11 | US-09-864-408A-5553  | Sequence 5553, Ap |
| 243 | 15.6 | 65.0 | 5190   | 17 | US-10-379-632-30     | Sequence 30, Appl  | 316   | 15.2 | 63.3 | 442   | 10 | US-09-918-993-37829  | Sequence 37829, A |
| 244 | 15.6 | 65.0 | 5232   | 17 | US-10-379-632-32     | Sequence 32, Appl  | c 317 | 15.2 | 63.3 | 457   | 17 | US-10-282-122A-11452 | Sequence 11452, A |
| 245 | 15.6 | 65.0 | 5243   | 17 | US-10-379-632-1      | Sequence 1, Appl   | c 318 | 15.2 | 63.3 | 459   | 10 | US-09-918-993-16808  | Sequence 16808, A |
| 246 | 15.6 | 65.0 | 5264   | 17 | US-10-379-632-77     | Sequence 77, Appl  | c 319 | 15.2 | 63.3 | 488   | 10 | US-09-918-993-25966  | Sequence 25966, A |
| 247 | 15.6 | 65.0 | 5271   | 17 | US-10-379-632-24     | Sequence 24, Appl  | c 320 | 15.2 | 63.3 | 489   | 10 | US-09-918-993-3278   | Sequence 3278, Ap |
| 248 | 15.6 | 65.0 | 5280   | 17 | US-10-379-632-79     | Sequence 79, Appl  | 321   | 15.2 | 63.3 | 502   | 19 | US-10-696-639-2327   | Sequence 2327, Ap |
| 249 | 15.6 | 65.0 | 5285   | 17 | US-10-379-632-74     | Sequence 74, Appl  | c 322 | 15.2 | 63.3 | 507   | 19 | US-10-696-639-2998   | Sequence 2998, Ap |
| 250 | 15.6 | 65.0 | 5287   | 17 | US-10-379-632-29     | Sequence 29, Appl  | c 323 | 15.2 | 63.3 | 513   | 9  | US-09-864-761-12432  | Sequence 12432, A |
| 251 | 15.6 | 65.0 | 5319   | 9  | US-09-826-752-7      | Sequence 7, Appl   | 324   | 15.2 | 63.3 | 533   | 18 | US-10-437-963-82686  | Sequence 82686, A |
| 252 | 15.6 | 65.0 | 5319   | 11 | US-09-968-007A-360   | Sequence 360, Appl | 325   | 15.2 | 63.3 | 539   | 19 | US-10-696-639-2093   | Sequence 2093, Ap |
| 253 | 15.6 | 65.0 | 5319   | 19 | US-10-912-434-7      | Sequence 7, Appl   | 326   | 15.2 | 63.3 | 555   | 16 | US-10-029-386-5280   | Sequence 5280, Ap |
| 254 | 15.6 | 65.0 | 5339   | 17 | US-10-379-632-27     | Sequence 27, Appl  | 327   | 15.2 | 63.3 | 567   | 16 | US-10-029-386-10175  | Sequence 10175, A |
| 255 | 15.6 | 65.0 | 5359   | 14 | US-10-197-666A-139   | Sequence 139, Appl | 328   | 15.2 | 63.3 | 576   | 9  | US-09-758-593A-3     | Sequence 3, Appl  |
| 256 | 15.6 | 65.0 | 5361   | 17 | US-10-379-632-76     | Sequence 76, Appl  | 329   | 15.2 | 63.3 | 576   | 15 | US-10-328-704-3      | Sequence 3, Appl  |
| 257 | 15.6 | 65.0 | 5366   | 17 | US-10-379-632-46     | Sequence 46, Appl  | 330   | 15.2 | 63.3 | 581   | 13 | US-10-027-632-203288 | Sequence 203288,  |
| 258 | 15.6 | 65.0 | 5368   | 17 | US-10-379-632-23     | Sequence 23, Appl  | 331   | 15.2 | 63.3 | 581   | 13 | US-10-027-632-203289 | Sequence 203289,  |
| 259 | 15.6 | 65.0 | 5382   | 17 | US-10-379-632-73     | Sequence 73, Appl  | 332   | 15.2 | 63.3 | 581   | 17 | US-10-027-632-203288 | Sequence 203288,  |
| 260 | 15.6 | 65.0 | 5390   | 18 | US-10-684-422-241    | Sequence 241, App  | 333   | 15.2 | 63.3 | 581   | 17 | US-10-027-632-203289 | Sequence 203289,  |
| 261 | 15.6 | 65.0 | 5434   | 17 | US-10-379-632-31     | Sequence 31, Appl  | 334   | 15.2 | 63.3 | 618   | 13 | US-10-027-632-277149 | Sequence 277149,  |
| 262 | 15.6 | 65.0 | 5436   | 17 | US-10-379-632-26     | Sequence 26, Appl  | 335   | 15.2 | 63.3 | 618   | 17 | US-10-027-632-277149 | Sequence 277149,  |
| 263 | 15.6 | 65.0 | 5463   | 17 | US-10-379-632-48     | Sequence 48, Appl  | 336   | 15.2 | 63.3 | 672   | 9  | US-09-764-864-110    | Sequence 110, App |
| 264 | 15.6 | 65.0 | 5531   | 17 | US-10-379-632-20     | Sequence 20, Appl  | 337   | 15.2 | 63.3 | 678   | 17 | US-10-240-425-967    | Sequence 967, App |
| 265 | 15.6 | 65.0 | 5782   | 18 | US-10-437-963-26437  | Sequence 26437, A  | c 338 | 15.2 | 63.3 | 702   | 13 | US-10-027-632-34070  | Sequence 34070, A |
| 266 | 15.6 | 65.0 | 5909   | 18 | US-10-602-494-142    | Sequence 142, App  | c 339 | 15.2 | 63.3 | 702   | 13 | US-10-027-632-34071  | Sequence 34071, A |
| 267 | 15.6 | 65.0 | 5984   | 17 | US-10-379-632-45     | Sequence 45, Appl  | c 340 | 15.2 | 63.3 | 702   | 13 | US-10-027-632-34070  | Sequence 34071, A |
| 268 | 15.6 | 65.0 | 6136   | 17 | US-10-275-287-57     | Sequence 57, Appl  | c 341 | 15.2 | 63.3 | 702   | 17 | US-10-027-632-34071  | Sequence 34071, A |
| 269 | 15.6 | 65.0 | 6138   | 17 | US-10-275-287-4      | Sequence 4, Appl   | 342   | 15.2 | 63.3 | 722   | 18 | US-10-425-115-36512  | Sequence 36512, A |
| 270 | 15.6 | 65.0 | 6141   | 17 | US-10-275-287-3      | Sequence 3, Appl   | 343   | 15.2 | 63.3 | 829   | 17 | US-10-027-632-167931 | Sequence 167931,  |
| 271 | 15.6 | 65.0 | 7032   | 9  | US-09-764-847-1429   | Sequence 1429, Ap  | 344   | 15.2 | 63.3 | 829   | 17 | US-10-027-632-167931 | Sequence 167931,  |
| 272 | 15.6 | 65.0 | 7032   | 14 | US-10-092-154-1429   | Sequence 1429, Ap  | 345   | 15.2 | 63.3 | 876   | 13 | US-10-027-632-135124 | Sequence 135124,  |
| 273 | 15.6 | 65.0 | 7646   | 17 | US-10-275-287-1      | Sequence 1, Appl   | c 346 | 15.2 | 63.3 | 876   | 13 | US-10-027-632-135125 | Sequence 135125,  |
| 274 | 15.6 | 65.0 | 7650   | 17 | US-10-275-287-56     | Sequence 56, Appl  | 347   | 15.2 | 63.3 | 876   | 17 | US-10-027-632-135124 | Sequence 135124,  |
| 275 | 15.6 | 65.0 | 11990  | 9  | US-09-969-708-569    | Sequence 569, App  | 348   | 15.2 | 63.3 | 876   | 17 | US-10-027-632-135125 | Sequence 135125,  |
| 276 | 15.6 | 65.0 | 11990  | 10 | US-09-873-367C-161   | Sequence 161, App  | c 349 | 15.2 | 63.3 | 933   | 13 | US-10-027-632-121365 | Sequence 121365,  |
| 277 | 15.6 | 65.0 | 11990  | 17 | US-10-240-425-1326   | Sequence 1326, Ap  | c 350 | 15.2 | 63.3 | 933   | 17 | US-10-027-632-121365 | Sequence 121365,  |
| 278 | 15.6 | 65.0 | 15549  | 17 | US-10-275-287-58     | Sequence 58, Appl  | c 351 | 15.2 | 63.3 | 969   | 11 | US-09-938-842A-2446  | Sequence 2446, Ap |
| 279 | 15.6 | 65.0 | 16570  | 17 | US-10-275-287-2      | Sequence 2, Appl   | c 352 | 15.2 | 63.3 | 969   | 11 | US-09-938-842A-2446  | Sequence 2446, Ap |
| 280 | 15.6 | 65.0 | 18318  | 16 | US-10-394-848-6      | Sequence 6, Appl   | 353   | 15.2 | 63.3 | 1002  | 16 | US-10-204-456-1      | Sequence 1, Appl  |
| 281 | 15.6 | 65.0 | 18876  | 17 | US-10-329-079-42     | Sequence 42, Appl  | 354   | 15.2 | 63.3 | 1026  | 15 | US-10-156-761-1549   | Sequence 1549, Ap |
| 282 | 15.6 | 65.0 | 25473  | 18 | US-10-719-993-7034   | Sequence 7034, Ap  | 355   | 15.2 | 63.3 | 1148  | 18 | US-10-719-993-245    | Sequence 245, App |
| 283 | 15.6 | 65.0 | 26180  | 19 | US-10-741-600-17763  | Sequence 17763, A  | 356   | 15.2 | 63.3 | 1158  | 9  | US-09-880-192-48     | Sequence 48, Appl |
| 284 | 15.6 | 65.0 | 61944  | 16 | US-10-329-079-34     | Sequence 34, Appl  | 357   | 15.2 | 63.3 | 1158  | 9  | US-09-758-593A-2     | Sequence 2, Appl  |
| 285 | 15.6 | 65.0 | 185695 | 14 | US-10-020-141-11     | Sequence 11, Appl  | 358   | 15.2 | 63.3 | 1158  | 15 | US-10-328-704-2      | Sequence 48, Appl |
| 286 | 15.6 | 65.0 | 185695 | 14 | US-10-017-721-11     | Sequence 1, Appl   | 359   | 15.2 | 63.3 | 1158  | 16 | US-10-427-348-48     | Sequence 246, App |
| 287 | 15.6 | 65.0 | 219352 | 18 | US-10-322-281-45     | Sequence 45, Appl  | 360   | 15.2 | 63.3 | 1159  | 18 | US-10-719-993-246    | Sequence 246, App |
| 288 | 15.6 | 65.0 | 400660 | 18 | US-10-388-838-68     | Sequence 68, Appl  | c 361 | 15.2 | 63.3 | 1260  | 18 | US-10-739-930-59     | Sequence 59, Appl |
| 289 | 15.6 | 65.0 | 225646 | 18 | US-10-470-585-1      | Sequence 1, Appl   | 362   | 15.2 | 63.3 | 1392  | 17 | US-10-369-493-3373   | Sequence 35373, A |
| 290 | 15.4 | 64.2 | 660    | 13 | US-10-027-632-131659 | Sequence 131659,   | 363   | 15.2 | 63.3 | 1407  | 18 | US-10-719-993-244    | Sequence 244, App |
| 291 | 15.4 | 64.2 | 660    | 13 | US-10-027-632-131660 | Sequence 131660,   | c 364 | 15.2 | 63.3 | 1416  | 17 | US-10-282-122A-20170 | Sequence 20170, A |
| 292 | 15.4 | 64.2 | 660    | 17 | US-10-027-632-131659 | Sequence 131659,   | 365   | 15.2 | 63.3 | 1452  | 17 | US-10-094-749-1245   | Sequence 1245, Ap |
| 293 | 15.4 | 64.2 | 660    | 17 | US-10-027-632-131660 | Sequence 131660,   | 366   | 15.2 | 63.3 | 1475  | 18 | US-10-723-860-5560   | Sequence 5560, Ap |
| 294 | 15.4 | 64.2 | 840    | 13 | US-10-027-632-166031 | Sequence 166031,   | 367   | 15.2 | 63.3 | 1475  | 18 | US-10-723-860-6074   | Sequence 6074, Ap |
| 295 | 15.4 | 64.2 | 840    | 13 | US-10-027-632-166032 | Sequence 166032,   | c 368 | 15.2 | 63.3 | 1492  | 14 | US-10-062-548-23     | Sequence 23, Appl |
| 296 | 15.4 | 64.2 | 840    | 17 | US-10-027-632-166031 | Sequence 166031,   | c 369 | 15.2 | 63.3 | 1492  | 19 | US-10-918-446-23     | Sequence 23, Appl |
| 297 | 15.4 | 64.2 | 840    | 17 | US-10-027-632-166032 | Sequence 166032,   | c 370 | 15.2 | 63.3 | 1508  | 17 | US-10-108-260A-967   | Sequence 967, App |
| 298 | 15.4 | 64.2 | 913    | 13 | US-10-027-632-153508 | Sequence 153508,   | 371   | 15.2 | 63.3 | 1590  | 18 | US-10-739-930-4996   | Sequence 4996, Ap |
| 299 | 15.4 | 64.2 | 913    | 13 | US-10-027-632-153509 | Sequence 153509,   | c 372 | 15.2 | 63.3 | 1611  | 9  | US-09-808-701-13     | Sequence 13, Appl |
| 300 | 15.4 | 64.2 | 913    | 17 | US-10-027-632-153508 | Sequence 153508,   | c 373 | 15.2 | 63.3 | 1611  | 14 | US-10-233-131-13     | Sequence 13, Appl |
| 301 | 15.4 | 64.2 | 913    | 17 | US-10-027-632-153509 | Sequence 153509,   | c 374 | 15.2 | 63.3 | 1619  | 10 | US-09-873-367C-329   | Sequence 329, App |
| 302 | 15.4 | 64.2 | 1119   | 18 | US-10-425-115-67486  | Sequence 67486, A  | c 375 | 15.2 | 63.3 | 1633  | 17 | US-10-369-493-27750  | Sequence 27750, A |
| 303 | 15.4 | 64.2 | 1937   | 18 | US-10-357-930-24785  | Sequence 24785, A  | c 376 | 15.2 | 63.3 | 1665  | 10 | US-09-946-374-159    | Sequence 159, App |

|       |      |      |      |    |                   |                   |                   |
|-------|------|------|------|----|-------------------|-------------------|-------------------|
| C 377 | 15.2 | 63.3 | 1665 | 13 | US-10-006-867-85  | Sequence 85, Appl | Sequence 85, Appl |
| C 378 | 15.2 | 63.3 | 1665 | 13 | US-10-052-586-285 | Sequence 285, App | Sequence 285, App |
| C 379 | 15.2 | 63.3 | 1665 | 13 | US-10-063-547-85  | Sequence 85, Appl | Sequence 85, Appl |
| C 380 | 15.2 | 63.3 | 1665 | 13 | US-10-063-551-85  | Sequence 85, Appl | Sequence 85, App  |
| C 381 | 15.2 | 63.3 | 1665 | 14 | US-10-174-590-285 | Sequence 285, App | Sequence 285, App |
| C 382 | 15.2 | 63.3 | 1665 | 14 | US-10-176-758-285 | Sequence 285, App | Sequence 285, App |
| C 383 | 15.2 | 63.3 | 1665 | 14 | US-10-175-737-285 | Sequence 285, App | Sequence 285, App |
| C 384 | 15.2 | 63.3 | 1665 | 14 | US-10-063-616-85  | Sequence 85, Appl | Sequence 285, App |
| C 385 | 15.2 | 63.3 | 1665 | 14 | US-10-174-581-285 | Sequence 285, App | Sequence 285, App |
| C 386 | 15.2 | 63.3 | 1665 | 14 | US-10-176-483-285 | Sequence 285, App | Sequence 285, App |
| C 387 | 15.2 | 63.3 | 1665 | 14 | US-10-176-749-285 | Sequence 285, App | Sequence 285, App |
| C 388 | 15.2 | 63.3 | 1665 | 14 | US-10-176-914-285 | Sequence 285, App | Sequence 285, App |
| C 389 | 15.2 | 63.3 | 1665 | 14 | US-10-176-915-285 | Sequence 285, App | Sequence 285, App |
| C 390 | 15.2 | 63.3 | 1665 | 14 | US-10-063-569-85  | Sequence 85, Appl | Sequence 285, App |
| C 391 | 15.2 | 63.3 | 1665 | 14 | US-10-063-511-85  | Sequence 85, Appl | Sequence 285, App |
| C 392 | 15.2 | 63.3 | 1665 | 14 | US-10-063-512-85  | Sequence 85, Appl | Sequence 285, App |
| C 393 | 15.2 | 63.3 | 1665 | 14 | US-10-063-512-85  | Sequence 85, Appl | Sequence 285, App |
| C 394 | 15.2 | 63.3 | 1665 | 14 | US-10-173-706-285 | Sequence 285, App | Sequence 285, App |
| C 395 | 15.2 | 63.3 | 1665 | 14 | US-10-175-738-285 | Sequence 285, App | Sequence 285, App |
| C 396 | 15.2 | 63.3 | 1665 | 14 | US-10-175-752-285 | Sequence 285, App | Sequence 285, App |
| C 397 | 15.2 | 63.3 | 1665 | 14 | US-10-176-482-285 | Sequence 285, App | Sequence 285, App |
| C 398 | 15.2 | 63.3 | 1665 | 14 | US-10-176-757-285 | Sequence 285, App | Sequence 285, App |
| C 399 | 15.2 | 63.3 | 1665 | 14 | US-10-176-911-285 | Sequence 285, App | Sequence 285, App |
| C 400 | 15.2 | 63.3 | 1665 | 14 | US-10-180-552-285 | Sequence 285, App | Sequence 285, App |
| C 401 | 15.2 | 63.3 | 1665 | 14 | US-10-180-557-285 | Sequence 285, App | Sequence 285, App |
| C 402 | 15.2 | 63.3 | 1665 | 14 | US-10-063-502-85  | Sequence 85, Appl | Sequence 285, App |
| C 403 | 15.2 | 63.3 | 1665 | 14 | US-10-173-700-285 | Sequence 285, App | Sequence 285, App |
| C 404 | 15.2 | 63.3 | 1665 | 14 | US-10-174-572-285 | Sequence 285, App | Sequence 285, App |
| C 405 | 15.2 | 63.3 | 1665 | 14 | US-10-174-579-285 | Sequence 285, App | Sequence 285, App |
| C 406 | 15.2 | 63.3 | 1665 | 14 | US-10-174-582-285 | Sequence 285, App | Sequence 285, App |
| C 407 | 15.2 | 63.3 | 1665 | 14 | US-10-174-588-285 | Sequence 285, App | Sequence 285, App |
| C 408 | 15.2 | 63.3 | 1665 | 14 | US-10-175-739-285 | Sequence 285, App | Sequence 285, App |
| C 409 | 15.2 | 63.3 | 1665 | 14 | US-10-175-743-285 | Sequence 285, App | Sequence 285, App |
| C 410 | 15.2 | 63.3 | 1665 | 14 | US-10-175-743-285 | Sequence 285, App | Sequence 285, App |
| C 411 | 15.2 | 63.3 | 1665 | 14 | US-10-176-488-285 | Sequence 285, App | Sequence 285, App |
| C 412 | 15.2 | 63.3 | 1665 | 14 | US-10-176-492-285 | Sequence 285, App | Sequence 285, App |
| C 413 | 15.2 | 63.3 | 1665 | 14 | US-10-176-747-285 | Sequence 285, App | Sequence 285, App |
| C 414 | 15.2 | 63.3 | 1665 | 14 | US-10-176-750-285 | Sequence 285, App | Sequence 285, App |
| C 415 | 15.2 | 63.3 | 1665 | 14 | US-10-176-985-285 | Sequence 285, App | Sequence 285, App |
| C 416 | 15.2 | 63.3 | 1665 | 14 | US-10-176-987-285 | Sequence 285, App | Sequence 285, App |
| C 417 | 15.2 | 63.3 | 1665 | 14 | US-10-176-992-285 | Sequence 285, App | Sequence 285, App |
| C 418 | 15.2 | 63.3 | 1665 | 14 | US-10-176-999-285 | Sequence 285, App | Sequence 285, App |
| C 419 | 15.2 | 63.3 | 1665 | 14 | US-10-184-650-285 | Sequence 285, App | Sequence 285, App |
| C 420 | 15.2 | 63.3 | 1665 | 14 | US-10-184-650-285 | Sequence 285, App | Sequence 285, App |
| C 421 | 15.2 | 63.3 | 1665 | 14 | US-10-176-991-285 | Sequence 285, App | Sequence 285, App |
| C 422 | 15.2 | 63.3 | 1665 | 14 | US-10-063-549-85  | Sequence 85, Appl | Sequence 285, App |
| C 423 | 15.2 | 63.3 | 1665 | 14 | US-10-173-697-285 | Sequence 285, App | Sequence 285, App |
| C 424 | 15.2 | 63.3 | 1665 | 14 | US-10-173-703-285 | Sequence 285, App | Sequence 285, App |
| C 425 | 15.2 | 63.3 | 1665 | 14 | US-10-174-576-285 | Sequence 285, App | Sequence 285, App |
| C 426 | 15.2 | 63.3 | 1665 | 14 | US-10-174-585-285 | Sequence 285, App | Sequence 285, App |
| C 427 | 15.2 | 63.3 | 1665 | 14 | US-10-174-585-285 | Sequence 285, App | Sequence 285, App |
| C 428 | 15.2 | 63.3 | 1665 | 14 | US-10-175-747-285 | Sequence 285, App | Sequence 285, App |
| C 429 | 15.2 | 63.3 | 1665 | 14 | US-10-176-481-285 | Sequence 285, App | Sequence 285, App |
| C 430 | 15.2 | 63.3 | 1665 | 14 | US-10-176-485-285 | Sequence 285, App | Sequence 285, App |
| C 431 | 15.2 | 63.3 | 1665 | 14 | US-10-176-487-285 | Sequence 285, App | Sequence 285, App |
| C 432 | 15.2 | 63.3 | 1665 | 14 | US-10-176-493-285 | Sequence 285, App | Sequence 285, App |
| C 433 | 15.2 | 63.3 | 1665 | 14 | US-10-176-756-285 | Sequence 285, App | Sequence 285, App |
| C 434 | 15.2 | 63.3 | 1665 | 14 | US-10-176-911-285 | Sequence 285, App | Sequence 285, App |
| C 435 | 15.2 | 63.3 | 1665 | 14 | US-10-176-919-285 | Sequence 285, App | Sequence 285, App |
| C 436 | 15.2 | 63.3 | 1665 | 14 | US-10-176-925-285 | Sequence 285, App | Sequence 285, App |
| C 437 | 15.2 | 63.3 | 1665 | 14 | US-10-176-978-285 | Sequence 285, App | Sequence 285, App |
| C 438 | 15.2 | 63.3 | 1665 | 14 | US-10-180-549-285 | Sequence 285, App | Sequence 285, App |
| C 439 | 15.2 | 63.3 | 1665 | 14 | US-10-180-550-285 | Sequence 285, App | Sequence 285, App |
| C 440 | 15.2 | 63.3 | 1665 | 14 | US-10-180-543-285 | Sequence 285, App | Sequence 285, App |
| C 441 | 15.2 | 63.3 | 1665 | 14 | US-10-180-544-285 | Sequence 285, App | Sequence 285, App |
| C 442 | 15.2 | 63.3 | 1665 | 14 | US-10-180-546-285 | Sequence 285, App | Sequence 285, App |
| C 443 | 15.2 | 63.3 | 1665 | 14 | US-10-180-547-285 | Sequence 285, App | Sequence 285, App |
| C 444 | 15.2 | 63.3 | 1665 | 14 | US-10-180-549-285 | Sequence 285, App | Sequence 285, App |
| C 445 | 15.2 | 63.3 | 1665 | 14 | US-10-180-555-285 | Sequence 285, App | Sequence 285, App |
| C 446 | 15.2 | 63.3 | 1665 | 14 | US-10-180-559-285 | Sequence 285, App | Sequence 285, App |
| C 447 | 15.2 | 63.3 | 1665 | 14 | US-10-181-000-285 | Sequence 285, App | Sequence 285, App |
| C 448 | 15.2 | 63.3 | 1665 | 14 | US-10-183-010-285 | Sequence 285, App | Sequence 285, App |
| C 449 | 15.2 | 63.3 | 1665 | 14 | US-10-183-012-285 | Sequence 285, App | Sequence 285, App |
| C 450 | 15.2 | 63.3 | 1665 | 14 | US-10-184-614-285 | Sequence 285, App | Sequence 285, App |

ALIGNMENTS

RESULT 1  
 US-10-688-489-74  
 ; Sequence 74, Application US/10688489  
 ; Publication No. US20040259108A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Linmen, Jeffrey M.  
 ; APPLICANT: Pollner, Reinhold B.  
 ; APPLICANT: Wu, Wen  
 ; APPLICANT: Dennis, Geoffrey G.  
 ; APPLICANT: Darby, Paul M.  
 ; TITLE OF INVENTION: Compositions and Methods for Detecting  
 ; FILE OF INVENTION: West Nile Virus  
 ; FILE REFERENCE: GP140-04.UT  
 ; CURRENT APPLICATION NUMBER: US/10/688,489  
 ; CURRENT FILING DATE: 2003-10-16  
 ; PRIOR APPLICATION NUMBER: 60/418,891  
 ; PRIOR FILING DATE: 2002-10-16



; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 74  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: West Nile Virus  
US-10-688-489-74

Query Match 100.0%; Score 24; DB 18; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24  
|||||  
Db 1 TCCGAGACGGTCTCTGAGGGCTTAC 24

RESULT 2  
US-10-688-489-75  
; Sequence 75, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; TITLE OF INVENTION: West Nile Virus  
; FILE REFERENCE: GP140-04.UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 75  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: West Nile Virus  
US-10-688-489-75

Query Match 100.0%; Score 24; DB 18; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24  
|||||  
Db 1 TCCGAGACGGTCTCTGAGGGCTTAC 24

RESULT 3  
US-10-815-480-1/c  
; Sequence 1, Application US/10815480  
; Publication No. US20040229261A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Karen K. Y.  
; APPLICANT: Roche Molecular Systems, Inc.  
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain  
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese  
; TITLE OF INVENTION: Encephalitis Virus Serogroup  
; FILE REFERENCE: 022101-000230US  
; CURRENT APPLICATION NUMBER: US/10/815,480  
; CURRENT FILING DATE: 2004-03-31  
; PRIOR APPLICATION NUMBER: US 60/459,491

; PRIOR FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/552,454  
; PRIOR FILING DATE: 2004-03-12  
; PRIOR APPLICATION NUMBER: US 60/555,530  
; PRIOR FILING DATE: 2004-03-22  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: region of  
; OTHER INFORMATION: conserved sequence in 3' untranslated region of  
; OTHER INFORMATION: the genomes of flaviviruses  
US-10-815-480-1

Query Match 100.0%; Score 24; DB 18; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24  
|||||  
Db 24 TCCGAGACGGTCTCTGAGGGCTTAC 1

RESULT 4  
US-10-815-480-2  
; Sequence 2, Application US/10815480  
; Publication No. US20040229261A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Karen K. Y.  
; APPLICANT: Roche Molecular Systems, Inc.  
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain  
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese  
; FILE REFERENCE: 022101-000230US  
; CURRENT APPLICATION NUMBER: US/10/815,480  
; CURRENT FILING DATE: 2004-03-31  
; PRIOR APPLICATION NUMBER: US 60/459,491  
; PRIOR FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/552,454  
; PRIOR FILING DATE: 2004-03-12  
; PRIOR APPLICATION NUMBER: US 60/555,530  
; PRIOR FILING DATE: 2004-03-22  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: complement to  
; OTHER INFORMATION: SEQ ID NO:1  
US-10-815-480-2

Query Match 100.0%; Score 24; DB 18; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24  
|||||  
Db 2 TCCGAGACGGTCTCTGAGGGCTTAC 25

RESULT 5  
US-10-815-480-7/c  
; Sequence 7, Application US/10815480  
; Publication No. US20040229261A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Karen K. Y.  
; APPLICANT: Roche Molecular Systems, Inc.  
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain

```

; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; FILE OF INVENTION: Encephalitis Virus Serogroup
; FILE REFERENCE: 022101-0002300S
; CURRENT APPLICATION NUMBER: US/10/815,480
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/459,491
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/552,454
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/555,530
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Koutango virus
; OTHER INFORMATION: Primer 1
US-10-815-480-7

```

```

Query Match      100.0%; Score 24; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TCCGAGACGGTCTCGAGGGCTTAC 24
    |||||
Db 24 TCCGAGACGGTCTCGAGGGCTTAC 1

```

```

RESULT 6
US-10-815-480-8/c
; Sequence 8, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K. Y.
; APPLICANT: Roche Molecular Systems, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; FILE REFERENCE: 022101-0002300S
; CURRENT APPLICATION NUMBER: US/10/815,480
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/459,491
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/552,454
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/555,530
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Example Primer
; OTHER INFORMATION: 1
US-10-815-480-8

```

```

Query Match      100.0%; Score 24; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TCCGAGACGGTCTCGAGGGCTTAC 24
    |||||
Db 24 TCCGAGACGGTCTCGAGGGCTTAC 1

```

```

RESULT 7
US-10-688-489-73
; Sequence 73, Application US/10688489

```

```

; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 48
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-73

```

```

Query Match      100.0%; Score 24; DB 18; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TCCGAGACGGTCTCGAGGGCTTAC 24
    |||||
Db 1 TCCGAGACGGTCTCGAGGGCTTAC 24

```

```

RESULT 8
US-10-688-489-84
; Sequence 84, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 84
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(27)
; OTHER INFORMATION: T7 promoter sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28)...(51)
; OTHER INFORMATION: WNV-complementary sequence
US-10-688-489-84

```

```

Query Match      100.0%; Score 24; DB 18; Length 51;

```

Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24  
Db 28 TCCGAGACGGTCTCTGAGGGCTTAC 51

RESULT 9

US-10-688-489-72  
; Sequence 72, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GP140-04.UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 72  
; LENGTH: 70  
; TYPE: DNA  
; ORGANISM: West Nile virus  
US-10-688-489-72

Query Match 100.0%; Score 24; DB 18; Length 70;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24  
Db 1 TCCGAGACGGTCTCTGAGGGCTTAC 24

RESULT 10

US-10-815-480-71/c  
; Sequence 71, Application US/10815480  
; Publication No. US20040229261A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Karen K. Y.  
; APPLICANT: Roche Molecular Systems, Inc.  
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain  
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese  
; TITLE OF INVENTION: Encephalitis Virus Serogroup  
; FILE REFERENCE: 022101-000230US  
; CURRENT APPLICATION NUMBER: US/10/815,480  
; CURRENT FILING DATE: 2004-03-31  
; PRIOR APPLICATION NUMBER: US 60/459,491  
; PRIOR FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/552,454  
; PRIOR FILING DATE: 2004-03-12  
; PRIOR APPLICATION NUMBER: US 60/555,530  
; PRIOR FILING DATE: 2004-03-22  
; NUMBER OF SEQ ID NOS: 74  
; SEQ ID NO 71  
; LENGTH: 98  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:region of

; OTHER INFORMATION: conserved sequence in 3' untranslated region of  
; OTHER INFORMATION: the genome of flavivirus AF196835

US-10-815-480-71  
Query Match 100.0%; Score 24; DB 18; Length 98;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24  
Db 68 TCCGAGACGGTCTCTGAGGGCTTAC 45

RESULT 11

US-10-361-002-5/c  
; Sequence 5, Application US/10361002  
; Publication No. US20040170954A1  
; GENERAL INFORMATION:  
; APPLICANT: Clearant, Inc.  
; APPLICANT: McKenney, Keith  
; APPLICANT: Gillmeister, Lidja  
; APPLICANT: Marlowe, Kristina  
; APPLICANT: Armistead, David  
; TITLE OF INVENTION: Pathogen Inactivation Assay  
; FILE REFERENCE: CI-0043  
; CURRENT APPLICATION NUMBER: US/10/361,002  
; CURRENT FILING DATE: 2003-02-10  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 10945  
; TYPE: DNA  
; ORGANISM: West Nile virus  
US-10-361-002-5

Query Match 100.0%; Score 24; DB 18; Length 10945;  
Best Local Similarity 100.0%; Pred. No. 0.05;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24  
Db 10587 TCCGAGACGGTCTCTGAGGGCTTAC 10564

RESULT 12

US-10-361-004-5/c  
; Sequence 5, Application US/10361004  
; Publication No. US20040170991A1  
; GENERAL INFORMATION:  
; APPLICANT: Clearant, Inc.  
; APPLICANT: McKenney, Keith  
; APPLICANT: Gillmeister, Lidja  
; APPLICANT: Marlowe, Kristina  
; APPLICANT: Armistead, David  
; TITLE OF INVENTION: Real-Time Polymerase Chain Reaction Using Large Target Amplicons  
; FILE REFERENCE: CI-0042  
; CURRENT APPLICATION NUMBER: US/10/361,004  
; CURRENT FILING DATE: 2003-02-10  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 10945  
; TYPE: DNA  
; ORGANISM: West Nile virus  
US-10-361-004-5

Query Match 100.0%; Score 24; DB 18; Length 10945;  
Best Local Similarity 100.0%; Pred. No. 0.05;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24  
Db 10587 TCCGAGACGGTCTCTGAGGGCTTAC 10564

RESULT 13  
US-10-699-550-1/c  
; Sequence 1, Application US/10699550  
; Publication No. US20040197769A1  
; GENERAL INFORMATION:  
; APPLICANT: WONG, SUSAN J.  
; APPLICANT: SHI, PEI-YONG  
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS  
; FILE REFERENCE: 454311-2232.1  
; CURRENT APPLICATION NUMBER: US/10/699,550  
; PRIOR FILING DATE: 2003-10-31  
; PRIOR APPLICATION NUMBER: 60/476,513  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: 60/422,755  
; PRIOR FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: PCT/US02/09036  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: 60/402,860  
; PRIOR FILING DATE: 2002-08-08  
; PRIOR APPLICATION NUMBER: 60/281,947  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/275,025  
; PRIOR FILING DATE: 2001-03-12  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 10975  
; TYPE: DNA  
; ORGANISM: West Nile virus  
US-10-699-550-1

Query Match 100.0%; Score 24; DB 18; Length 10975;  
Best Local Similarity 100.0%; Pred. No. 0.05;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGAGACGGTTCGAGGGCTTAC 24  
Db 10611 TCCGAGACGGTTCGAGGGCTTAC 10588

RESULT 14  
US-10-699-550-2/c  
; Sequence 2, Application US/10699550  
; Publication No. US20040197769A1  
; GENERAL INFORMATION:  
; APPLICANT: WONG, SUSAN J.  
; APPLICANT: SHI, PEI-YONG  
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS  
; FILE REFERENCE: 454311-2232.1  
; CURRENT APPLICATION NUMBER: US/10/699,550  
; PRIOR FILING DATE: 2003-10-31  
; PRIOR APPLICATION NUMBER: 60/476,513  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: 60/422,755  
; PRIOR FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: PCT/US02/09036  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: 60/402,860  
; PRIOR FILING DATE: 2002-08-08  
; PRIOR APPLICATION NUMBER: 60/281,947  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/275,025  
; PRIOR FILING DATE: 2001-03-12  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 2  
; LENGTH: 11029  
; TYPE: DNA  
; ORGANISM: West Nile virus  
US-10-699-550-2

Query Match 100.0%; Score 24; DB 18; Length 11029;  
Best Local Similarity 100.0%; Pred. No. 0.05;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGAGACGGTTCGAGGGCTTAC 24  
Db 10629 TCCGAGACGGTTCGAGGGCTTAC 10606  
RESULT 15  
US-10-679-520A-66/c  
; Sequence 66, Application US/10679520A  
; Publication No. US20050031641A1  
; GENERAL INFORMATION:  
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE FRANCIS  
; APPLICANT: LOOSMORE, SHEENA MAY  
; APPLICANT: MINKE, JULES MAARTEN  
; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS  
; FILE REFERENCE: 574313-3161.4  
; CURRENT APPLICATION NUMBER: US/10/679,520A  
; PRIOR FILING DATE: 2003-10-06  
; PRIOR APPLICATION NUMBER: 10/374,953  
; PRIOR FILING DATE: 2003-02-26  
; PRIOR APPLICATION NUMBER: 10/116,298  
; PRIOR FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: 60/281,923  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: PCT/FR02/01200  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: FR 01/04737  
; PRIOR FILING DATE: 2001-04-06  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 66  
; LENGTH: 11029  
; TYPE: DNA  
; ORGANISM: West Nile virus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (97)..(10395)  
US-10-679-520A-66

Query Match 100.0%; Score 24; DB 19; Length 11029;  
Best Local Similarity 100.0%; Pred. No. 0.05;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGAGACGGTTCGAGGGCTTAC 24  
Db 10629 TCCGAGACGGTTCGAGGGCTTAC 10606  
RESULT 16  
US-10-706-892-1/c  
; Sequence 1, Application US/10706892  
; Publication No. US20050058987A1  
; GENERAL INFORMATION:  
; APPLICANT: SHI, PEI-YONG  
; TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY  
; FILE REFERENCE: 454311-2231.1  
; CURRENT APPLICATION NUMBER: US/10/706,892  
; PRIOR FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/427,117  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 11029  
; TYPE: DNA  
; ORGANISM: West Nile virus  
US-10-706-892-1  
Query Match 100.0%; Score 24; DB 19; Length 11029;  
Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTCTGAGGGCTTAC 24  
|||||  
Db 10629 TCCGAGACGGTCTCTGAGGGCTTAC 10606

## RESULT 17

US-10-688-489-76  
; Sequence 76, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GP140-04.UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 76  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: West Nile Virus  
US-10-688-489-76

Query Match 95.8%; Score 23; DB 18; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.17;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTCTGAGGGCTTA 23  
|||||  
Db 1 TCCGAGACGGTCTCTGAGGGCTTA 23

## RESULT 18

US-10-688-489-85  
; Sequence 85, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GP140-04.UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 85  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

; NAME/KEY: misc.feature  
; LOCATION: (1)...(27)  
; OTHER INFORMATION: T7 promoter sequence  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (28)...(50)  
; OTHER INFORMATION: WNV-complementary sequence  
US-10-688-489-85

Query Match 95.8%; Score 23; DB 18; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.17;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTCTGAGGGCTTA 23  
|||||  
Db 28 TCCGAGACGGTCTCTGAGGGCTTA 50

## RESULT 19

US-10-706-892-2/c  
; Sequence 2, Application US/10706892  
; Publication No. US20050058987A1  
; GENERAL INFORMATION:  
; APPLICANT: SHI, PEI-YONG  
; TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY  
; FILE REFERENCE: 454311-2231.1  
; CURRENT APPLICATION NUMBER: US/10/706,892  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/427,117  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 2  
; LENGTH: 11029  
; TYPE: DNA  
; ORGANISM: West Nile virus  
US-10-706-892-2

Query Match 93.3%; Score 22.4; DB 19; Length 11029;  
Best Local Similarity 95.8%; Pred. No. 0.31;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTCTGAGGGCTTAC 24  
|||||  
Db 10629 TCCGAGACGGTCTCTGAGGGCTTAC 10606

## RESULT 20

US-10-688-489-77  
; Sequence 77, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GP140-04.UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 77  
; LENGTH: 22  
; TYPE: DNA

; ORGANISM: West Nile Virus  
US-10-688-489-77

Query Match 91.7%; Score 22; DB 18; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.54;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGCGGTTCTGAGGGCTT 22  
| | | | | | | | | | | | | | | | | | | | | |  
DB 1 TCCGAGCGGTTCTGAGGGCTT 22

## RESULT 21

US-10-688-489-86  
; Sequence 86, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GPI40-04.UT  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: US/10/688,489  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 86  
; LENGTH: 49  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(27)  
; OTHER INFORMATION: T7 promoter sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (28)...(49)  
; OTHER INFORMATION: WNV-complementary sequence  
US-10-688-489-86

Query Match 91.7%; Score 22; DB 18; Length 49;  
Best Local Similarity 100.0%; Pred. No. 0.53;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGCGGTTCTGAGGGCTT 22  
| | | | | | | | | | | | | | | | | | | | | |  
DB 28 TCCGAGCGGTTCTGAGGGCTT 49

## RESULT 22

US-10-688-489-149  
; Sequence 149, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GPI40-04.UT  
; CURRENT FILING DATE: 2003-10-16

; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 149  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: West Nile Virus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(23)  
; OTHER INFORMATION: 2'-OME nucleotide analogs  
US-10-688-489-149

Query Match 87.5%; Score 21; DB 18; Length 23;  
Best Local Similarity 76.2%; Pred. No. 1.7;  
Matches 16; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCTGAGGGCTTAC 24  
| | | | | | | | | | | | | | | | | | | | | |  
DB 1 GAGACGGUUCUGAGGGCUUAC 21

## RESULT 23

US-10-688-489-116/c  
; Sequence 116, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GPI40-04.UT  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: US/10/688,489  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 116  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: West Nile Virus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(19)  
; OTHER INFORMATION: 2'-OME nucleotide analogs  
US-10-688-489-116

Query Match 79.2%; Score 19; DB 18; Length 19;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACGGTTCTGAGGGCTTAC 24  
| | | | | | | | | | | | | | | | | | | | | |  
DB 19 GACGGTTCTGAGGGCTTAC 1

## RESULT 24

US-10-688-489-101/c  
; Sequence 101, Application US/10688489  
; Publication No. US20040259108A1

; GENERAL INFORMATION:  
 ; APPLICANT: Linnen, Jeffrey M.  
 ; APPLICANT: Pollner, Reinhold B.  
 ; APPLICANT: Wu, Wen  
 ; APPLICANT: Dennis, Geoffrey G.  
 ; APPLICANT: Darby, Paul M.  
 ; TITLE OF INVENTION: Compositions and Methods for Detecting  
 ; TITLE OF INVENTION: West Nile Virus  
 ; FILE REFERENCE: GP140-04.UT  
 ; CURRENT APPLICATION NUMBER: US/10/688,489  
 ; PRIOR FILING DATE: 2003-10-16  
 ; PRIOR FILING DATE: 2002-10-16  
 ; PRIOR FILING DATE: 2002-10-16  
 ; PRIOR FILING DATE: 2002-11-25  
 ; PRIOR FILING DATE: 2002-11-25  
 ; PRIOR FILING DATE: 2003-02-24  
 ; NUMBER OF SEQ ID NOS: 196  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 101  
 ; LENGTH: 87  
 ; TYPE: DNA  
 ; ORGANISM: West Nile Virus  
 US-10-688-489-101

Query Match 79.2%; Score 19; DB 18; Length 87;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAGCGTTCTGAGGCTTAC 24  
 DB 87 GAGCGTTCTGAGGCTTAC 69

RESULT 25  
 US-10-425-114-6462  
 ; Sequence 6462, Application US/10425114  
 ; Publication No. US2004003488A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E.  
 ; APPLICANT: Tabaska, Jack E.  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53313)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,114  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 73128  
 ; SEQ ID NO 6462  
 ; LENGTH: 434  
 ; TYPE: DNA  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: 700565822\_FLI  
 US-10-425-114-6462

Query Match 74.2%; Score 17.8; DB 17; Length 434;  
 Best Local Similarity 90.5%; Pred. No. 62;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGACGGTTCTGAGGCTTAC 24  
 DB 29 GATACGGTTCTGAGGGATTAC 49

RESULT 26  
 US-10-424-599-28488  
 ; Sequence 28488, Application US/10424599  
 ; Publication No. US20040031072A1  
 ; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J  
 ; APPLICANT: Kovalic David K  
 ; APPLICANT: Zhou Yihua  
 ; APPLICANT: Cao Yongwei  
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53223)B  
 ; CURRENT APPLICATION NUMBER: US/10/424,599  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 285684  
 ; SEQ ID NO 28488  
 ; LENGTH: 1831  
 ; TYPE: DNA  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_125726C.1  
 US-10-424-599-28488

Query Match 74.2%; Score 17.8; DB 17; Length 1831;  
 Best Local Similarity 90.5%; Pred. No. 61;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGACGGTTCTGAGGCTTAC 24  
 DB 1202 GATACGGTTCTGAGGGATTAC 1222

RESULT 27  
 US-10-225-066A-1045/c  
 ; Sequence 1045, Application US/10225066A  
 ; Publication No. US20030226173A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mendel Biotechnology, Inc.  
 ; APPLICANT: RATCLIFFE, Oliver  
 ; APPLICANT: RIESCHMANN, Jose Luis  
 ; APPLICANT: ADAM, Luc J  
 ; APPLICANT: DUBELL, Arnold T  
 ; APPLICANT: HEARD, Jacqueline E  
 ; APPLICANT: PILGRIM, Marsha L  
 ; APPLICANT: JIANG, Cai-Zhong  
 ; APPLICANT: REUBER, T. Lynne  
 ; APPLICANT: CREELMAN, Robert A  
 ; APPLICANT: PINEDA, Omalra  
 ; APPLICANT: YU, Guo-Liang  
 ; APPLICANT: BROUN, Pierre E  
 ; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants  
 ; FILE REFERENCE: MEI0036-2 US  
 ; CURRENT APPLICATION NUMBER: US/10/225,066A  
 ; CURRENT FILING DATE: 2002-08-09  
 ; PRIOR FILING DATE: 2002-08-09  
 ; PRIOR FILING DATE: 2001-04-18  
 ; PRIOR FILING DATE: 2001-04-18  
 ; PRIOR FILING DATE: 2001-04-18  
 ; PRIOR FILING DATE: 2001-08-09  
 ; PRIOR FILING DATE: 2001-08-09  
 ; PRIOR FILING DATE: 2001-12-05  
 ; PRIOR FILING DATE: 2001-12-05  
 ; PRIOR FILING DATE: 2001-12-11  
 ; PRIOR FILING DATE: 2001-12-11  
 ; PRIOR FILING DATE: 2002-06-14  
 ; NUMBER OF SEQ ID NOS: 1122  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1045  
 ; LENGTH: 1661  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 US-10-225-066A-1045

Query Match 73.3%; Score 17.6; DB 17; Length 1661;  
 Best Local Similarity 83.3%; Pred. No. 76;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGACGCGTTCTGAGGCTTAC 24  
 |||||

Db 610 TCCAGTCGGTTCGTGAGGCTAC 587

RESULT 28

US-10-302-267-29/c  
; Sequence 29, Application US/10302267  
; Publication No. US20030229915A1  
; GENERAL INFORMATION:

; APPLICANT: Keddle, James  
; APPLICANT: Fromm, Michael  
; APPLICANT: Heard, Jacqueline  
; APPLICANT: Riechmann, Jose Luis  
; APPLICANT: Adam, Luc  
; APPLICANT: Broun, Pierre  
; APPLICANT: Pineda, Omaira  
; APPLICANT: Reuber, Lynne  
; APPLICANT: Zhang, James  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Jiang, Cai-Zhong  
; APPLICANT: Samaha, Raymond  
; APPLICANT: Pilgrim, Marsha  
; APPLICANT: Creelman, Robert

; TITLE OF INVENTION: PLANT GENE SEQUENCES II

; FILE REFERENCE: MBI-0007

; CURRENT APPLICATION NUMBER: US/10/302,267

; CURRENT FILING DATE: 2002-11-22

; PRIOR APPLICATION NUMBER: US/09/506,720

; PRIOR FILING DATE: 2000-02-17

; PRIOR APPLICATION NUMBER: 60/120,880

; PRIOR FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: 60/121,037

; PRIOR FILING DATE: 1999-02-22

; PRIOR APPLICATION NUMBER: 60/124,278

; PRIOR FILING DATE: 1999-03-11

; PRIOR APPLICATION NUMBER: 60/129,450

; PRIOR FILING DATE: 1999-04-15

; PRIOR APPLICATION NUMBER: 60/135,134

; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: 60/144,153

; PRIOR FILING DATE: 1999-07-15

; PRIOR APPLICATION NUMBER: 60/161,143

; PRIOR FILING DATE: 1999-10-22

; PRIOR APPLICATION NUMBER: 60/162,656

; PRIOR FILING DATE: 1999-11-01

; NUMBER OF SEQ ID NOS: 218

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 29

; LENGTH: 1661

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (190)..(1458)

; OTHER INFORMATION: G631

US-10-302-267-29

Query Match 73.3%; Score 17.6; DB 17; Length 1661;

Best Local Similarity 83.3%; Pred. No. 76;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGTGAGGCTTAC 24

|||||

Db 610 TCCAGTCGGTTCGTGAGGCTAC 587

RESULT 29

US-10-374-780A-2387/c

; Sequence 2387, Application US/10374780A

; Publication No. US20040019927A1

; GENERAL INFORMATION:

; APPLICANT: Sherman, Bradley K

; APPLICANT: Riechmann, Jose Luis

; APPLICANT: Jiang, Cai-Zhong

; APPLICANT: Heard, Jacqueline E  
; APPLICANT: Haake, Volker  
; APPLICANT: Creelman, Robert A  
; APPLICANT: Ratcliffe, Oliver  
; APPLICANT: Adam, Luc J  
; APPLICANT: Reuber, T. Lynne  
; APPLICANT: Keddle, James  
; APPLICANT: Broun, Pierre E  
; APPLICANT: Pilgrim, Marsha L  
; APPLICANT: Dubell III, Arnold T  
; APPLICANT: Pineda, Omaira  
; APPLICANT: Yu, Guo-Liang

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS

; FILE REFERENCE: MBI-0047 CIP

; CURRENT APPLICATION NUMBER: US/10/374,780A

; CURRENT FILING DATE: 2003-02-25

; PRIOR APPLICATION NUMBER: 09/837,944

; PRIOR FILING DATE: 2001-04-18

; PRIOR APPLICATION NUMBER: 60/310,847

; PRIOR FILING DATE: 2001-08-09

; PRIOR APPLICATION NUMBER: 09/934,455

; PRIOR FILING DATE: 2001-08-22

; PRIOR APPLICATION NUMBER: 60/336,049

; PRIOR FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/338,692

; PRIOR FILING DATE: 2001-12-11

; PRIOR APPLICATION NUMBER: 10/171,468

; PRIOR FILING DATE: 2002-06-14

; PRIOR APPLICATION NUMBER: 10/225,066

; PRIOR FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: 10/225,067

; PRIOR FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: 10/225,068

; PRIOR FILING DATE: 2002-08-09

; NUMBER OF SEQ ID NOS: 2906

; SOFTWARE: Patent In version 3.2

; SEQ ID NO 2387

; LENGTH: 1661

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; OTHER INFORMATION: G631

US-10-374-780A-2387

Query Match 73.3%; Score 17.6; DB 17; Length 1661;

Best Local Similarity 83.3%; Pred. No. 76;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGTGAGGCTTAC 24

|||||

Db 610 TCCAGTCGGTTCGTGAGGCTAC 587

RESULT 30

US-10-412-699B-411/c

; Sequence 411, Application US/10412699B

; Publication No. US20040045049A1

; GENERAL INFORMATION:

; APPLICANT: Mendel Biotechnology, Inc.

; APPLICANT: Zhang, James

; APPLICANT: Fromm, Michael E.

; APPLICANT: Heard, Jacqueline E.

; APPLICANT: Riechmann, Jose Luis

; APPLICANT: Adam, Luc J.

; APPLICANT: Broun, Pierre E.

; APPLICANT: Pineda, Omaira

; APPLICANT: Reuber, T. Lynne

; APPLICANT: Keddle, James S.

; APPLICANT: Yu, Guo-Liang

; APPLICANT: Jiang, Cai-Zhong

; APPLICANT: Samaha, Raymond R.

; APPLICANT: Pilgrim, Marsha L.

; APPLICANT: Creelman, Robert A.





US-10-815-480-4

Query Match 70.0%; Score 16.8; DB 18; Length 26;  
Best Local Similarity 78.9%; Pred. No. 2e+02;  
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGC 19  
|||||:|||||:|  
Db 25 TCCGARRCGGTCTGRNG 7

RESULT 34

US-09-918-995-5377/c  
; Sequence 5377, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5377  
; LENGTH: 487  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(487)  
; OTHER INFORMATION: n = A,T,C or G

US-09-918-995-5377

Query Match 70.0%; Score 16.8; DB 10; Length 487;  
Best Local Similarity 90.0%; Pred. No. 1.9e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGC 20  
|||||:|||||:|  
Db 47 TCCGGCGCGGTTCGAGGC 28

RESULT 35

US-10-437-963-80309/c  
; Sequence 80309, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 80309  
; LENGTH: 704  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(704)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_79946C.1  
US-10-437-963-80309

Query Match 70.0%; Score 16.8; DB 18; Length 704;  
Best Local Similarity 90.0%; Pred. No. 1.9e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTTCGAGGGCT 21  
|||||:|||||:|  
Db 566 CCGAGACGGTTCGAGGGCT 547

RESULT 36

US-10-437-963-21906  
; Sequence 21906, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 21906  
; LENGTH: 1416  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_27132C.1

US-10-437-963-21906

Query Match 70.0%; Score 16.8; DB 18; Length 1416;  
Best Local Similarity 90.0%; Pred. No. 1.9e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGC 20  
|||||:|||||:|  
Db 1091 TCCGAGACGGATCGAGGC 1110

RESULT 37

US-10-261-175A-3  
; Sequence 3, Application US/10261175A  
; Publication No. US20040038222A1  
; GENERAL INFORMATION:  
; APPLICANT: DIETRICH, WILLIAM  
; APPLICANT: WATERS, JAMES W.  
; TITLE OF INVENTION: ANTHRAX SUSCEPTIBILITY GENE  
; FILE REFERENCE: 56491(71250)  
; CURRENT APPLICATION NUMBER: US/10/261,175A  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: 60/325,864  
; PRIOR FILING DATE: 2001-09-29  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 2802  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: KifLC nucleic  
; OTHER INFORMATION: acid sequence

US-10-261-175A-3

Query Match 70.0%; Score 16.8; DB 17; Length 2802;

```

Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTCTCTGAGGGCT 21
    ||||| ||||| ||||| |||||
Db 444 CCGAGGAGGTTCTGAGGGCT 463

RESULT 38
US-10-085-117-235
; Sequence 235, Application US/10085117
; Publication No. US20030232334A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235
; LENGTH: 33488
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)...(33488)
; OTHER INFORMATION: n = any nucleotide
US-10-085-117-235

Query Match 70.0%; Score 16.8; DB 17; Length 33488;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGACGGTCTCTGAGGGCTTAC 24
    ||||| ||||| ||||| |||||
Db 31534 AGAGGGTCTCTGAGGGCTTCC 31553

RESULT 39
US-10-322-281-232
; Sequence 232, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 232
; LENGTH: 135827
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(135827)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-232

Query Match 70.0%; Score 16.8; DB 18; Length 135827;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGC 20
    ||||| ||||| ||||| |||||
Db 21789 TCCAGAGGTTCTGAGGC 21808

Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTCTCTGAGGGCT 21
    ||||| ||||| ||||| |||||
Db 444 CCGAGGAGGTTCTGAGGGCT 463

RESULT 40
US-10-357-930-55914
; Sequence 55914, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55914
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 28
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-55914

Query Match 69.2%; Score 16.6; DB 18; Length 597;
Best Local Similarity 82.6%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTA 23
    ||||| ||||| ||||| |||||
Db 65 TCAGAAACGGTCTGTGAGGCTTA 87

RESULT 41
US-09-919-580-6
; Sequence 6, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 643, 670, 694, 721
; OTHER INFORMATION: n = A,T,C or G

```

## US-09-919-580-6

Query Match 69.2%; Score 16.6; DB 9; Length 723;  
Best Local Similarity 79.2%; Pred. No. 2.4e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGCGTTAC 24  
DB 689 TCACACACTTCTGAGGCGTTAC 712

## RESULT 42

US-10-369-493-24654  
; Sequence 24654, Application US/10369493  
; Publication No. US20030233675A1

## GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 24654

; LENGTH: 1671

; TYPE: DNA

; ORGANISM: Archaeoglobus fulgidus

US-10-369-493-24654

Query Match 69.2%; Score 16.6; DB 17; Length 1671;  
Best Local Similarity 82.6%; Pred. No. 2.4e+02;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CCGAGACGGTTCTGAGGCGTTAC 24  
DB 554 CGGACCGTTGAGGCGTTAC 576

## RESULT 43

US-10-815-480-5/c

; Sequence 5, Application US/10815480

; Publication No. US20040229261A1

## GENERAL INFORMATION:

; APPLICANT: Young, Karen K. Y.

; APPLICANT: Roche Molecular Systems, Inc.

; TITLE OF INVENTION: Compositions and Methods for Detecting Certain

; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese

; TITLE OF INVENTION: Encephalitis Virus Serogroup

; FILE REFERENCE: 022101-000230US

; CURRENT APPLICATION NUMBER: US/10/815,480

; CURRENT FILING DATE: 2004-03-31

; PRIOR APPLICATION NUMBER: US 60/459,491

; PRIOR FILING DATE: 2003-03-31

; PRIOR APPLICATION NUMBER: US 60/552,454

; PRIOR FILING DATE: 2004-03-12

; PRIOR APPLICATION NUMBER: US 60/555,530

; PRIOR FILING DATE: 2004-03-22

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 5

; LENGTH: 26

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Japanese

; OTHER INFORMATION: encephalitis virus Primer 1

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (8)

; OTHER INFORMATION: n = absent

US-10-815-480-5

Query Match 68.3%; Score 16.4; DB 18; Length 26;  
Best Local Similarity 73.7%; Pred. No. 3.2e+02;  
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGG 19  
DB 25 TCCGACACRGTTTGGAGNG 7

## RESULT 44

US-09-938-842A-1241

; Sequence 1241, Application US/09938842A

; Patent No. US20020160378A1

## GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; TITLE OF INVENTION: SAME, AND METHODS OF USE

; FILE REFERENCE: SCRIPT300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 1241

; LENGTH: 1929

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-938-842A-1241

Query Match 68.3%; Score 16.4; DB 9; Length 1929;  
Best Local Similarity 94.4%; Pred. No. 3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGACGGTTCTGAGGCGTT 22  
DB 1535 AGACGGTTCTGAGGCGATT 1552

## RESULT 45

US-09-938-842A-1241

; Sequence 1241, Application US/09938842A

; Publication No. US20040009476A9

## GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; TITLE OF INVENTION: SAME, AND METHODS OF USE

; FILE REFERENCE: SCRIPT300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 1241

; LENGTH: 1929

```
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1241

Query Match      68.3%; Score 16.4; DB 11; Length 1929;
Best Local Similarity 94.4%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGACGGTTCTGAGGGCTT 22
    |||||
Db 1535 AGACGGTTCTGAGGGATT 1552

RESULT 46
US-10-449-857A-67/c
; Sequence 67, Application US/10449857A
; Publication No. US20040043931A1
; GENERAL INFORMATION:
; APPLICANT: Hereshberg, Robert M.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raedoh
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF INFLAMMATORY BOWEL DISEASE
; FILE REFERENCE: 584C1
; CURRENT APPLICATION NUMBER: US/10/449,857A
; CURRENT FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 67
; LENGTH: 616
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Unknown Bacterium
US-10-449-857A-67

Query Match      67.5%; Score 16.2; DB 17; Length 616;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCGACACGGTTCTGAGGGCT 21
    |||||
Db 444 TCCGACACGGTTCTGATAGCT 424

RESULT 47
US-10-425-114-6252
; Sequence 6252, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 6252
; LENGTH: 1055
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700558722_FLI
US-10-425-114-6252

Query Match      67.5%; Score 16.2; DB 17; Length 1055;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;

US-10-688-489-75.rnpb

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GAGACGGTTCTGAGGGCTTAC 24
    |||||
Db 339 GAGACGGTTCTGAGGGCTAAC 359

RESULT 48
US-10-424-599-35449
; Sequence 35449, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 35449
; LENGTH: 1122
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1122)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_132013C.1
US-10-424-599-35449

Query Match      67.5%; Score 16.2; DB 17; Length 1122;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GAGACGGTTCTGAGGGCTTAC 24
    |||||
Db 406 GAGACGGTTCTGAGGGCTAAC 426

RESULT 49
US-10-424-599-73661/c
; Sequence 73661, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 73661
; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_37530C.1
US-10-424-599-73661

Query Match      67.5%; Score 16.2; DB 17; Length 1275;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGAGACGGTTCTGAGGGCTTA 23
    |||||
Db 44 CGGACGAGTCTGAGGGCTTA 24
```

RESULT 50  
US-10-437-963-83700  
; Sequence 83700, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 83700  
; LENGTH: 1685  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_83005C.1  
US-10-437-963-83700

Query Match 67.5%; Score 16.2; DB 18; Length 1685;  
Best Local Similarity 85.7%; Pred. No. 3.8e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CCGAGACGGTTCTGAGGGCTT 22  
|||||  
Db 361 CCGAGTCGGTTCAGAGGGTTT 361

Search completed: March 25, 2005, 14:03:20  
Job time : 305.714 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 09:34:25 ; Search time 663.429 Seconds  
(without alignments)  
1314.676 Million cell updates/sec

Title: US-10-688-489-64

Perfect score: 18

Sequence: 1 cgccaccggaagttagt 18

Scoring table: IDENTITY.NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_scs.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 18    | 100.0       | 456    | 14 | AF458351 Kunjin vi |
| 2          | 18    | 100.0       | 458    | 14 | AF458356 Kunjin vi |
| 3          | 18    | 100.0       | 462    | 14 | AF458350 West Nile |
| 4          | 18    | 100.0       | 463    | 14 | AF458343 West Nile |
| 5          | 18    | 100.0       | 463    | 14 | AF458344 West Nile |
| 6          | 18    | 100.0       | 463    | 14 | AF458347 West Nile |
| 7          | 18    | 100.0       | 463    | 14 | AF458348 West Nile |
| 8          | 18    | 100.0       | 463    | 14 | AF458355 West Nile |
| 9          | 18    | 100.0       | 463    | 14 | AF458360 West Nile |
| 10         | 18    | 100.0       | 463    | 14 | AF458361 West Nile |
| 11         | 18    | 100.0       | 464    | 14 | AF590190 West Nile |
| 12         | 18    | 100.0       | 464    | 14 | AF590191 West Nile |
| 13         | 18    | 100.0       | 464    | 14 | AF590192 West Nile |
| 14         | 18    | 100.0       | 464    | 14 | AF590193 West Nile |
| 15         | 18    | 100.0       | 464    | 14 | AF590194 West Nile |
| 16         | 18    | 100.0       | 464    | 14 | AF590195 West Nile |
| 17         | 18    | 100.0       | 464    | 14 | AF590196 West Nile |
| 18         | 18    | 100.0       | 464    | 14 | AF590197 West Nile |
| 19         | 18    | 100.0       | 464    | 14 | AF590198 West Nile |

|    |    |       |       |    |           |                    |
|----|----|-------|-------|----|-----------|--------------------|
| 20 | 18 | 100.0 | 464   | 14 | AY590199  | West Nile          |
| 21 | 18 | 100.0 | 464   | 14 | AY590200  | West Nile          |
| 22 | 18 | 100.0 | 464   | 14 | AY590201  | West Nile          |
| 23 | 18 | 100.0 | 464   | 14 | AY590202  | West Nile          |
| 24 | 18 | 100.0 | 464   | 14 | AY590203  | West Nile          |
| 25 | 18 | 100.0 | 464   | 14 | AY590204  | West Nile          |
| 26 | 18 | 100.0 | 464   | 14 | AY590205  | West Nile          |
| 27 | 18 | 100.0 | 464   | 14 | AY590206  | West Nile          |
| 28 | 18 | 100.0 | 464   | 14 | AY590207  | West Nile          |
| 29 | 18 | 100.0 | 464   | 14 | AY590208  | West Nile          |
| 30 | 18 | 100.0 | 464   | 14 | AY590209  | West Nile          |
| 31 | 18 | 100.0 | 542   | 14 | AF297854  | Kunjin vi          |
| 32 | 18 | 100.0 | 545   | 14 | AF297850  | Kunjin vi          |
| 33 | 18 | 100.0 | 585   | 14 | AF297840  | Kunjin vi          |
| 34 | 18 | 100.0 | 587   | 14 | KUNNS5GAA | L48978 Kunjin viru |
| 35 | 18 | 100.0 | 587   | 14 | KUNNS5GAB | L48979 Kunjin viru |
| 36 | 18 | 100.0 | 593   | 14 | AF297847  | AF297847 Kunjin vi |
| 37 | 18 | 100.0 | 593   | 14 | AF297852  | AF297852 Kunjin vi |
| 38 | 18 | 100.0 | 594   | 14 | AF297853  | AF297853 Kunjin vi |
| 39 | 18 | 100.0 | 600   | 14 | AF297846  | AF297846 Kunjin vi |
| 40 | 18 | 100.0 | 601   | 14 | AF297844  | AF297844 Kunjin vi |
| 41 | 18 | 100.0 | 607   | 14 | AF297841  | AF297841 Kunjin vi |
| 42 | 18 | 100.0 | 609   | 14 | AF297856  | AF297856 Kunjin vi |
| 43 | 18 | 100.0 | 616   | 14 | AF297845  | AF297845 Kunjin vi |
| 44 | 18 | 100.0 | 620   | 14 | AF297859  | AF297859 Kunjin vi |
| 45 | 18 | 100.0 | 622   | 14 | AF297842  | AF297842 Kunjin vi |
| 46 | 18 | 100.0 | 623   | 14 | AF297843  | AF297843 Kunjin vi |
| 47 | 18 | 100.0 | 627   | 14 | KUNNONCOB | L24512 Kunjin viru |
| 48 | 18 | 100.0 | 633   | 14 | AF297858  | AF297858 Kunjin vi |
| 49 | 18 | 100.0 | 644   | 14 | AF297848  | AF297848 Kunjin vi |
| 50 | 18 | 100.0 | 645   | 14 | AY187012  | AY187012 West Nile |
| 51 | 18 | 100.0 | 645   | 14 | AY187013  | AY187013 West Nile |
| 52 | 18 | 100.0 | 645   | 14 | AY187014  | AY187014 West Nile |
| 53 | 18 | 100.0 | 645   | 14 | AY187015  | AY187015 West Nile |
| 54 | 18 | 100.0 | 652   | 14 | AF297855  | AF297855 Kunjin vi |
| 55 | 18 | 100.0 | 657   | 14 | AF297849  | AF297849 Kunjin vi |
| 56 | 18 | 100.0 | 659   | 14 | AF196536  | AF196536 West Nile |
| 57 | 18 | 100.0 | 669   | 14 | AF196541  | AF196541 West Nile |
| 58 | 18 | 100.0 | 670   | 14 | AF196542  | AF196542 West Nile |
| 59 | 18 | 100.0 | 1524  | 14 | AF017254  | AF017254 West Nile |
| 60 | 18 | 100.0 | 10842 | 14 | AF278442  | AF278442 West Nile |
| 61 | 18 | 100.0 | 10845 | 14 | AY277252  | AY277252 West Nile |
| 62 | 18 | 100.0 | 10945 | 14 | AF202541  | AF202541 West Nile |
| 63 | 18 | 100.0 | 10972 | 14 | AF317203  | AF317203 West Nile |
| 64 | 18 | 100.0 | 10975 | 14 | AF206518  | AF206518 West Nile |
| 65 | 18 | 100.0 | 10984 | 14 | AY262283  | AY262283 West Nile |
| 66 | 18 | 100.0 | 10989 | 14 | AY268132  | AY268132 West Nile |
| 67 | 18 | 100.0 | 10989 | 14 | AY268133  | AY268133 West Nile |
| 68 | 18 | 100.0 | 10998 | 14 | AY278441  | AY278441 West Nile |
| 69 | 18 | 100.0 | 11022 | 14 | AY274504  | AY274504 Kunjin vi |
| 70 | 18 | 100.0 | 11022 | 14 | AY274505  | AY274505 Kunjin vi |
| 71 | 18 | 100.0 | 11028 | 14 | AY490240  | AY490240 West Nile |
| 72 | 18 | 100.0 | 11028 | 6  | AX576542  | AX576542 Sequence  |
| 73 | 18 | 100.0 | 11029 | 6  | AX577796  | AX577796 Sequence  |
| 74 | 18 | 100.0 | 11029 | 14 | AB185914  | AB185914 West Nile |
| 75 | 18 | 100.0 | 11029 | 14 | AB185915  | AB185915 West Nile |
| 76 | 18 | 100.0 | 11029 | 14 | AB185916  | AB185916 West Nile |
| 77 | 18 | 100.0 | 11029 | 14 | AB185917  | AB185917 West Nile |
| 78 | 18 | 100.0 | 11029 | 14 | AF196835  | AF196835 West Nile |
| 79 | 18 | 100.0 | 11029 | 14 | AF260967  | AF260967 West Nile |
| 80 | 18 | 100.0 | 11029 | 14 | AF260968  | AF260968 West Nile |
| 81 | 18 | 100.0 | 11029 | 14 | AF260969  | AF260969 West Nile |
| 82 | 18 | 100.0 | 11029 | 14 | AF404753  | AF404753 West Nile |
| 83 | 18 | 100.0 | 11029 | 14 | AF404754  | AF404754 West Nile |
| 84 | 18 | 100.0 | 11029 | 14 | AF404755  | AF404755 West Nile |
| 85 | 18 | 100.0 | 11029 | 14 | AF404756  | AF404756 West Nile |
| 86 | 18 | 100.0 | 11029 | 14 | AF404757  | AF404757 West Nile |
| 87 | 18 | 100.0 | 11029 | 14 | AF481864  | AF481864 West Nile |
| 88 | 18 | 100.0 | 11029 | 14 | AF533540  | AF533540 West Nile |
| 89 | 18 | 100.0 | 11029 | 14 | AY289214  | AY289214 West Nile |
| 90 | 17 | 94.4  | 395   | 14 | AF458358  | AF458358 West Nile |
| 91 | 17 | 94.4  | 481   | 14 | AF458349  | AF458349 West Nile |
| 92 | 17 | 94.4  | 481   | 14 | AF458359  | AF458359 West Nile |

|     |      |      |        |    |             |                    |       |      |      |        |    |            |
|-----|------|------|--------|----|-------------|--------------------|-------|------|------|--------|----|------------|
| 93  | 17   | 94.4 | 483    | 14 | AF458345    | West Nile          | 166   | 15.4 | 85.6 | 163970 | 3  | AC010580   |
| 94  | 17   | 94.4 | 483    | 14 | AF458357    | West Nile          | 167   | 15.4 | 85.6 | 169902 | 3  | AC008209   |
| 95  | 17   | 94.4 | 484    | 14 | AF458354    | West Nile          | C 168 | 15.4 | 85.6 | 170750 | 2  | AC103898   |
| 96  | 17   | 94.4 | 497    | 14 | AF458346    | West Nile          | C 169 | 15.4 | 85.6 | 173603 | 10 | AC1032222  |
| 97  | 17   | 94.4 | 591    | 14 | AF196543    | West Nile          | C 170 | 15.4 | 85.6 | 178602 | 9  | AC078859   |
| 98  | 17   | 94.4 | 593    | 14 | AF196543    | West Nile          | C 171 | 15.4 | 85.6 | 178357 | 9  | AC013286   |
| 99  | 17   | 94.4 | 677    | 14 | AF196535    | West Nile          | C 172 | 15.4 | 85.6 | 178965 | 9  | AC012048   |
| 100 | 17   | 94.4 | 687    | 14 | AF196535    | West Nile          | C 173 | 15.4 | 85.6 | 179305 | 9  | AC144411   |
| 101 | 17   | 94.4 | 917    | 14 | AF208017    | West Nile          | C 174 | 15.4 | 85.6 | 182408 | 9  | HS4535K18  |
| 102 | 17   | 94.4 | 10962  | 14 | WNFCG       | West Nile          | C 175 | 15.4 | 85.6 | 186008 | 2  | AC018776   |
| 103 | 17   | 94.4 | 11057  | 14 | AF688948    | West Nile          | C 176 | 15.4 | 85.6 | 188458 | 2  | AC074052   |
| 104 | 17   | 94.4 | 11064  | 14 | AF453412    | Usuru vir          | 177   | 15.4 | 85.6 | 190187 | 5  | BS511138   |
| 105 | 17   | 94.4 | 11066  | 14 | AF453411    | Usuru vir          | 178   | 15.4 | 85.6 | 191810 | 2  | AC137503   |
| 106 | 16.4 | 91.1 | 451    | 14 | AF458352    | West Nile          | 179   | 15.4 | 85.6 | 193050 | 1  | AJ414149   |
| 107 | 16.4 | 91.1 | 583    | 14 | AF2397857   | West Nile          | 180   | 15.4 | 85.6 | 202798 | 2  | AC026553   |
| 108 | 16.4 | 91.1 | 604    | 14 | KUNNS5      | West Nile          | C 181 | 15.4 | 85.6 | 204922 | 2  | AF325177   |
| 109 | 16.4 | 91.1 | 644    | 14 | AF196538    | West Nile          | 182   | 15.4 | 85.6 | 205602 | 10 | AF325177   |
| 110 | 16.4 | 91.1 | 648    | 14 | AF196540    | West Nile          | 183   | 15.4 | 85.6 | 206082 | 2  | AC128554   |
| 111 | 16.4 | 91.1 | 654    | 14 | AF196537    | West Nile          | C 184 | 15.4 | 85.6 | 207345 | 9  | AC009062   |
| 112 | 16.4 | 91.1 | 10741  | 14 | AV277251    | West Nile          | C 185 | 15.4 | 85.6 | 207441 | 2  | AC140719   |
| 113 | 16.4 | 91.1 | 110000 | 2  | AC006497_5  | Continuation (6 of | C 186 | 15.4 | 85.6 | 209113 | 2  | CR388368   |
| 114 | 16.4 | 91.1 | 137296 | 2  | AC014162    | Mus muscu          | C 187 | 15.4 | 85.6 | 211278 | 10 | AC093346   |
| 115 | 16.4 | 91.1 | 150975 | 5  | AX663976    | Sequence           | 188   | 15.4 | 85.6 | 212620 | 9  | AC093731   |
| 116 | 16.4 | 91.1 | 174539 | 9  | AC103558    | Continuation (15 o | C 189 | 15.4 | 85.6 | 220515 | 2  | AC113303   |
| 117 | 16.4 | 91.1 | 177384 | 9  | AC097639    | Continuation (15 o | C 190 | 15.4 | 85.6 | 220922 | 2  | AC103466   |
| 118 | 16.4 | 91.1 | 184541 | 2  | AC073715    | Mus muscu          | C 191 | 15.4 | 85.6 | 226793 | 3  | AE003753   |
| 119 | 16.4 | 91.1 | 241836 | 10 | AC019302    | Mus muscu          | 192   | 15.4 | 85.6 | 230200 | 2  | AC129375   |
| 120 | 16   | 88.9 | 1323   | 6  | AX663976    | Sequence           | 193   | 15.4 | 85.6 | 232124 | 2  | AC102984   |
| 121 | 16   | 88.9 | 3931   | 10 | AB041543    | Mus muscu          | C 194 | 15.4 | 85.6 | 233428 | 2  | AC011064   |
| 122 | 16   | 88.9 | 3986   | 10 | BC066816    | Mus muscu          | C 195 | 15.4 | 85.6 | 235612 | 2  | AC113621   |
| 123 | 16   | 88.9 | 4000   | 10 | AK128931    | Mus muscu          | C 196 | 15.4 | 85.6 | 241151 | 2  | AC125675   |
| 124 | 16   | 88.9 | 5753   | 10 | AK173281    | Mus muscu          | C 197 | 15.4 | 85.6 | 245444 | 2  | AC136836   |
| 125 | 16   | 88.9 | 31068  | 6  | CO612365    | Sequence           | C 200 | 15.4 | 85.6 | 255763 | 2  | AC099281   |
| 126 | 16   | 88.9 | 61969  | 2  | CO614103    | Drosophil          | C 201 | 15.4 | 85.6 | 256032 | 2  | AC114054   |
| 127 | 16   | 88.9 | 110000 | 1  | AE000516_14 | Continuation (15 o | C 202 | 15.4 | 85.6 | 256511 | 2  | AC135040   |
| 128 | 16   | 88.9 | 124373 | 10 | AC012104    | Mus muscu          | C 203 | 15.4 | 85.6 | 256807 | 2  | AC105547   |
| 129 | 16   | 88.9 | 169273 | 3  | AC009916    | Mus muscu          | C 204 | 15.4 | 85.6 | 262721 | 2  | AC106265   |
| 130 | 16   | 88.9 | 215711 | 3  | AC008205    | Drosophil          | C 205 | 15.4 | 85.6 | 262721 | 2  | AC099478   |
| 131 | 16   | 88.9 | 228433 | 3  | AE003749    | Drosophil          | C 206 | 15.4 | 85.6 | 290680 | 2  | AE017135   |
| 132 | 16   | 88.9 | 299450 | 1  | BX248338    | Mycobacte          | C 207 | 15.4 | 85.6 | 291326 | 1  | AE017135   |
| 133 | 16   | 88.9 | 348264 | 1  | BX842576    | Mycobacte          | C 208 | 15   | 83.3 | 436    | 6  | AR305566   |
| 134 | 15.6 | 85.7 | 21     | 6  | CO815914    | Sequence           | C 209 | 15   | 83.3 | 600    | 6  | AR305579   |
| 135 | 15.4 | 85.6 | 391    | 8  | AF203459    | Arabidops          | C 210 | 15   | 83.3 | 600    | 8  | BT008964   |
| 136 | 15.4 | 85.6 | 524    | 14 | AF297851    | Arabidops          | C 211 | 15   | 83.3 | 616    | 6  | BT008964   |
| 137 | 15.4 | 85.6 | 562    | 14 | FVMSNSGAH   | Arabidops          | C 212 | 15   | 83.3 | 673    | 6  | AR305576   |
| 138 | 15.4 | 85.6 | 741    | 6  | CO805118    | Sequence           | C 213 | 15   | 83.3 | 1863   | 6  | AR305575   |
| 139 | 15.4 | 85.6 | 741    | 8  | AY039999    | Arabidops          | C 214 | 15   | 83.3 | 1863   | 6  | BD162638   |
| 140 | 15.4 | 85.6 | 882    | 8  | AY085388    | Arabidops          | C 215 | 15   | 83.3 | 1969   | 6  | AX120521   |
| 141 | 15.4 | 85.6 | 931    | 8  | AF360183    | Arabidops          | C 216 | 15   | 83.3 | 35652  | 2  | AX773825   |
| 142 | 15.4 | 85.6 | 2329   | 5  | DRU57973    | Arabidops          | C 217 | 15   | 83.3 | 52872  | 2  | AC017428   |
| 143 | 15.4 | 85.6 | 2878   | 8  | SCU18116    | Arabidops          | C 218 | 15   | 83.3 | 110000 | 2  | CQ576911   |
| 144 | 15.4 | 85.6 | 6947   | 1  | AB033988    | Arabidops          | C 219 | 15   | 83.3 | 134728 | 8  | AX927234_2 |
| 145 | 15.4 | 85.6 | 9923   | 1  | AB033780    | Arabidops          | C 220 | 15   | 83.3 | 139182 | 2  | AC109917   |
| 146 | 15.4 | 85.6 | 10863  | 9  | AC005678    | Arabidops          | C 221 | 15   | 83.3 | 147702 | 2  | AC109917   |
| 147 | 15.4 | 85.6 | 37346  | 9  | AC137601    | Arabidops          | C 222 | 15   | 83.3 | 152383 | 9  | HSF18108   |
| 148 | 15.4 | 85.6 | 37972  | 2  | AC137601    | Arabidops          | C 223 | 15   | 83.3 | 169283 | 10 | AC131581   |
| 149 | 15.4 | 85.6 | 45133  | 2  | AC142207    | Arabidops          | C 224 | 15   | 83.3 | 171105 | 3  | AC007532   |
| 150 | 15.4 | 85.6 | 63314  | 2  | AC017803    | Arabidops          | C 225 | 15   | 83.3 | 181009 | 3  | AC007575   |
| 151 | 15.4 | 85.6 | 80770  | 8  | AB005240    | Arabidops          | C 226 | 15   | 83.3 | 195696 | 10 | AC125058   |
| 152 | 15.4 | 85.6 | 84761  | 9  | AC093648    | Arabidops          | C 227 | 15   | 83.3 | 206167 | 2  | AC113586   |
| 153 | 15.4 | 85.6 | 98348  | 9  | ATF136103   | Human DNA          | C 228 | 15   | 83.3 | 214508 | 2  | AC103532   |
| 154 | 15.4 | 85.6 | 98008  | 8  | AF158117    | Arabidops          | C 229 | 15   | 83.3 | 215391 | 2  | AC120168   |
| 155 | 15.4 | 85.6 | 107074 | 8  | AP003911    | Arabidops          | C 230 | 15   | 83.3 | 216912 | 2  | AC114349   |
| 156 | 15.4 | 85.6 | 110000 | 1  | AE016827_21 | Continuation (22 o | C 231 | 15   | 83.3 | 227299 | 10 | AC138722   |
| 157 | 15.4 | 85.6 | 110000 | 1  | BX936398_28 | Continuation (29 o | C 232 | 15   | 83.3 | 295289 | 3  | AE003603   |
| 158 | 15.4 | 85.6 | 127725 | 9  | AC023813_2  | Continuation (3 of | C 233 | 15   | 83.3 | 307337 | 1  | BE426556   |
| 159 | 15.4 | 85.6 | 130665 | 10 | AF289666    | Continuation (3 of | C 234 | 15   | 83.3 | 328050 | 2  | AP005275   |
| 160 | 15.4 | 85.6 | 132742 | 2  | AC145412    | Continuation (3 of | C 235 | 15   | 83.3 | 328050 | 1  | AP005275   |
| 161 | 15.4 | 85.6 | 146185 | 8  | AF005542    | Continuation (3 of | C 236 | 15   | 83.3 | 340000 | 9  | HS21C046   |
| 162 | 15.4 | 85.6 | 151457 | 8  | AP003410    | Continuation (3 of | C 237 | 15   | 83.3 | 349887 | 1  | BE426556   |
| 163 | 15.4 | 85.6 | 151457 | 8  | AP003410    | Continuation (3 of | C 238 | 15   | 83.3 | 349887 | 1  | BE426556   |
| 164 | 15.4 | 85.6 | 156850 | 8  | AP002901    | Continuation (3 of | C 239 | 15   | 83.3 | 349887 | 1  | BE426556   |
| 165 | 15.4 | 85.6 | 163240 | 2  | AC069422    | Continuation (3 of | C 240 | 15   | 83.3 | 349887 | 1  | BE426556   |





|     |      |      |        |    |           |                    |                      |
|-----|------|------|--------|----|-----------|--------------------|----------------------|
| 385 | 14.8 | 82.2 | 212373 | 9  | AP004288  | Homo sapi          | AP004288 Homo sapi   |
| 386 | 14.8 | 82.2 | 213047 | 2  | AC099622  | Mus muscu          | AC099622 Mus muscu   |
| 387 | 14.8 | 82.2 | 214363 | 2  | AC109876  | Rattus no          | AC109876 Rattus no   |
| 388 | 14.8 | 82.2 | 214937 | 5  | BC010986  | Zebrafish          | BC010986 Zebrafish   |
| 389 | 14.8 | 82.2 | 216190 | 2  | AC116280  | Rattus no          | AC116280 Rattus no   |
| 390 | 14.8 | 82.2 | 220548 | 2  | AC109260  | Mus muscu          | AC109260 Mus muscu   |
| 391 | 14.8 | 82.2 | 225005 | 2  | AC102985  | Rattus no          | AC102985 Rattus no   |
| 392 | 14.8 | 82.2 | 226361 | 2  | AC094681  | Rattus no          | AC094681 Rattus no   |
| 393 | 14.8 | 82.2 | 227903 | 2  | AC111923  | Rattus no          | AC111923 Rattus no   |
| 394 | 14.8 | 82.2 | 243118 | 2  | AC126821  | Rattus no          | AC126821 Rattus no   |
| 395 | 14.8 | 82.2 | 244534 | 2  | AC125559  | Rattus no          | AC125559 Rattus no   |
| 396 | 14.8 | 82.2 | 251219 | 2  | CR388422  | Danio rer          | CR388422 Danio rer   |
| 397 | 14.8 | 82.2 | 253188 | 2  | AC130748  | Rattus no          | AC130748 Rattus no   |
| 398 | 14.8 | 82.2 | 254962 | 2  | AC127877  | Rattus no          | AC127877 Rattus no   |
| 399 | 14.8 | 82.2 | 255541 | 2  | AC097730  | Rattus no          | AC097730 Rattus no   |
| 400 | 14.8 | 82.2 | 266557 | 1  | AP002559  | Escherich          | AP002559 Escherich   |
| 401 | 14.8 | 82.2 | 290582 | 1  | AE016984  | Shigella           | AE016984 Shigella    |
| 402 | 14.8 | 82.2 | 297293 | 2  | AC125863  | Rattus no          | AC125863 Rattus no   |
| 403 | 14.8 | 82.2 | 300861 | 1  | AE016928  | Bacteroid          | AE016928 Bacteroid   |
| 404 | 14.8 | 82.2 | 301443 | 1  | AE012560  | Xylella f          | AE012560 Xylella f   |
| 405 | 14.8 | 82.2 | 309400 | 6  | AX127153  | Sequence           | AX127153 Sequence    |
| 406 | 14.8 | 82.2 | 310990 | 3  | AE003431  | Drosophil          | AE003431 Drosophil   |
| 407 | 14.8 | 82.2 | 311443 | 1  | AE016762  | Escherich          | AE016762 Escherich   |
| 408 | 14.8 | 82.2 | 314957 | 3  | AE003581  | Drosophil          | AE003581 Drosophil   |
| 409 | 14.8 | 82.2 | 325651 | 1  | AP005281  | Coryneb            | AP005281 Coryneb     |
| 410 | 14.8 | 82.2 | 326150 | 1  | AP005089  | Vibrio pa          | AP005089 Vibrio pa   |
| 411 | 14.8 | 82.2 | 335862 | 1  | AP005281  | Coryneb            | AP005281 Coryneb     |
| 412 | 14.8 | 82.2 | 340750 | 1  | BX294135  | Pirellula          | BX294135 Pirellula   |
| 413 | 14.8 | 82.2 | 349136 | 1  | BX297155  | Coryneb            | BX297155 Coryneb     |
| 414 | 14.8 | 82.2 | 349535 | 1  | BX248357  | Coryneb            | BX248357 Coryneb     |
| 415 | 14.8 | 82.2 | 349980 | 6  | AX127151  | Sequence           | AX127151 Sequence    |
| 416 | 14.4 | 80.0 | 24     | 6  | AX445342  | Sequence           | AX445342 Sequence    |
| 417 | 14.4 | 80.0 | 348    | 14 | HCU56588  | Hepatitis C        | HCU56588 Hepatitis C |
| 418 | 14.4 | 80.0 | 348    | 14 | HCU56589  | Hepatitis C        | HCU56589 Hepatitis C |
| 419 | 14.4 | 80.0 | 348    | 14 | HCU56590  | Hepatitis C        | HCU56590 Hepatitis C |
| 420 | 14.4 | 80.0 | 348    | 14 | HCU56591  | Hepatitis C        | HCU56591 Hepatitis C |
| 421 | 14.4 | 80.0 | 348    | 14 | HCU56592  | Hepatitis C        | HCU56592 Hepatitis C |
| 422 | 14.4 | 80.0 | 348    | 14 | HCU56593  | Hepatitis C        | HCU56593 Hepatitis C |
| 423 | 14.4 | 80.0 | 372    | 6  | CO729410  | Sequence           | CO729410 Sequence    |
| 424 | 14.4 | 80.0 | 401    | 11 | BV192841  | BV192841 sqm17593  | BV192841 sqm17593    |
| 425 | 14.4 | 80.0 | 401    | 11 | BV192841  | BV192841 sqm17593  | BV192841 sqm17593    |
| 426 | 14.4 | 80.0 | 435    | 6  | AR304290  | Sequence           | AR304290 Sequence    |
| 427 | 14.4 | 80.0 | 452    | 3  | AK174773  | Ciona int          | AK174773 Ciona int   |
| 428 | 14.4 | 80.0 | 475    | 6  | AX401535  | Sequence           | AX401535 Sequence    |
| 429 | 14.4 | 80.0 | 524    | 10 | RATIP3RA  | M64699 Rat inosito | M64699 Rat inosito   |
| 430 | 14.4 | 80.0 | 673    | 11 | BV061217  | BV061217 S212P6010 | BV061217 S212P6010   |
| 431 | 14.4 | 80.0 | 746    | 10 | RNU38665  | U38665 Rattus norv | U38665 Rattus norv   |
| 432 | 14.4 | 80.0 | 755    | 6  | BD129383  | BD129383 Human gen | BD129383 Human gen   |
| 433 | 14.4 | 80.0 | 771    | 3  | AX250754  | Reissita           | AX250754 Reissita    |
| 434 | 14.4 | 80.0 | 843    | 9  | HSA322895 | AY045849 Arabidops | AY045849 Arabidops   |
| 435 | 14.4 | 80.0 | 881    | 8  | AY045849  | Arabidops          | AY045849 Arabidops   |
| 436 | 14.4 | 80.0 | 1245   | 6  | AX654494  | Sequence           | AX654494 Sequence    |
| 437 | 14.4 | 80.0 | 1296   | 6  | AR302627  | Sequence           | AR302627 Sequence    |
| 438 | 14.4 | 80.0 | 1296   | 6  | AX043798  | Sequence           | AX043798 Sequence    |
| 439 | 14.4 | 80.0 | 1296   | 6  | AX360794  | Sequence           | AX360794 Sequence    |
| 440 | 14.4 | 80.0 | 1296   | 6  | AX428162  | Sequence           | AX428162 Sequence    |
| 441 | 14.4 | 80.0 | 1327   | 8  | AY114016  | Arabidops          | AY114016 Arabidops   |
| 442 | 14.4 | 80.0 | 1330   | 5  | BC049528  | Danio rer          | BC049528 Danio rer   |
| 443 | 14.4 | 80.0 | 1481   | 8  | AY045952  | Arabidops          | AY045952 Arabidops   |
| 444 | 14.4 | 80.0 | 1525   | 8  | AY087634  | Arabidops          | AY087634 Arabidops   |
| 445 | 14.4 | 80.0 | 1570   | 8  | AK106688  | Oryza sat          | AK106688 Oryza sat   |
| 446 | 14.4 | 80.0 | 1612   | 8  | PSA133722 | AF137722 Pium sat  | AF137722 Pium sat    |
| 447 | 14.4 | 80.0 | 1628   | 8  | AF378882  | Arabidops          | AF378882 Arabidops   |
| 448 | 14.4 | 80.0 | 1833   | 6  | BD165869  | Synthetic          | BD165869 Synthetic   |
| 449 | 14.4 | 80.0 | 1833   | 6  | E37593    | Synthetic 9        | E37593 Synthetic 9   |
| 450 | 14.4 | 80.0 | 1833   | 6  | T08209    | 108209 Sequence 4  | 108209 Sequence 4    |
| 451 | 14.4 | 80.0 | 1833   | 12 | AGCR1111A | AK109643 Oryza sat | AK109643 Oryza sat   |
| 452 | 14.4 | 80.0 | 1938   | 8  | AK099643  | Oryza sat          | AK099643 Oryza sat   |
| 453 | 14.4 | 80.0 | 1964   | 8  | AK099986  | Oryza sat          | AK099986 Oryza sat   |
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QY 1 CGCCACCGGAGTTGAGT 18
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Db 293 CGCCACCGGAGTTGAGT 310

RESULT 2
AF458356 458 bp RNA linear VRL 18-JUN-2003
LOCUS Kunjin virus strain K6453 nonstructural protein 5 gene, partial cds.
DEFINITION Kunjin virus
ACCESSION AF458356.1 GI:21636491
VERSION AF458356.1
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM Kunjin virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 458)
AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 458)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO Collaborating Center for Tropical Diseases, The University of Texas Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA

FEATURES
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Db 293 CGCCACCGGAGTTGAGT 310

RESULT 3
AF458350 462 bp RNA linear VRL 18-JUN-2003
LOCUS West Nile virus strain And-27875 nonstructural protein 5 gene, partial cds.
DEFINITION West Nile virus
ACCESSION AF458350
VERSION AF458350.1 GI:21636479
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 462)
AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 462)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO Collaborating Center for Tropical Diseases, The University of Texas Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA

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Db 299 CGCCACCGGAGTTGAGT 316

RESULT 4
AF458343 463 bp RNA linear VRL 18-JUN-2003
LOCUS West Nile virus strain ArB310/67 nonstructural protein 5 gene, partial cds.
DEFINITION West Nile virus
ACCESSION AF458343
VERSION AF458343.1 GI:21636465
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 463)
AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies

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depending upon virus genotype
Virology 296 (1), 17-23 (2002)
MEDLINE
PUBMED
REFERENCE
2 (bases 1 to 463)
Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
Direct Submission
Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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QY 1 CGCCACCGGAAGTTGAGT 18
|||||
Db 300 CGCCACCGGAAGTTGAGT 317

RESULT 5
AF458344
LOCUS
DEFINITION
West Nile virus strain 68856 nonstructural protein 5 gene,
partial cds.
ACCESSION
AF458344
VERSION
AF458344.1 GI:21636467
KEYWORDS
SOURCE
West Nile virus (WNV)
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 463)
AUTHORS
Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE
Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
Virology 296 (1), 17-23 (2002)
MEDLINE
PUBMED
12036314
REFERENCE
2 (bases 1 to 463)
AUTHORS
Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE
Direct Submission
JOURNAL
Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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QY 1 CGCCACCGGAAGTTGAGT 18
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Db 300 CGCCACCGGAAGTTGAGT 317

RESULT 7
AF458348
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DEFINITION
West Nile virus strain IBAN7019 nonstructural protein 5 gene,
partial cds.

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
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Db 300 CGCCACCGGAAGTTGAGT 317

RESULT 6
AF458347
LOCUS
DEFINITION
West Nile virus strain Ethn4766 nonstructural protein 5 gene,
partial cds.
ACCESSION
AF458347
VERSION
AF458347.1 GI:21636473
KEYWORDS
SOURCE
West Nile virus (WNV)
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 463)
AUTHORS
Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE
Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
Virology 296 (1), 17-23 (2002)
MEDLINE
PUBMED
12036387
REFERENCE
2 (bases 1 to 463)
AUTHORS
Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE
Direct Submission
JOURNAL
Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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QY 1 CGCCACCGGAAGTTGAGT 18
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Db 300 CGCCACCGGAAGTTGAGT 317

RESULT 7
AF458348
LOCUS
DEFINITION
West Nile virus strain IBAN7019 nonstructural protein 5 gene,
partial cds.

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ACCESSION AF458348
VERSION AF458348.1 GI:21636475
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus (WNV)
REFERENCE Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Flavivirus; Japanese encephalitis virus group.
TITLE 1 (bases 1 to 463)
JOURNAL Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
MEDLINE Mouse neuroinvasive phenotype of West Nile virus strains varies
PUBMED depending upon virus genotype
22033887 Virology 296 (1), 17-23 (2002)
12036314 PUBMED
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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QY 1 CGCCACCGGAAGTTGAGT 18
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RESULT 9
AF458360
LOCUS West Nile virus strain 385-99 nonstructural protein 5 gene, partial
DEFINITION cds.
ACCESSION AF458360
VERSION AF458360.1 GI:21636499
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus
REFERENCE Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 463)
Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
Location/Qualifiers
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Db 300 CGCCACCGGAAGTTGAGT 317
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AF458355
LOCUS West Nile virus (WNV)
DEFINITION Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
partial cds.
ACCESSION AF458355
VERSION AF458355.1 GI:21636489
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus
REFERENCE Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 463)
Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCCACCGGAAGTTGAGT 18
Db 300 CGCCACCGGAAGTTGAGT 317
RESULT 8
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LOCUS West Nile virus (WNV)
DEFINITION Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
partial cds.
ACCESSION AF458355
VERSION AF458355.1 GI:21636489
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus
REFERENCE Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 463)
Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
Location/Qualifiers
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QY 1 CGCCACCGGAAGTTGAGT 18
Db 300 CGCCACCGGAAGTTGAGT 317

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Qy 1 CGCCACCGGAAGTTGAGT 18
    |||||
Db 300 CGCCACCGGAAGTTGAGT 317

RESULT 10
LOCUS AF458361
DEFINITION West Nile virus strain 31A nonstructural protein 5 gene, partial cds.
ACCESSION AF458361
VERSION AF458361.1 GI:21636501
KEYWORDS West Nile virus (WNV)
SOURCE West Nile virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 463)
AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
FURNED 12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO Collaborating Center for Tropical Diseases, The University of Texas Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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ORIGIN
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Qy 1 CGCCACCGGAAGTTGAGT 18
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RESULT 11
LOCUS AY590190
DEFINITION West Nile virus strain 03002094 3' UTR, partial sequence.
ACCESSION AY590190
VERSION AY590190.1 GI:47121677
KEYWORDS West Nile virus (WNV)
SOURCE West Nile virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York, 2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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Db 1 CGCCACCGGAAGTTGAGT 18

RESULT 13

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JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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Qy 1 CGCCACCGGAAGTTGAGT 18
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Db 1 CGCCACCGGAAGTTGAGT 18

RESULT 12
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ACCESSION AY590191
VERSION AY590191.1 GI:47121678
KEYWORDS West Nile virus (WNV)
SOURCE West Nile virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York, 2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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AY590192      AY590192      464 bp      RNA      linear      VRL 30-MAY-2004
LOCUS      West Nile virus strain 03001087 3' UTR, partial sequence.
DEFINITION      AY590192
ACCESSION      AY590192
VERSION      AY590192.1 GI:47121679
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM      West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE      1 (bases 1 to 464)
AUTHORS      Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE      Genetic and phenotypic variation of West Nile virus in New York,
            2000-2003
JOURNAL      Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE      2 (bases 1 to 464)
AUTHORS      Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE      Direct Submission
JOURNAL      Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
            Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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AY590193      AY590193      464 bp      RNA      linear      VRL 30-MAY-2004
LOCUS      West Nile virus strain 03001426 3' UTR, partial sequence.
DEFINITION      AY590193
ACCESSION      AY590193
VERSION      AY590193.1 GI:47121680
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM      West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE      1 (bases 1 to 464)
AUTHORS      Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE      Genetic and phenotypic variation of West Nile virus in New York,
            2000-2003
JOURNAL      Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE      2 (bases 1 to 464)
AUTHORS      Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE      Direct Submission
JOURNAL      Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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RESULT 16
AY590195      AY590195      464 bp      RNA      linear      VRL 30-MAY-2004
LOCUS      West Nile virus strain 03001543 3' UTR, partial sequence.
DEFINITION      AY590195
ACCESSION      AY590195
VERSION      AY590195.1 GI:47121682
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM      West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE      1 (bases 1 to 464)
AUTHORS      Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE      Genetic and phenotypic variation of West Nile virus in New York,
            2000-2003
JOURNAL      Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE      2 (bases 1 to 464)
AUTHORS      Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE      Direct Submission
JOURNAL      Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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RESULT 15
AY590194      AY590194      464 bp      RNA      linear      VRL 30-MAY-2004
LOCUS      West Nile virus strain 03001516 3' UTR, partial sequence.
DEFINITION      AY590194
ACCESSION      AY590194
VERSION      AY590194.1 GI:47121681
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM      West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE      1 (bases 1 to 464)
AUTHORS      Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE      Genetic and phenotypic variation of West Nile virus in New York,
            2000-2003
JOURNAL      Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE      2 (bases 1 to 464)
AUTHORS      Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE      Direct Submission
JOURNAL      Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
            Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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RESULT 16
AY590195      AY590195      464 bp      RNA      linear      VRL 30-MAY-2004
LOCUS      West Nile virus strain 03001543 3' UTR, partial sequence.
DEFINITION      AY590195
ACCESSION      AY590195
VERSION      AY590195.1 GI:47121682
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM      West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE      1 (bases 1 to 464)
AUTHORS      Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE      Genetic and phenotypic variation of West Nile virus in New York,
            2000-2003
JOURNAL      Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE      2 (bases 1 to 464)
AUTHORS      Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE      Direct Submission
JOURNAL      Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
            Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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2000-2003
JOURNAL      Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE    2 (bases 1 to 464)
AUTHORS      Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
              Kramer,L.D.
TITLE        Direct Submission
JOURNAL      Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
              Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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Db 1 CGCCACCGGAAGTTGAGT 18

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DEFINITION   West Nile virus strain 03001619 3' UTR, partial sequence.
ACCESSION    AY590196
VERSION      AY590196.1 GI:47121683
KEYWORDS
SOURCE       West Nile virus (WNV)
ORGANISM     Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
              Flavivirus; Japanese encephalitis virus group.
REFERENCE    1 (bases 1 to 464)
AUTHORS      Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
              Kramer,L.D.
TITLE        Genetic and phenotypic variation of West Nile virus in New York,
              2000-2003
JOURNAL      Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE    2 (bases 1 to 464)
AUTHORS      Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
              Kramer,L.D.
TITLE        Direct Submission
JOURNAL      Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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Db 1 CGCCACCGGAAGTTGAGT 18

2000-2003
JOURNAL      Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE    2 (bases 1 to 464)
AUTHORS      Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
              Kramer,L.D.
TITLE        Direct Submission
JOURNAL      Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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Db 1 CGCCACCGGAAGTTGAGT 18

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RESULT 18
AY590197
LOCUS        West Nile virus strain 03001700 3' UTR, partial sequence.
DEFINITION   West Nile virus strain 03001700 3' UTR, partial sequence.
ACCESSION    AY590197
VERSION      AY590197.1 GI:47121684
KEYWORDS
SOURCE       West Nile virus (WNV)
ORGANISM     Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
              Flavivirus; Japanese encephalitis virus group.
REFERENCE    1 (bases 1 to 464)
AUTHORS      Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
              Kramer,L.D.
TITLE        Genetic and phenotypic variation of West Nile virus in New York,
              2000-2003
JOURNAL      Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE    2 (bases 1 to 464)
AUTHORS      Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
              Kramer,L.D.
TITLE        Direct Submission
JOURNAL      Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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Db 1 CGCCACCGGAAGTTGAGT 18

RESULT 19
AY590198
LOCUS        West Nile virus strain 03001721 3' UTR, partial sequence.
DEFINITION   West Nile virus strain 03001721 3' UTR, partial sequence.
ACCESSION    AY590198
VERSION      AY590198.1 GI:47121685
KEYWORDS
SOURCE       West Nile virus (WNV)
ORGANISM     Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
              Flavivirus; Japanese encephalitis virus group.
REFERENCE    1 (bases 1 to 464)
AUTHORS      Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
              Kramer,L.D.
TITLE        Genetic and phenotypic variation of West Nile virus in New York,
              2000-2003
JOURNAL      Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE    2 (bases 1 to 464)
AUTHORS      Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
              Kramer,L.D.
TITLE        Direct Submission
JOURNAL      Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
              Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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Best Local Similarity 100.0%; Pred. No. 14;
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Db 1 CGCCACCGGAAGTTGAGT 18

RESULT 20
AY590199
LOCUS      464 bp RNA linear VRL 30-MAY-2004
DEFINITION West Nile virus strain 03001734 3' UTR, partial sequence.
ACCESSION  AY590199
VERSION     AY590199.1 GI:47121686
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE   1 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Genetic and phenotypic variation of West Nile virus in New York,
            2000-2003
JOURNAL     Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE   2 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Direct Submission
JOURNAL     Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
            Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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Best Local Similarity 100.0%; Pred. No. 14;
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Db 1 CGCCACCGGAAGTTGAGT 18

RESULT 21
AY590200
LOCUS      464 bp RNA linear VRL 30-MAY-2004
DEFINITION West Nile virus strain 03001816 3' UTR, partial sequence.
ACCESSION  AY590200
VERSION     AY590200.1 GI:47121687
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE   1 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.

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TITLE       Genetic and phenotypic variation of West Nile virus in New York,
            2000-2003
JOURNAL     Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE   2 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Direct Submission
JOURNAL     Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
            Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
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Db 1 CGCCACCGGAAGTTGAGT 18

RESULT 22
AY590201
LOCUS      464 bp RNA linear VRL 30-MAY-2004
DEFINITION West Nile virus strain 03001869 3' UTR, partial sequence.
ACCESSION  AY590201
VERSION     AY590201.1 GI:47121688
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE   1 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Genetic and phenotypic variation of West Nile virus in New York,
            2000-2003
JOURNAL     Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE   2 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Direct Submission
JOURNAL     Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
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Db 1 CGCCACCGGAAGTTGAGT 18

RESULT 23
AY590202
LOCUS      464 bp RNA linear VRL 30-MAY-2004
DEFINITION West Nile virus strain 03001816 3' UTR, partial sequence.
ACCESSION  AY590202
VERSION     AY590202.1 GI:47121687
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE   1 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.

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RESULT 23
AY590202
LOCUS      AY590202                464 bp    RNA        linear    VRL 30-MAY-2004
DEFINITION West Nile virus strain 03001895 3' UTR, partial sequence.
ACCESSION  AY590202
VERSION     AY590202.1 GI:47121689
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE   1 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Genetic and phenotypic variation of West Nile virus in New York,
            2000-2003
JOURNAL     Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE   2 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Direct Submission
JOURNAL     Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
            Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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QY 1 CGCCACCGGAGTTGAGT 18
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Db 1 CGCCACCGGAGTTGAGT 18

RESULT 24
AY590203
LOCUS      AY590203                464 bp    RNA        linear    VRL 30-MAY-2004
DEFINITION West Nile virus strain 03001956 3' UTR, partial sequence.
ACCESSION  AY590203
VERSION     AY590203.1 GI:47121690
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE   1 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Genetic and phenotypic variation of West Nile virus in New York,
            2000-2003
JOURNAL     Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE   2 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Direct Submission
JOURNAL     Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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DEFINITION West Nile virus strain 03001986 3' UTR, partial sequence.
ACCESSION  AY590204
VERSION     AY590204.1 GI:47121691
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE   1 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Genetic and phenotypic variation of West Nile virus in New York,
            2000-2003
JOURNAL     Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE   2 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Direct Submission
JOURNAL     Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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Db 1 CGCCACCGGAGTTGAGT 18

RESULT 26
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LOCUS      AY590205                464 bp    RNA        linear    VRL 30-MAY-2004
DEFINITION West Nile virus strain 03002018 3' UTR, partial sequence.
ACCESSION  AY590205
VERSION     AY590205.1 GI:47121692
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE   1 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and

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Kramer,L.D.
Genetic and phenotypic variation of West Nile virus in New York,
2000-2003.
TITLE
JOURNAL
REFERENCE
AUTHORS
2 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
Direct Submission
Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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LOCUS
DEFINITION
West Nile virus strain 03002031 3' UTR, partial sequence.
ACCESSION
AY590206
VERSION
AY590206.1 GI:47121693
KEYWORDS
SOURCE
ORGANISM
West Nile virus (WNV)
West Nile virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
Am. J. Trop. Med. Hyg. (2004) In press
2 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
Direct Submission
Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
JOURNAL
REFERENCE
AUTHORS
2 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
Direct Submission
Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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LOCUS
DEFINITION
West Nile virus strain 03002035 3' UTR, partial sequence.
ACCESSION
AY590207
VERSION
AY590207.1 GI:47121694
KEYWORDS
SOURCE
ORGANISM
West Nile virus (WNV)
West Nile virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
Am. J. Trop. Med. Hyg. (2004) In press
2 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
Direct Submission
Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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AUTHORS
2 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
Direct Submission
Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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Db 1 CGCCACCGGAAGTTGAGT 18
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West Nile virus strain 03002066 3' UTR, partial sequence.
ACCESSION
AY590208
VERSION
AY590208.1 GI:47121695
KEYWORDS
SOURCE
ORGANISM
West Nile virus (WNV)
West Nile virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
Am. J. Trop. Med. Hyg. (2004) In press
2 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
Direct Submission
Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
JOURNAL
REFERENCE
AUTHORS
2 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
Direct Submission
Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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Db 1 CGCCACCGGAAGTTGAGT 18

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| 1   | (bases 1 to 542) | Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.<br>The relationships between West Nile and Kunjin viruses<br>Emerging Infect. Dis. 7 (4), 697-705 (2001) |
| 2   | (bases 1 to 542) | Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.<br>Definitive studies of the relationships between West Nile and Kunjin viruses<br>Unpublished   |
| 3   | (bases 1 to 542) | Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.<br>Direct Submission   |
| Submitted   | (22-AUG-2000)    | Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia  |
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| /db_xref="GI:11991999"  |                  |   |
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| VERSION   |                  |   |
| AF297850.1  |                  | GI:11991990   |
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| Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.  |                  |   |
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| Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.<br>The relationships between West Nile and Kunjin viruses<br>Emerging Infect. Dis. 7 (4), 697-705 (2001) |                  |   |
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| 11585535  |                  |   |
| 2 (bases 1 to 545)  |                  |   |
| Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.<br>Definitive studies of the relationships between West Nile and Kunjin viruses<br>Unpublished   |                  |   |
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| Kunjin virus  |                  |   |
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| Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.<br>Definitive studies of the relationships between West Nile and Kunjin viruses<br>Unpublished   |                  |   |
| 3 (bases 1 to 545)  |                  |   |
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| Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.  |                  |   |
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| 3 (bases 1 to 545)  |                  |   |
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| Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.  |                  |   |
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| Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom  |                  |   |

JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia

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RESULT 33  
LOCUS AF297840 585 bp RNA linear VRL 05-WAR-2002  
DEFINITION Kunjin virus isolate Boort nonstructural protein 5 gene, partial cds.  
ACCESSION AF297840  
VERSION AF297840.1 GI:11991970  
KEYWORDS  
SOURCE Kunjin virus  
ORGANISM Kunjin virus  
REFERENCE 1 (bases 1 to 585)  
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,F., Gould,E.A. and Hall,R.A.  
TITLE The relationships between West Nile and Kunjin viruses  
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)  
MEDLINE 21469816  
PUBMED 11595535  
REFERENCE 2 (bases 1 to 585)  
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.  
TITLE Definitive studies of the relationships between West Nile and Kunjin viruses  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 585)  
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.  
TITLE Direct Submission  
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia

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LOCUS KUNNSGAA 587 bp ss-RNA linear VRL 07-JUN-1996  
DEFINITION Kunjin virus nonstructural protein (NS5) gene, 3' end of cds.  
ACCESSION L48978  
VERSION L48978.1 GI:1066802  
KEYWORDS NS5 gene; nonstructural protein.  
SOURCE Kunjin virus  
ORGANISM Kunjin virus  
REFERENCE 1 (bases 1 to 587)  
AUTHORS Poldinger,M., Hall,R.A. and Mackenzie,J.S.  
TITLE Molecular characterization of the Japanese encephalitis serocomplex of the flavivirus genus  
JOURNAL Virology 218 (2), 417-421 (1996)  
MEDLINE 96193756  
PUBMED 8610471  
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DEFINITION Kunjin virus nonstructural protein (NS5) gene, 3' end of cds.  
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VERSION L48979.1 GI:1066804  
KEYWORDS NS5 gene; nonstructural protein.  
SOURCE Kunjin virus  
ORGANISM Kunjin virus  
REFERENCE 1 (bases 1 to 587)  
AUTHORS Poldinger,M., Hall,R.A. and Mackenzie,J.S.  
TITLE Molecular characterization of the Japanese encephalitis serocomplex of the flavivirus genus  
JOURNAL Virology 218 (2), 417-421 (1996)

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MEDLINE      96193756
PUBMED       8610471
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CGCCACCGGAAGTTGAGT 18
        |||||
Db      356 CGCCACCGGAAGTTGAGT 373
        |||||

RESULT 36
AF297847
LOCUS      Kunjin virus isolate Hu6774 nonstructural protein 5 gene, partial
cds.
ACCESSION  AF297847.1 GI:11991984
VERSION     1
KEYWORDS
SOURCE      Kunjin virus
ORGANISM    Kunjin virus
REFERENCE   1 (bases 1 to 593)
AUTHORS    Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
            Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE      The relationships between West Nile and Kunjin viruses
JOURNAL    Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE    21469816
PUBMED     11585535
REFERENCE   2 (bases 1 to 593)
AUTHORS    Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
            Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE      Definitive studies of the relationships between West Nile and
            Kunjin viruses
JOURNAL    Unpublished
REFERENCE   3 (bases 1 to 593)
AUTHORS    Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
            Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE      Direct Submission
JOURNAL    Submitted (22-AUG-2000) Microbiology and Parasitology, University
            of Queensland, St Lucia, QLD 4072, Australia
FEATURES
  source     Location/Qualifiers
            1..593
            /organism="Kunjin virus"
            /mol_type="genomic RNA"
            /isolate="Hu6774"
            /db_xref="taxon:11077"
            <1..247
            /note="NS5"
            /codon_start=2
            /product="nonstructural protein 5"
            /protein_id="AA02385.1"
            /db_xref="GI:11991985"
            /translation="NMEDKTPVENWSDVPYSGKREDIWCGSLIGTRARATWAENIQ
            VAINQVRSINGDENVYDYMSSSKSSEDTTLVEDTVL"
CDS
  1..247
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  /db_xref="GI:11991985"
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/db_xref="GI:11991985"
/translation="KMKLMEDKTPVEKMSDVPYSGKREDIWCGSLIGTRARATWAENI
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ORIGIN
Query Match      100.0%; Score 18; DB 14; Length 593;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CGCCACCGGAAGTTGAGT 18
        |||||
Db      368 CGCCACCGGAAGTTGAGT 385
        |||||

RESULT 37
AF297852
LOCUS      Kunjin virus isolate M695 nonstructural protein 5 gene, partial
cds.
ACCESSION  AF297852.1 GI:11991994
VERSION     1
KEYWORDS
SOURCE      Kunjin virus
ORGANISM    Kunjin virus
REFERENCE   1 (bases 1 to 593)
AUTHORS    Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
            Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
            Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE      The relationships between West Nile and Kunjin viruses
JOURNAL    Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE    21469816
PUBMED     11585535
REFERENCE   2 (bases 1 to 593)
AUTHORS    Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
            Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE      Definitive studies of the relationships between West Nile and
            Kunjin viruses
JOURNAL    Unpublished
REFERENCE   3 (bases 1 to 593)
AUTHORS    Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
            Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE      Direct Submission
JOURNAL    Submitted (22-AUG-2000) Microbiology and Parasitology, University
            of Queensland, St Lucia, QLD 4072, Australia
FEATURES
  source     Location/Qualifiers
            1..593
            /organism="Kunjin virus"
            /mol_type="genomic RNA"
            /isolate="M695"
            /db_xref="taxon:11077"
            <1..244
            /note="NS5"
            /codon_start=2
            /product="nonstructural protein 5"
            /protein_id="AA042390.1"
            /db_xref="GI:11991995"
            /translation="NMEDKTPVENWSDVPYSGKREDIWCGSLIGTRARATWAENIQ
            VAINQVRSINGDENVYDYMSSSKSSEDTTLVEDTVL"
CDS
  1..244
  /product="nonstructural protein 5"
  /protein_id="AA042390.1"
  /db_xref="GI:11991995"
  /translation="NMEDKTPVENWSDVPYSGKREDIWCGSLIGTRARATWAENIQ
  VAINQVRSINGDENVYDYMSSSKSSEDTTLVEDTVL"
ORIGIN
Query Match      100.0%; Score 18; DB 14; Length 593;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CGCCACCGGAAGTTGAGT 18
        |||||
Db      365 CGCCACCGGAAGTTGAGT 382
        |||||

RESULT 38
AF297853
LOCUS      Kunjin virus isolate M695 nonstructural protein 5 gene, partial
cds.
ACCESSION  AF297853.1 GI:11991994
VERSION     1
KEYWORDS
SOURCE      Kunjin virus
ORGANISM    Kunjin virus
REFERENCE   1 (bases 1 to 593)
AUTHORS    Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
            Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
            Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE      The relationships between West Nile and Kunjin viruses
JOURNAL    Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE    21469816
PUBMED     11585535
REFERENCE   2 (bases 1 to 593)
AUTHORS    Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
            Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE      Definitive studies of the relationships between West Nile and
            Kunjin viruses
JOURNAL    Unpublished
REFERENCE   3 (bases 1 to 593)
AUTHORS    Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
            Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE      Direct Submission
JOURNAL    Submitted (22-AUG-2000) Microbiology and Parasitology, University
            of Queensland, St Lucia, QLD 4072, Australia
FEATURES
  source     Location/Qualifiers
            1..593
            /organism="Kunjin virus"
            /mol_type="genomic RNA"
            /isolate="Hu6774"
            /db_xref="taxon:11077"
            <1..247
            /note="NS5"
            /codon_start=2
            /product="nonstructural protein 5"
            /protein_id="AA042385.1"
            /db_xref="GI:11991985"
            /translation="NMEDKTPVENWSDVPYSGKREDIWCGSLIGTRARATWAENIQ
            VAINQVRSINGDENVYDYMSSSKSSEDTTLVEDTVL"
CDS
  1..247
  /product="nonstructural protein 5"
  /protein_id="AA042385.1"
  /db_xref="GI:11991985"
  /translation="NMEDKTPVENWSDVPYSGKREDIWCGSLIGTRARATWAENIQ
  VAINQVRSINGDENVYDYMSSSKSSEDTTLVEDTVL"

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DEFINITION Kunjin virus isolate SH183 nonstructural protein 5 gene, partial cds.

ACCESSION AF297853

VERSION AF297853.1 GI:11991996

KEYWORDS Kunjin virus

SOURCE Kunjin virus

ORGANISM Kunjin virus

REFERENCE 1 (bases 1 to 594)  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.

TITLE The relationships between West Nile and Kunjin viruses

JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)

MEDLINE 21469816

PUBMED 11585535

REFERENCE 2 (bases 1 to 594)  
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.

AUTHORS Definitive studies of the relationships between West Nile and Kunjin viruses

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 594)  
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.

AUTHORS Direct Submission

TITLE Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia

JOURNAL Location/Qualifiers

MEDLINE 1..594

PUBMED /organism="Kunjin virus"

REFERENCE /mol\_type="genomic RNA"

AUTHORS /isolate="SH183"

TITLE /db\_xref="taxon:11077"

JOURNAL <1..243

MEDLINE /note="NS5"

PUBMED /codon\_start=1

REFERENCE /product="nonstructural protein 5"

AUTHORS /protein\_id="AAG42391.1"

TITLE /GI:11991997"

JOURNAL /translation="NEWMDKTPVEKMSDVPYSGKREDIWCGSLIGTRATWAEINQ

MEDLINE VAINQVRSIIIGDEKYVDYMSWKRYEDTTLVEDTVL"

PUBMED

ORIGIN

Query Match 100.0%; Score 18; DB 14; Length 594;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18  
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Db 364 CGCCACCGGAAGTTGAGT 381  
|||||

RESULT 39

AF297846

LOCUS AF297846.1 GI:11991982

DEFINITION Kunjin virus isolate FC15 nonstructural protein 5 gene, partial cds.

ACCESSION AF297846

VERSION AF297846.1 GI:11991982

KEYWORDS Kunjin virus

SOURCE Kunjin virus

ORGANISM Kunjin virus

REFERENCE 1 (bases 1 to 600)  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.

TITLE The relationships between West Nile and Kunjin viruses

JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)

MEDLINE 21469816

PUBMED 11585535

REFERENCE 2 (bases 1 to 600)  
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.

AUTHORS Definitive studies of the relationships between West Nile and Kunjin viruses

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 600)  
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.

AUTHORS Direct Submission

TITLE Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia

JOURNAL Location/Qualifiers

MEDLINE 1..600

PUBMED /organism="Kunjin virus"

REFERENCE /mol\_type="genomic RNA"

AUTHORS /isolate="FC15"

TITLE /db\_xref="taxon:11077"

JOURNAL <1..236

MEDLINE /note="NS5"

PUBMED /codon\_start=3

REFERENCE /product="nonstructural protein 5"

AUTHORS /protein\_id="AAG42384.1"

TITLE /GI:11991983"

JOURNAL /translation="MEDTTPVEKMSDVPYSGKREDIWCGSLIGTRATWAEIDQVAI

MEDLINE NQVRSIIIGDEKYVDYMSLSKRYEDTTLVEDTVL"

PUBMED

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.

TITLE Definitive studies of the relationships between West Nile and Kunjin viruses

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 600)  
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.

AUTHORS Direct Submission

TITLE Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia

JOURNAL Location/Qualifiers

MEDLINE 1..600

PUBMED /organism="Kunjin virus"

REFERENCE /mol\_type="genomic RNA"

AUTHORS /isolate="FC15"

TITLE /db\_xref="taxon:11077"

JOURNAL <1..236

MEDLINE /note="NS5"

PUBMED /codon\_start=3

REFERENCE /product="nonstructural protein 5"

AUTHORS /protein\_id="AAG42384.1"

TITLE /GI:11991983"

JOURNAL /translation="MEDTTPVEKMSDVPYSGKREDIWCGSLIGTRATWAEIDQVAI

MEDLINE NQVRSIIIGDEKYVDYMSLSKRYEDTTLVEDTVL"

PUBMED

ORIGIN

Query Match 100.0%; Score 18; DB 14; Length 600;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18  
|||||

Db 357 CGCCACCGGAAGTTGAGT 374  
|||||

RESULT 40

AF297844

LOCUS AF297844.1 GI:11991978

DEFINITION Kunjin virus isolate CH16549E nonstructural protein 5 gene, partial cds.

ACCESSION AF297844

VERSION AF297844.1 GI:11991978

KEYWORDS Kunjin virus

SOURCE Kunjin virus

ORGANISM Kunjin virus

REFERENCE 1 (bases 1 to 601)  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.

TITLE The relationships between West Nile and Kunjin viruses

JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)

MEDLINE 21469816

PUBMED 11585535

REFERENCE 2 (bases 1 to 601)  
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.

AUTHORS Definitive studies of the relationships between West Nile and Kunjin viruses

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 601)  
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.

AUTHORS Direct Submission

TITLE Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia

JOURNAL Location/Qualifiers

MEDLINE 1..601

PUBMED /organism="Kunjin virus"

REFERENCE /mol\_type="genomic RNA"

AUTHORS /isolate="CH16549E"

TITLE /db\_xref="taxon:11077"

JOURNAL

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CDS
<1..242
/note="NS5"
/codon_start=3
/product="nonstructural protein 5"
/protein_id="AAG42382.1"
/db_xref="GI:11991979"
/translations="EWMDTTPVEKSDVPYSGKREDIWCGSLIGTRARATWAEDIQV
AINQVRSIIIGDEKYDYNSLSKRYEDITLVETVL"

ORIGIN
Query Match 100.0%; Score 18; DB 14; Length 601;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAAGTTGAGT 18
|||||
Db 363 CGCCACCGGAAGTTGAGT 380

RESULT 41
AF297841
LOCUS
DEFINITION
Kunjin virus isolate CHI6465C nonstructural protein 5 gene, partial
cfs.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Kunjin virus
Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 607)
Schretter,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
The relationships between West Nile and Kunjin viruses
Emerging Infect. Dis. 7 (4), 697-705 (2001)
21469816
PUBMED
REFERENCE
2 (bases 1 to 609)
Schretter,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
REFERENCE
3 (bases 1 to 609)
Schretter,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Direct Submission
Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
Location/Qualifiers
1..609
/organism="Kunjin virus"
/mol_type="genomic RNA"
/isolate="P1553"
/db_xref="taxon:11077"
<1..255
/note="NS5"
/codon_start=3
/product="nonstructural protein 5"
/protein_id="AAG42394.1"
/db_xref="GI:11992003"
/translations="WIDENEMEDKTPVEKMSDVPYSGKREDIWCGSLIGTRARATWA
ENIQVAINQVRSIIIGDEKYDYNSLSKRYEDITLVETVL"

CDS
Query Match 100.0%; Score 18; DB 14; Length 609;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAAGTTGAGT 18
|||||
Db 385 CGCCACCGGAAGTTGAGT 402

RESULT 43
AF297845
LOCUS
DEFINITION
Kunjin virus isolate CX255 nonstructural protein 5 gene, partial
cfs.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Kunjin virus
Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 616)
Schretter,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.

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TITLE      The relationships between West Nile and Kunjin viruses
JOURNAL    Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE    21469816
PUBMED     11585535
REFERENCE  2 (bases 1 to 616)
AUTHORS    Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
            and Hall,R.A.
TITLE      Definitive studies of the relationships between West Nile and
JOURNAL    Kunjin viruses
REFERENCE  3 (bases 1 to 616)
AUTHORS    Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
            and Hall,R.A.
TITLE      Direct Submission
JOURNAL    Submitted (22-AUG-2000) Microbiology and Parasitology, University
REFERENCE  of Queensland, St Lucia, QLD 4072, Australia
AUTHORS    Location/Qualifiers
FEATURES   source
            1..616
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            /mol_type="genomic RNA"
            /isolate="CX255"
            /db_xref="taxon:11077"
            <1..226
            /note="NS5"
            /codon_start=2
            /product="nonstructural protein 5"
            /protein_id="AAG42383.1"
            /db_xref="GI:11991981"
            /translation="TTPVKWSDVPYSGKREDIWCGLIGTRATWAENIQVAITQV
            RSLIGDEKIVDNTSLKRYEDTTLVEDTVL"
ORIGIN
Query Match      100.0%; Score 18; DB 14; Length 616;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
    |||||
Db 347 CGCCACCGGAAGTTGAGT 364
    |||||

RESULT 44
LOCUS     AF297859
DEFINITION Kunjin virus isolate MRM5373 nonstructural protein 5 gene, partial cds
ACCESSION AF297859
VERSION    AF297859.1 GI:11992008
KEYWORDS   Kunjin virus
SOURCE     Kunjin virus
ORGANISM   Kunjin virus
REFERENCE  1 (bases 1 to 620)
AUTHORS    Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
            Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE      The relationships between West Nile and Kunjin viruses
JOURNAL    Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE    21469816
PUBMED     11585535
REFERENCE  2 (bases 1 to 620)
AUTHORS    Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
            and Hall,R.A.
TITLE      Definitive studies of the relationships between West Nile and
JOURNAL    Kunjin viruses
REFERENCE  3 (bases 1 to 620)
AUTHORS    Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
            and Hall,R.A.
TITLE      Direct Submission
JOURNAL    Submitted (22-AUG-2000) Microbiology and Parasitology, University
REFERENCE  of Queensland, St Lucia, QLD 4072, Australia
AUTHORS    Location/Qualifiers
FEATURES   source
            1..620
            /organism="Kunjin virus"
            /mol_type="genomic RNA"
            /isolate="CH16514C"
            /db_xref="taxon:11077"
            <1..245
            /note="NS5"
            /codon_start=3
            /product="nonstructural protein 5"
            /protein_id="AAG42380.1"
            /db_xref="GI:11991975"
            /translation="EENWMDKTPVEKWSDPYSGKREDIWCGLIGTRATWAENIQ
            VAINQVRSLIGDEKIVDYMSLSKRYEDTTLVEDTVL"
ORIGIN
Query Match      100.0%; Score 18; DB 14; Length 622;
Best Local Similarity 100.0%; Pred. No. 15;

QY 1 CGCCACCGGAAGTTGAGT 18
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Db 372 CGCCACCGGAAGTTGAGT 389
    |||||

RESULT 45
LOCUS     AF297842
DEFINITION Kunjin virus isolate CH16514C nonstructural protein 5 gene, partial cds
ACCESSION AF297842
VERSION    AF297842.1 GI:11991974
KEYWORDS   Kunjin virus
SOURCE     Kunjin virus
ORGANISM   Kunjin virus
REFERENCE  1 (bases 1 to 622)
AUTHORS    Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
            Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE      The relationships between West Nile and Kunjin viruses
JOURNAL    Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE    21469816
PUBMED     11585535
REFERENCE  2 (bases 1 to 622)
AUTHORS    Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
            and Hall,R.A.
TITLE      Definitive studies of the relationships between West Nile and
JOURNAL    Kunjin viruses
REFERENCE  3 (bases 1 to 622)
AUTHORS    Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
            and Hall,R.A.
TITLE      Direct Submission
JOURNAL    Submitted (22-AUG-2000) Microbiology and Parasitology, University
REFERENCE  of Queensland, St Lucia, QLD 4072, Australia
AUTHORS    Location/Qualifiers
FEATURES   source
            1..622
            /organism="Kunjin virus"
            /mol_type="genomic RNA"
            /isolate="CH16514C"
            /db_xref="taxon:11077"
            <1..245
            /note="NS5"
            /codon_start=3
            /product="nonstructural protein 5"
            /protein_id="AAG42380.1"
            /db_xref="GI:11991975"
            /translation="EENWMDKTPVEKWSDPYSGKREDIWCGLIGTRATWAENIQ
            VAINQVRSLIGDEKIVDYMSLSKRYEDTTLVEDTVL"
ORIGIN
Query Match      100.0%; Score 18; DB 14; Length 622;
Best Local Similarity 100.0%; Pred. No. 15;

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
Db 366 CGCCACCGGAAGTTGAGT 383

RESULT 46
LOCUS AF297843 623 bp RNA linear VRL 05-MAR-2002
DEFINITION Kunjin virus isolate CH16532C nonstructural protein 5 gene, partial cds.
ACCESSION AF297843
VERSION AF297843.1 GI:11991976
KEYWORDS Kunjin virus
SOURCE Kunjin virus
ORGANISM Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
REFERENCE 1 (bases 1 to 623)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 623)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 623)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia
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ORGANISM Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

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Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 627)
Cota,G., Parker,M.D., Speight,G., Byrne,M.E. and Westaway,E.G.
Nucleotide and complete amino acid sequences of Kunjin virus;
definitive gene order and characteristics of the virus-specified
proteins
J. Gen. Virol. 69 (Pt 1), 1-21 (1988)
MEDLINE 8809524
PUBMED 2826659
REFERENCE 2 (bases 1 to 627)
AUTHORS Khromykh,A.A. and Westaway,E.G.
TITLE Completion of Kunjin virus RNA sequence and recovery of an
infectious RNA transcribed from stably cloned full-length cDNA
J. Virol. 68 (7), 4580-4588 (1994)
MEDLINE 94267921
PUBMED 8207832
COMMENT Original source text: Kunjin virus (strain MRM 61C) mature RNA.
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KEYWORDS Kunjin virus
SOURCE Kunjin virus
ORGANISM Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
REFERENCE 1 (bases 1 to 633)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 633)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 633)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia
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ACCESSION AF297848 GI:11991986
KEYWORDS
SOURCE Kunjin virus
ORGANISM Kunjin virus
REFERENCE 1 (bases 1 to 644)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 644)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 644)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
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Best Local Similarity 100.0%; Pred. No. 16;
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DEFINITION
ACCESSION AY187012
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus
REFERENCE 1 (bases 1 to 645)
AUTHORS Beasley,D.W., Davis,C.T., Guzman,H., Vanlandingham,D.L., Travassos
da Rosa,A.P., Parsons,R.E., Higgs,S., Tesh,R.B. and Barrett,A.D.
TITLE Limited evolution of West Nile virus has occurred during its
southwesterly spread in the United States
JOURNAL Virology 309 (2), 190-195 (2003)
MEDLINE 22644768
PUBMED 12758166
REFERENCE 2 (bases 1 to 645)
AUTHORS Beasley,D.W.C., Davis,C.T., Guzman,H., Vanlandingham,D.L.,
Travassos da Rosa,A.P.A., Parsons,R.E., Higgs,S., Tesh,R.B. and
Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (26-NOV-2002) Pathology, University of Texas Medical
Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 09:32:36 ; Search time 171.857 Seconds

(without alignments)  
620.023 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 500 summaries

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2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

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7: Geneseqn2002bs:\*

8: Geneseqn2003as:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004as:\*

13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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| 7          | 18    | 100.0       | 10945  | ADR67768    | Adr67768 West Nile |
| 8          | 18    | 100.0       | 10975  | ADN98022    | Adn98022 West Nile |
| 9          | 18    | 100.0       | 11029  | 8 ABZ68481  | Abz68481 Nucleotid |
| 10         | 18    | 100.0       | 11029  | 10 ABV74821 | Abv74821 West Nile |
| 11         | 18    | 100.0       | 11029  | 12 ADN98023 | Adn98023 West Nile |
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| 13         | 17    | 94.4        | 17     | 6 ACN07465  | Acn07465 WNV minus |
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|--------------------|------------|
| Acn09627           | WNV minus  |
| Abz71129           | Mycobacte  |
| Aah51995           | Mycobacte  |
| Abi28588           | Drosophi   |
| Continuation (15 o |            |
| Continuation (15 o |            |
| Ado21519           | West Nile  |
| Adn73634           | Thale cre  |
| Aac48174           | Arabidops  |
| Aac35195           | Arabidops  |
| Ado39648           | Yeast Bdf  |
| Adq97983           | Mouse can  |
| Ado33203           | Human can  |
| Acn14228           | WNV minus  |
| Acn03350           | WNV Inozy  |
| Acn04649           | WNV Zinz   |
| Ac127596           | Human mic  |
| Acn03748           | Wheat ste  |
| Acn03761           | Wheat ste  |
| Acn03758           | Corn ster  |
| Acn03757           | Corn ster  |
| Aah65402           | C glutami  |
| Adl65984           | C. glutam  |
| Abi04952           | Drosophil  |
| Aah68525           | C glutami  |
| Acn72382           | E. coli K  |
| Acn72383           | E. coli K  |
| Adq16356           | Nucleotid  |
| Adq16357           | Nucleotid  |
| Aat64813           | Novel hum  |
| Aat64761           | Novel hum  |
| Abn63337           | Human can  |
| Aah07543           | Human cdn  |
| Aas78026           | DNA encod  |
| Abv28936           | Human pro  |
| Abv23098           | Human pro  |
| Abz13721           | Arabidops  |
| Aac42336           | Arabidops  |
| Aas73496           | DNA encod  |
| Aav31213           | E. coli J  |
| Aah68311           | C. glutami |
| Acn19044           | Prokaryot  |
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| Abd15999           | Pseudomon  |
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| Acn01132           | C. glutam  |
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| Adq63334           | Novel hum  |
| Adq30772           | Plant yie  |
| Adi41958           | Plant tra  |
| Adq64456           | Novel hum  |
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| Aag35297           | ZYMV geno  |
| Abi15493           | Drosophil  |
| Abf03152           | Bacteri    |
| Abi15493           | Drosophil  |
| Abq07520           | Oligonucl  |
| Abq01790           | Oligonucl  |
| Abk63304           | Rat seque  |
| Adb52117           | Primary r  |
| Abt41596           | Toxicity   |
| Adp72384           | Renal tox  |

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| C 95  | 14.4 | 80.0 | 550  | 9  | ACC73171 | Acc73171 Cat flea   | C 168 | 13.8 | 76.7 | 711 | 4  | RA556132 | Aas56132 Salmonell  |
| C 96  | 14.4 | 80.0 | 550  | 12 | ADL09816 | Adl09816 Cat flea   | C 169 | 13.8 | 76.7 | 711 | 8  | ACA52014 | Acas2014 Prokaryot  |
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| C 98  | 14.4 | 80.0 | 550  | 12 | ADL09816 | Adl09816 Cat flea   | C 171 | 13.8 | 76.7 | 720 | 10 | ADH82147 | Adh82147 Enteroococ |
| C 99  | 14.4 | 80.0 | 550  | 12 | ADL09816 | Adl09816 Cat flea   | C 172 | 13.8 | 76.7 | 744 | 2  | AAQ43288 | Aaq43288 Multivale  |
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| 103   | 14.4 | 80.0 | 936  | 12 | ADL62199 | Adl62199 DNA encod  | C 176 | 13.8 | 76.7 | 744 | 3  | AA59617  | Aas59617 DNA encod  |
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| C 108 | 14.4 | 80.0 | 1296 | 12 | ADJ26791 | Adj26791 Arabidops  | C 181 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
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| C 134 | 14.4 | 80.0 | 1296 | 12 | ADJ26791 | Adj26791 Arabidops  | C 207 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 135 | 14.4 | 80.0 | 1296 | 12 | ADJ26791 | Adj26791 Arabidops  | C 208 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 136 | 14.4 | 80.0 | 1296 | 12 | ADJ26791 | Adj26791 Arabidops  | C 209 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 137 | 14.4 | 80.0 | 1296 | 12 | ADJ26791 | Adj26791 Arabidops  | C 210 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 138 | 14.4 | 80.0 | 1296 | 12 | ADJ26791 | Adj26791 Arabidops  | C 211 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 139 | 14.4 | 80.0 | 1296 | 12 | ADJ26791 | Adj26791 Arabidops  | C 212 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 140 | 14.4 | 80.0 | 1296 | 12 | ADJ26791 | Adj26791 Arabidops  | C 213 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 141 | 14.4 | 80.0 | 1296 | 12 | ADJ26791 | Adj26791 Arabidops  | C 214 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 142 | 14.4 | 80.0 | 1296 | 12 | ADJ26791 | Adj26791 Arabidops  | C 215 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 143 | 14.4 | 80.0 | 1296 | 12 | ADJ26791 | Adj26791 Arabidops  | C 216 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 144 | 14.4 | 80.0 | 1296 | 12 | ADJ26791 | Adj26791 Arabidops  | C 217 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 145 | 14.4 | 80.0 | 1296 | 12 | ADJ26791 | Adj26791 Arabidops  | C 218 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 146 | 14.4 | 80.0 | 1296 | 12 | ADJ26791 | Adj26791 Arabidops  | C 219 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 147 | 14.4 | 80.0 | 1296 | 12 | ADJ26791 | Adj26791 Arabidops  | C 220 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 148 | 13.8 | 76.7 | 19   | 6  | ABA01459 | Abao1459 Streptococ | C 221 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 149 | 13.8 | 76.7 | 25   | 9  | ACI35252 | Act35252 Human mic  | C 222 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 150 | 13.8 | 76.7 | 69   | 10 | ADD55911 | Add55911 Chicken m  | C 223 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 151 | 13.8 | 76.7 | 100  | 8  | ACD80582 | Acd80582 E. coli K  | C 224 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 152 | 13.8 | 76.7 | 100  | 8  | ACD80582 | Acd80582 E. coli K  | C 225 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 153 | 13.8 | 76.7 | 195  | 8  | ABX54248 | Abx54248 Bovine ES  | C 226 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 154 | 13.8 | 76.7 | 271  | 7  | ADS70977 | AdS70977 Corn seed  | C 227 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 155 | 13.8 | 76.7 | 359  | 3  | AAZ58767 | Aaz58767 Human bun  | C 228 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 156 | 13.8 | 76.7 | 365  | 6  | ABT10291 | Abt10291 Human bre  | C 229 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 157 | 13.8 | 76.7 | 380  | 2  | AA411129 | Aa411129 Human sec  | C 230 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 158 | 13.8 | 76.7 | 406  | 12 | ADP57134 | Adp57134 Maize car  | C 231 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 159 | 13.8 | 76.7 | 420  | 3  | AAI16112 | Aai16112 Human sec  | C 232 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 160 | 13.8 | 76.7 | 466  | 9  | ACH34526 | Ach34526 Human end  | C 233 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 161 | 13.8 | 76.7 | 475  | 3  | AA433552 | Aa433552 Zea mays   | C 234 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 162 | 13.8 | 76.7 | 503  | 12 | ADN13034 | Adn13034 Human pro  | C 235 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 163 | 13.8 | 76.7 | 541  | 3  | AAA44532 | Aaa44532 Human sec  | C 236 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 164 | 13.8 | 76.7 | 628  | 6  | ABQ66147 | Abq66147 Arabidops  | C 237 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 165 | 13.8 | 76.7 | 632  | 2  | ADR01359 | Adr01359 A. gossyp  | C 238 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |
| C 166 | 13.8 | 76.7 | 660  | 4  | ABL24327 | AbL24327 Drosophil  | C 239 | 13.8 | 76.7 | 782 | 2  | AAV69288 | Aav69288 Single ch  |

|       |      |      |      |    |           |           |       |      |      |      |    |          |                     |
|-------|------|------|------|----|-----------|-----------|-------|------|------|------|----|----------|---------------------|
| C 240 | 13.8 | 76.7 | 978  | 12 | ADD78348  | Novel hum | C 313 | 13.8 | 76.7 | 2298 | 13 | ADS60815 | Ad608015 Bacterial  |
| C 241 | 13.8 | 76.7 | 978  | 12 | ADDE21171 | Novel hum | 314   | 13.8 | 76.7 | 2304 | 13 | ADS48003 | Ad480003 Bacterial  |
| C 242 | 13.8 | 76.7 | 978  | 12 | ADD77286  | Novel hum | C 315 | 13.8 | 76.7 | 2330 | 4  | ABL25027 | Ab125027 Drosophil  |
| C 243 | 13.8 | 76.7 | 978  | 12 | ADDE20433 | Novel hum | 316   | 13.8 | 76.7 | 2374 | 4  | ABL22972 | Ab122972 Drosophil  |
| C 244 | 13.8 | 76.7 | 978  | 12 | ADDE20433 | Novel hum | 317   | 13.8 | 76.7 | 2390 | 4  | ABL02769 | Ab102769 Drosophil  |
| C 245 | 13.8 | 76.7 | 978  | 12 | ADD74014  | Human PRO | C 318 | 13.8 | 76.7 | 2396 | 3  | AAA75081 | Aaa75081 CDNA enco  |
| C 246 | 13.8 | 76.7 | 978  | 12 | ADD74260  | Human PRO | C 319 | 13.8 | 76.7 | 2396 | 4  | AAA91113 | Aaa91113 Mouse hep  |
| C 247 | 13.8 | 76.7 | 978  | 12 | ADD75990  | Novel hum | C 320 | 13.8 | 76.7 | 2396 | 10 | ADG88833 | Adg88833 Mouse hpa  |
| C 248 | 13.8 | 76.7 | 978  | 12 | ADD85482  | Novel hum | C 321 | 13.8 | 76.7 | 2396 | 10 | ADG88835 | Adg88835 Mouse hpa  |
| C 249 | 13.8 | 76.7 | 978  | 12 | ADDE05031 | Human PRO | C 322 | 13.8 | 76.7 | 2396 | 12 | ADL16412 | Adl16412 Mouse cDN  |
| C 250 | 13.8 | 76.7 | 978  | 12 | ADDE05031 | Human PRO | C 323 | 13.8 | 76.7 | 2396 | 12 | ADL16414 | Adl16414 Mouse cDN  |
| C 251 | 13.8 | 76.7 | 978  | 12 | ADD75244  | Human PRO | C 324 | 13.8 | 76.7 | 2396 | 12 | ADM48749 | Adm48749 Mouse hpa  |
| C 252 | 13.8 | 76.7 | 978  | 12 | ADD76788  | Novel hum | C 325 | 13.8 | 76.7 | 2396 | 12 | ADM48751 | Adm48751 Mouse hpa  |
| C 253 | 13.8 | 76.7 | 978  | 12 | ADD86556  | Novel hum | C 326 | 13.8 | 76.7 | 2402 | 5  | AA569796 | Aa569796 DNA enco   |
| C 254 | 13.8 | 76.7 | 978  | 12 | ADD778024 | Novel hum | C 327 | 13.8 | 76.7 | 2538 | 4  | ABL15911 | Ab115911 Drosophil  |
| C 255 | 13.8 | 76.7 | 978  | 12 | ADD77532  | Novel hum | C 328 | 13.8 | 76.7 | 2540 | 4  | ABL24550 | Ab124550 Drosophil  |
| C 256 | 13.8 | 76.7 | 978  | 12 | ADD77778  | Novel hum | C 329 | 13.8 | 76.7 | 2554 | 6  | AA599908 | Aa599908 Polynucle  |
| C 257 | 13.8 | 76.7 | 978  | 12 | ADD85236  | Novel hum | C 330 | 13.8 | 76.7 | 2659 | 4  | AA160389 | Aa160389 Human pol  |
| C 258 | 13.8 | 76.7 | 978  | 12 | ADD73768  | Human PRO | C 331 | 13.8 | 76.7 | 2659 | 4  | AA160390 | Ab160390 Human pol  |
| C 259 | 13.8 | 76.7 | 978  | 12 | ADD74506  | Human PRO | C 332 | 13.8 | 76.7 | 2691 | 4  | ABL17111 | Ab117111 Drosophil  |
| C 260 | 13.8 | 76.7 | 978  | 12 | ADD77034  | Novel hum | C 333 | 13.8 | 76.7 | 2715 | 2  | AAV80665 | Aav80665 Human DNA  |
| C 261 | 13.8 | 76.7 | 978  | 12 | ADD85728  | Novel hum | C 334 | 13.8 | 76.7 | 2715 | 6  | AA26282  | Ad26282 Human DNA   |
| C 262 | 13.8 | 76.7 | 978  | 12 | ADDE05277 | Human PRO | C 335 | 13.8 | 76.7 | 2740 | 6  | ABQ76022 | Abq76022 Human mac  |
| C 263 | 13.8 | 76.7 | 978  | 12 | ADD74752  | Human PRO | C 336 | 13.8 | 76.7 | 2796 | 5  | AA594111 | Aa594111 DNA enco   |
| C 264 | 13.8 | 76.7 | 978  | 12 | ADG05564  | Novel hum | C 337 | 13.8 | 76.7 | 2859 | 11 | ABD17008 | Abd17008 Pseudomon  |
| C 265 | 13.8 | 76.7 | 978  | 12 | ADG27118  | Human PRO | C 338 | 13.8 | 76.7 | 2863 | 4  | ABL24326 | Ab124326 Drosophil  |
| C 266 | 13.8 | 76.7 | 978  | 12 | ADG11181  | Novel hum | C 339 | 13.8 | 76.7 | 2896 | 5  | AA580134 | Ad580134 DNA enco   |
| C 267 | 13.8 | 76.7 | 978  | 12 | ADG11960  | Novel hum | C 340 | 13.8 | 76.7 | 2969 | 4  | ABL10148 | Ab110148 Drosophil  |
| C 268 | 13.8 | 76.7 | 978  | 12 | ADF94517  | Novel hum | C 341 | 13.8 | 76.7 | 2975 | 10 | ADA53314 | Ada53314 Human cod  |
| C 269 | 13.8 | 76.7 | 978  | 12 | ADG06613  | Human PRO | C 342 | 13.8 | 76.7 | 2975 | 2  | AA338325 | Aa338325 Signal tr  |
| C 270 | 13.8 | 76.7 | 978  | 12 | ADH38957  | Novel hum | C 343 | 13.8 | 76.7 | 3027 | 8  | ABT18986 | Abt18986 Aspergill  |
| C 271 | 13.8 | 76.7 | 978  | 12 | ADG34047  | Novel hum | C 344 | 13.8 | 76.7 | 3029 | 10 | ACF36710 | Acf36710 Human Tol  |
| C 272 | 13.8 | 76.7 | 978  | 12 | ADI33517  | Human PRO | C 345 | 13.8 | 76.7 | 3029 | 10 | ADK61029 | Adk61029 Ovarian c  |
| C 273 | 13.8 | 76.7 | 978  | 12 | ADH69611  | Human PRO | C 346 | 13.8 | 76.7 | 3057 | 10 | ADK61029 | Adk61029 Ovarian c  |
| C 274 | 13.8 | 76.7 | 978  | 12 | ADI29772  | Novel hum | C 347 | 13.8 | 76.7 | 3057 | 10 | ACC72737 | Acc72737 Human can  |
| C 275 | 13.8 | 76.7 | 978  | 12 | ADM27169  | Human PRO | C 348 | 13.8 | 76.7 | 3057 | 12 | ADP56653 | Adp56653 Human Tol  |
| C 276 | 13.8 | 76.7 | 978  | 12 | ADK66527  | Human PRO | C 349 | 13.8 | 76.7 | 3057 | 12 | ADP48594 | Adp48594 Human Tol  |
| C 277 | 13.8 | 76.7 | 986  | 5  | AA569791  | DNA enco  | C 350 | 13.8 | 76.7 | 3081 | 8  | ABT18392 | Abt18392 Aspergill  |
| C 278 | 13.8 | 76.7 | 1056 | 6  | ABK43187  | DNA enco  | C 351 | 13.8 | 76.7 | 3180 | 2  | AAQ94645 | Aaq94645 Recombina  |
| C 279 | 13.8 | 76.7 | 1068 | 9  | ADA31143  | DNA enco  | C 352 | 13.8 | 76.7 | 3180 | 2  | AAQ94645 | Aaq94645 Recombina  |
| C 280 | 13.8 | 76.7 | 1101 | 4  | AAK63517  | Human imm | C 353 | 13.8 | 76.7 | 3198 | 8  | ABT20806 | Abt20806 Aspergill  |
| C 281 | 13.8 | 76.7 | 1107 | 3  | AA54915   | Arabidops | C 354 | 13.8 | 76.7 | 3210 | 6  | ABQ70990 | Abq70990 Listeria   |
| C 282 | 13.8 | 76.7 | 1110 | 3  | AA54027   | Arabidops | C 355 | 13.8 | 76.7 | 3311 | 13 | ADS48485 | Ad484848 Bacterial  |
| C 283 | 13.8 | 76.7 | 1133 | 4  | ABU13097  | Drosophil | C 356 | 13.8 | 76.7 | 3311 | 8  | ABT20208 | Abt20208 Aspergill  |
| C 284 | 13.8 | 76.7 | 1149 | 2  | AA302109  | Yeast FEN | C 357 | 13.8 | 76.7 | 3319 | 4  | ABL12634 | Ab112634 Drosophil  |
| C 285 | 13.8 | 76.7 | 1178 | 8  | ABZ57353  | Human zin | C 358 | 13.8 | 76.7 | 3584 | 8  | ABX63341 | Abx63341 Human cDN  |
| C 286 | 13.8 | 76.7 | 1179 | 8  | ADA69875  | Rice gene | C 359 | 13.8 | 76.7 | 3815 | 4  | ABL15910 | Ab115910 Drosophil  |
| C 287 | 13.8 | 76.7 | 1260 | 13 | ACN37649  | Tumour-as | C 360 | 13.8 | 76.7 | 3855 | 4  | ABL27710 | Ab127710 Drosophil  |
| C 288 | 13.8 | 76.7 | 1281 | 13 | AD45289   | Bacterial | C 361 | 13.8 | 76.7 | 4054 | 4  | ABL13096 | Ab113096 Drosophil  |
| C 289 | 13.8 | 76.7 | 1317 | 11 | ABD13141  | Pseudomon | C 362 | 13.8 | 76.7 | 4232 | 2  | AA133008 | Aa133008 Enterococ  |
| C 290 | 13.8 | 76.7 | 1380 | 2  | AA37261   | Murine he | C 363 | 13.8 | 76.7 | 4232 | 6  | ABS98803 | Ab98803 Enterococ   |
| C 291 | 13.8 | 76.7 | 1383 | 5  | AA570995  | DNA enco  | C 364 | 13.8 | 76.7 | 4233 | 3  | AAZ90198 | Aaz90198 Rat mdrib  |
| C 292 | 13.8 | 76.7 | 1411 | 6  | ABK43189  | DNA enco  | C 365 | 13.8 | 76.7 | 4233 | 4  | AAF27498 | Aaf27498 Rat mdrib  |
| C 293 | 13.8 | 76.7 | 1455 | 11 | ABD00580  | Klebsiell | C 366 | 13.8 | 76.7 | 4251 | 5  | ABA21002 | Ab21002 Human ner   |
| C 294 | 13.8 | 76.7 | 1460 | 2  | AAQ43291  | Sequence  | C 367 | 13.8 | 76.7 | 4347 | 3  | AAA70724 | Aaa70724 Thermsus t |
| C 295 | 13.8 | 76.7 | 1460 | 3  | AA504745  | DNA enco  | C 368 | 13.8 | 76.7 | 4701 | 5  | AA564813 | Aa564813 DNA enco   |
| C 296 | 13.8 | 76.7 | 1460 | 3  | AA59620   | DNA enco  | C 369 | 13.8 | 76.7 | 4701 | 13 | ADR14476 | Adr14476 Human NF-  |
| C 297 | 13.8 | 76.7 | 1460 | 3  | AA57093   | Divalent  | C 370 | 13.8 | 76.7 | 4851 | 8  | ACA37619 | Aca37619 Prokaryot  |
| C 298 | 13.8 | 76.7 | 1460 | 3  | AA595088  | DNA enco  | C 371 | 13.8 | 76.7 | 4892 | 4  | AA158604 | Aa158604 Human pol  |
| C 299 | 13.8 | 76.7 | 1460 | 3  | AA290342  | DNA enco  | C 372 | 13.8 | 76.7 | 4892 | 5  | ADQ98822 | Adq98822 DNA enco   |
| C 300 | 13.8 | 76.7 | 1460 | 5  | ACA62246  | Divalent  | C 373 | 13.8 | 76.7 | 4892 | 9  | ADB48582 | Adb48582 Human hum  |
| C 301 | 13.8 | 76.7 | 1617 | 12 | ADJ40236  | Plant cDN | C 374 | 13.8 | 76.7 | 4964 | 4  | AA158603 | Aa158603 Human pol  |
| C 302 | 13.8 | 76.7 | 1692 | 11 | ABD13283  | Pseudomon | C 375 | 13.8 | 76.7 | 4964 | 5  | ADQ98821 | Adq98821 DNA enco   |
| C 303 | 13.8 | 76.7 | 1702 | 6  | ABK43190  | DNA enco  | C 376 | 13.8 | 76.7 | 4964 | 9  | ADB48581 | Adb48581 Novel hum  |
| C 304 | 13.8 | 76.7 | 1737 | 13 | ADR07621  | Full leng | C 377 | 13.8 | 76.7 | 5081 | 8  | ABT17798 | Abt17798 Aspergill  |
| C 305 | 13.8 | 76.7 | 1845 | 10 | ADD47716  | Human gen | C 378 | 13.8 | 76.7 | 5226 | 6  | ADI39469 | Adi39469 Arabidops  |
| C 306 | 13.8 | 76.7 | 2000 | 10 | ACC60755  | Gene sequ | C 379 | 13.8 | 76.7 | 5311 | 8  | ABT19612 | Abt19612 Aspergill  |
| C 307 | 13.8 | 76.7 | 2000 | 10 | ADK61933  | Disease t | C 380 | 13.8 | 76.7 | 5513 | 3  | AA563529 | Aa563529 Slit prot  |
| C 308 | 13.8 | 76.7 | 2005 | 3  | AA290422  | Maize ace | C 381 | 13.8 | 76.7 | 5650 | 8  | ACD13203 | Adc13203 cDNA enco  |
| C 309 | 13.8 | 76.7 | 2061 | 13 | ADS47086  | Bacterial | C 382 | 13.8 | 76.7 | 5874 | 6  | ADI39470 | Adi39470 A thalian  |
| C 310 | 13.8 | 76.7 | 2148 | 11 | ABD04060  | Pseudomon | C 383 | 13.8 | 76.7 | 6106 | 4  | ABL22974 | Ab122974 Drosophil  |
| C 311 | 13.8 | 76.7 | 2163 | 11 | ABD04406  | Pseudomon | C 384 | 13.8 | 76.7 | 6120 | 10 | ADE63138 | Ad63138 Human gen   |
| C 312 | 13.8 | 76.7 | 2291 | 10 | ADA52811  | Human cod | C 385 | 13.8 | 76.7 | 6120 | 10 | ADD46316 | Ad46316 Human gen   |

|       |      |      |        |    |             |                                |     |      |      |     |    |          |                     |
|-------|------|------|--------|----|-------------|--------------------------------|-----|------|------|-----|----|----------|---------------------|
| C 386 | 13.8 | 76.7 | 6270   | 4  | ABL25026    | Ab125026 Drosophil             | 459 | 13.4 | 74.4 | 458 | 12 | ADJ42714 | Adj42714 Plant CDN  |
| C 387 | 13.8 | 76.7 | 6291   | 4  | ABL16851    | Ab116851 Drosophil             | 460 | 13.4 | 74.4 | 459 | 12 | ACH86212 | ACH86212 Human gen  |
| C 388 | 13.8 | 76.7 | 6291   | 13 | ADQ89605    | Adq89605 Antagonis             | 461 | 13.4 | 74.4 | 463 | 9  | ACH28627 | ACH28627 Human adu  |
| C 389 | 13.8 | 76.7 | 6957   | 10 | ADBS2723    | Adbs2723 Primary r             | 462 | 13.4 | 74.4 | 471 | 12 | ADJ43189 | Adj43189 Plant CDN  |
| C 390 | 13.8 | 76.7 | 7106   | 4  | ABL14908    | Ab114908 Drosophil             | 463 | 13.4 | 74.4 | 474 | 3  | AAC44074 | Aac44074 Zea mays   |
| C 391 | 13.8 | 76.7 | 8265   | 4  | AAS42165    | Aas42165 Genomic s             | 464 | 13.4 | 74.4 | 478 | 3  | AAC46697 | Aac46697 Zea mays   |
| C 392 | 13.8 | 76.7 | 8527   | 4  | ABL16850    | Ab116850 Drosophil             | 465 | 13.4 | 74.4 | 480 | 4  | AAR89812 | Aar89812 Human pol  |
| C 393 | 13.8 | 76.7 | 9434   | 4  | ABL17110    | Ab117110 Drosophil             | 466 | 13.4 | 74.4 | 484 | 4  | AAR11681 | Aar11681 Probe #16  |
| C 394 | 13.8 | 76.7 | 9636   | 4  | AAK90449    | Aak90449 Human dig             | 467 | 13.4 | 74.4 | 484 | 4  | ABA53374 | Abas53374 Human foe |
| C 395 | 13.8 | 76.7 | 10401  | 4  | AAS42164    | Aas42164 Genomic s             | 468 | 13.4 | 74.4 | 484 | 4  | AAI32981 | Aai32981 Probe #16  |
| C 396 | 13.8 | 76.7 | 14460  | 6  | ABA01440    | Abao1440 Streptoco             | 469 | 13.4 | 74.4 | 484 | 4  | ABA42953 | Abas42953 Human bre |
| C 397 | 13.8 | 76.7 | 15441  | 4  | ABL06029    | Ab106029 Drosophil             | 470 | 13.4 | 74.4 | 484 | 4  | ABA23154 | Abas23154 Probe #16 |
| C 398 | 13.8 | 76.7 | 20706  | 4  | ABL06028    | Ab106028 Drosophil             | 471 | 13.4 | 74.4 | 484 | 4  | AAK27086 | Aak27086 Human bon  |
| C 399 | 13.8 | 76.7 | 21646  | 11 | ACN44454    | Acn44454 Human gen             | 472 | 13.4 | 74.4 | 484 | 4  | AAK01643 | Aak01643 Human liv  |
| C 400 | 13.8 | 76.7 | 22157  | 6  | ABA01448    | Abao1448 Streptoco             | 473 | 13.4 | 74.4 | 484 | 4  | ABS26673 | Abas26673 Human liv |
| C 401 | 13.8 | 76.7 | 27459  | 13 | ABD32620    | Abd32620 Human can             | 474 | 13.4 | 74.4 | 484 | 5  | AAI01606 | Aai01606 Probe #15  |
| C 402 | 13.8 | 76.7 | 33012  | 8  | ABS55899    | Abss5899 Bovine ad             | 475 | 13.4 | 74.4 | 484 | 6  | ABS01654 | Abes01654 Human gen |
| C 403 | 13.8 | 76.7 | 33113  | 8  | ABS55900    | Abss5900 Bovine ad             | 476 | 13.4 | 74.4 | 500 | 12 | ADJ42742 | Adj42742 Plant CDN  |
| C 404 | 13.8 | 76.7 | 33306  | 8  | ABS55901    | Abss5901 Bovine ad             | 477 | 13.4 | 74.4 | 502 | 12 | ADJ43242 | Adj43242 Plant CDN  |
| C 405 | 13.8 | 76.7 | 33310  | 8  | ABS55902    | Abss5902 Bovine ad             | 478 | 13.4 | 74.4 | 507 | 12 | ADJ42759 | Adj42759 Plant CDN  |
| C 406 | 13.8 | 76.7 | 34079  | 8  | ABS55903    | Abss5903 Bovine ad             | 479 | 13.4 | 74.4 | 516 | 12 | ADJ43261 | Adj43261 Plant CDN  |
| C 407 | 13.8 | 76.7 | 34185  | 3  | AAC62130    | Aac62130 Nucleotid             | 480 | 13.4 | 74.4 | 518 | 12 | ADJ42752 | Adj42752 Plant CDN  |
| C 408 | 13.8 | 76.7 | 34185  | 8  | ABS55888    | Abss5888 Bovine ad             | 481 | 13.4 | 74.4 | 519 | 4  | AAK61881 | Aak61881 Human imm  |
| C 409 | 13.8 | 76.7 | 34185  | 10 | ADC17118    | Adc17118 Bovine ad             | 482 | 13.4 | 74.4 | 529 | 5  | AAH87936 | Aah87936 Peppermin  |
| C 410 | 13.8 | 76.7 | 35133  | 4  | ABL50991    | Ab150991 Thermus c             | 483 | 13.4 | 74.4 | 532 | 8  | ABX73138 | Abx73138 Metabolic  |
| C 411 | 13.8 | 76.7 | 35134  | 4  | ABL50990    | Ab150990 Thermus c             | 484 | 13.4 | 74.4 | 535 | 10 | ABX57422 | Abx57422 Arabidops  |
| C 412 | 13.8 | 76.7 | 38734  | 2  | AA232020    | Aa232020 Human MFR             | 485 | 13.4 | 74.4 | 536 | 4  | AAI43411 | Aai43411 Probe #12  |
| C 413 | 13.8 | 76.7 | 38734  | 5  | AAC90077    | Aac90077 AL021529              | 486 | 13.4 | 74.4 | 536 | 12 | ADJ42743 | Adj42743 Plant CDN  |
| C 414 | 13.8 | 76.7 | 47066  | 4  | ABU11514    | Abu11514 Drosophil             | 487 | 13.4 | 74.4 | 542 | 12 | ADJ43279 | Adj43279 Plant CDN  |
| C 415 | 13.8 | 76.7 | 51259  | 2  | ACN45164    | Acn45164 Mouse gen             | 488 | 13.4 | 74.4 | 543 | 12 | ADJ42748 | Adj42748 Plant CDN  |
| C 416 | 13.8 | 76.7 | 58665  | 11 | ADN01773    | Adn01773 Human hun             | 489 | 13.4 | 74.4 | 544 | 12 | ADJ42753 | Adj42753 Plant CDN  |
| C 417 | 13.8 | 76.7 | 65454  | 12 | ADN01773    | Adn01773 Human hun             | 490 | 13.4 | 74.4 | 545 | 4  | AAI19273 | Aai19273 Probe #92  |
| C 418 | 13.8 | 76.7 | 81098  | 11 | ACN45202    | Acn45202 Human gen             | 491 | 13.4 | 74.4 | 545 | 4  | ABA64285 | Abas64285 Human foe |
| C 419 | 13.8 | 76.7 | 88853  | 11 | ACN43904    | Acn43904 Mouse gen             | 492 | 13.4 | 74.4 | 545 | 4  | AAI44442 | Aai44442 Probe #13  |
| C 420 | 13.8 | 76.7 | 110000 | 4  | AA199682_30 | AA199682_30 Continuation (31 o | 493 | 13.4 | 74.4 | 545 | 4  | ABA31421 | Abas31421 Probe #98 |
| C 421 | 13.8 | 76.7 | 110000 | 4  | AA199682_31 | AA199682_31 Continuation (32 o | 494 | 13.4 | 74.4 | 545 | 4  | AAK38474 | Aak38474 Human bon  |
| C 422 | 13.8 | 76.7 | 110000 | 4  | AA199683_30 | AA199683_30 Continuation (31 o | 495 | 13.4 | 74.4 | 545 | 4  | AAK12753 | Aak12753 Human bra  |
| C 423 | 13.8 | 76.7 | 110000 | 4  | AA199683_31 | AA199683_31 Continuation (32 o | 496 | 13.4 | 74.4 | 545 | 4  | ABS38061 | Abes38061 Human liv |
| C 424 | 13.8 | 76.7 | 151826 | 3  | AAF22291    | Aaf22291 BAC conta             | 497 | 13.4 | 74.4 | 545 | 6  | ABS12539 | Abes12539 Human gen |
| C 425 | 13.8 | 76.7 | 175561 | 8  | AD55694     | Ad55694 Human THB              | 498 | 13.4 | 74.4 | 548 | 4  | AAH09413 | Aah09413 Human gen  |
| C 426 | 13.8 | 76.7 | 175561 | 12 | ADL08129    | Adl08129 Human gen             | 499 | 13.4 | 74.4 | 548 | 12 | ADJ42761 | Adj42761 Plant CDN  |
| C 427 | 13.8 | 76.7 | 226475 | 9  | AD58279     | Ad58279 Human tum              | 500 | 13.4 | 74.4 | 552 | 12 | ADJ43263 | Adj43263 Plant CDN  |
| C 428 | 13.8 | 76.7 | 304905 | 11 | ADP75180    | Adp75180 Human can             |     |      |      |     |    |          |                     |
| C 429 | 13.8 | 76.7 | 348101 | 12 | ADQ97146    | Adq97146 Human can             |     |      |      |     |    |          |                     |
| C 430 | 13.8 | 76.7 | 349980 | 5  | AAH41225    | Aah41225 Pyrococcu             |     |      |      |     |    |          |                     |
| C 431 | 13.4 | 74.4 | 20     | 4  | AD11810     | Ad11810 Salmonell              |     |      |      |     |    |          |                     |
| C 432 | 13.4 | 74.4 | 25     | 9  | ACI27597    | Act27597 Human mic             |     |      |      |     |    |          |                     |
| C 433 | 13.4 | 74.4 | 100    | 8  | ACD80252    | Act80252 E. coli K             |     |      |      |     |    |          |                     |
| C 434 | 13.4 | 74.4 | 134    | 4  | AAI20894    | Aai20894 Probe #10             |     |      |      |     |    |          |                     |
| C 435 | 13.4 | 74.4 | 134    | 4  | ABA65966    | Abas65966 Human foe            |     |      |      |     |    |          |                     |
| C 436 | 13.4 | 74.4 | 134    | 4  | AAI46133    | Aai46133 Probe #14             |     |      |      |     |    |          |                     |
| C 437 | 13.4 | 74.4 | 134    | 4  | ABA48081    | Abas48081 Human bre            |     |      |      |     |    |          |                     |
| C 438 | 13.4 | 74.4 | 134    | 4  | ABA33058    | Abas33058 Probe #11            |     |      |      |     |    |          |                     |
| C 439 | 13.4 | 74.4 | 134    | 4  | AAK40118    | Aak40118 Human bon             |     |      |      |     |    |          |                     |
| C 440 | 13.4 | 74.4 | 134    | 4  | AAK14389    | Aak14389 Human bra             |     |      |      |     |    |          |                     |
| C 441 | 13.4 | 74.4 | 134    | 4  | ABS39703    | Abas39703 Human liv            |     |      |      |     |    |          |                     |
| C 442 | 13.4 | 74.4 | 134    | 5  | AAI06602    | Aai06602 Probe #65             |     |      |      |     |    |          |                     |
| C 443 | 13.4 | 74.4 | 134    | 6  | ABS14185    | Abas14185 Human gen            |     |      |      |     |    |          |                     |
| C 444 | 13.4 | 74.4 | 151    | 7  | ADS68645    | Ades68645 Corn seed            |     |      |      |     |    |          |                     |
| C 445 | 13.4 | 74.4 | 189    | 8  | ACC48810    | Acc48810 Human EVI             |     |      |      |     |    |          |                     |
| C 446 | 13.4 | 74.4 | 275    | 7  | ABS70372    | Abse70372 Corn seed            |     |      |      |     |    |          |                     |
| C 447 | 13.4 | 74.4 | 275    | 10 | ABX86179    | Abx86179 Corn ear-             |     |      |      |     |    |          |                     |
| C 448 | 13.4 | 74.4 | 322    | 13 | ADS4782     | Ades4782 Bacterial             |     |      |      |     |    |          |                     |
| C 449 | 13.4 | 74.4 | 324    | 10 | ADF02123    | Adf02123 Bacterial             |     |      |      |     |    |          |                     |
| C 450 | 13.4 | 74.4 | 334    | 3  | AAA31143    | Aaa31143 Plant mic             |     |      |      |     |    |          |                     |
| C 451 | 13.4 | 74.4 | 366    | 2  | AAQ61221    | Aaq61221 Human bra             |     |      |      |     |    |          |                     |
| C 452 | 13.4 | 74.4 | 377    | 6  | ABL78745    | Ab178745 Human ova             |     |      |      |     |    |          |                     |
| C 453 | 13.4 | 74.4 | 381    | 11 | ACH98703    | Ach98703 Klebsiell             |     |      |      |     |    |          |                     |
| C 454 | 13.4 | 74.4 | 390    | 6  | ABN27012    | Abn27012 Human ORF             |     |      |      |     |    |          |                     |
| C 455 | 13.4 | 74.4 | 414    | 4  | AAC91317    | Aac91317 Human pol             |     |      |      |     |    |          |                     |
| C 456 | 13.4 | 74.4 | 435    | 8  | ABX35016    | Abx35016 Bovine ES             |     |      |      |     |    |          |                     |
| C 457 | 13.4 | 74.4 | 454    | 3  | AAA31071    | Aaa31071 Plant mic             |     |      |      |     |    |          |                     |
| C 458 | 13.4 | 74.4 | 456    | 11 | ABD02030    | Abd02030 Pseudomon             |     |      |      |     |    |          |                     |

## ALIGNMENTS

RESULT 1  
ADN36742  
ID ADN36742 standard; DNA; 18 BP.  
XX  
XX  
AC ADN36742;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE West Nile virus detection-related PCR primer SeqID64.  
XX  
KW hybridisation assay probe; nucleic acid detection;  
KW target-complementary sequence; flavivirus; West Nile virus; WNV;  
KW RNA virus; infection; meningitis; encephalitis;  
KW high throughput screening; PCR; primer; ss.  
XX  
OS West Nile virus.  
XX  
PN WO2004036190-A2.  
XX  
PD 29-APR-2004.  
XX  
PF 10-OCT-2003; 2003WO-US033639.  
XX  
PR 16-OCT-2002; 2002US-0418891P.  
PR 23-NOV-2002; 2002US-0429006P.  
PR 24-FEB-2003; 2003US-0449810P.



XX (GENP-) GEN-PROBE INC.  
 XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;  
 XX WPI; 2004-389590/36.  
 XX New hybridization assay probe comprising target-complementary sequence of  
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
 XX Claim 26; SEQ ID NO 64; 135pp; English.  
 XX This invention relates to a novel hybridisation assay probe, for  
 CC detecting a nucleic acid, which is a probe sequence that comprises a  
 CC target-complementary sequence of bases, and optionally one or more base  
 CC sequences that are not complementary to the nucleic acid that is to be  
 CC detected. The hybridisation assay probes and the kits are useful in  
 CC detecting and amplifying a target nucleic acid sequence, for example  
 CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC birds and culex mosquitoes, with humans and horses serving as incidental  
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
 CC invention may allow for accurate and efficient high throughput screening.  
 CC The present sequence is that of a PCR primer which is related to the  
 CC invention.  
 XX Sequence 18 BP; 4 A; 5 C; 6 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 18; DB 12; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.5;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CGCCACCGGAGTTGAGT 18  
 DB 1 CGCCACCGGAGTTGAGT 18  
 RESULT 2  
 ADN36744  
 ID ADN36744 standard; DNA; 19 BP.  
 XX AC ADN36744;  
 XX 15-JUL-2004 (first entry)  
 XX West Nile virus detection-related oligonucleotide probe SeqID66.  
 XX hybridisation assay probe; nucleic acid detection;  
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;  
 KW RNA virus; infection; meningitis; encephalitis;  
 KW high throughput screening; probe; ss.  
 XX West Nile virus.  
 OS WO2004036190-A2.  
 XX 29-APR-2004.  
 XX 10-OCT-2003; 2003WO-US033639.  
 XX 16-OCT-2002; 2002US-0418891P.  
 XX 25-NOV-2002; 2002US-0429006P.  
 XX 24-FEB-2003; 2003US-0449810P.  
 XX (GENP-) GEN-PROBE INC.  
 XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;  
 XX WPI; 2004-389590/36.  
 XX New hybridization assay probe comprising target-complementary sequence of  
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
 XX

PS Claim 26; SEQ ID NO 66; 135pp; English.  
 XX This invention relates to a novel hybridisation assay probe, for  
 CC detecting a nucleic acid, which is a probe sequence that comprises a  
 CC target-complementary sequence of bases, and optionally one or more base  
 CC sequences that are not complementary to the nucleic acid that is to be  
 CC detected. The hybridisation assay probes and the kits are useful in  
 CC detecting and amplifying a target nucleic acid sequence, for example  
 CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC birds and culex mosquitoes, with humans and horses serving as incidental  
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
 CC invention may allow for accurate and efficient high throughput screening.  
 CC The present sequence is that of an oligonucleotide probe which is related  
 CC to the invention.  
 XX Sequence 19 BP; 5 A; 5 C; 6 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 19; DB 12; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.6;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CGCCACCGGAGTTGAGT 18  
 DB 1 CGCCACCGGAGTTGAGT 18  
 RESULT 3  
 ADN36740  
 ID ADN36740 standard; DNA; 20 BP.  
 XX AC ADN36740;  
 XX 15-JUL-2004 (first entry)  
 XX West Nile virus detection-related oligonucleotide probe SeqID62.  
 XX hybridisation assay probe; nucleic acid detection;  
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;  
 KW RNA virus; infection; meningitis; encephalitis;  
 KW high throughput screening; probe; ss.  
 XX West Nile virus.  
 OS WO2004036190-A2.  
 XX 29-APR-2004.  
 XX 10-OCT-2003; 2003WO-US033639.  
 XX 16-OCT-2002; 2002US-0418891P.  
 XX 25-NOV-2002; 2002US-0429006P.  
 XX 24-FEB-2003; 2003US-0449810P.  
 XX (GENP-) GEN-PROBE INC.  
 XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;  
 XX WPI; 2004-389590/36.  
 XX New hybridization assay probe comprising target-complementary sequence of  
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
 XX Claim 26; SEQ ID NO 62; 135pp; English.  
 XX This invention relates to a novel hybridisation assay probe, for  
 CC detecting a nucleic acid, which is a probe sequence that comprises a  
 CC target-complementary sequence of bases, and optionally one or more base  
 CC sequences that are not complementary to the nucleic acid that is to be  
 CC detected. The hybridisation assay probes and the kits are useful in  
 CC detecting and amplifying a target nucleic acid sequence, for example  
 CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC

CC birds and culex mosquitoes, with humans and horses serving as incidental  
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
 CC invention may allow for accurate and efficient high throughput screening.  
 CC The present sequence is that of an oligonucleotide probe which is related  
 CC to the invention.  
 XX

SQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.6;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18  
 |||||  
 DB 3 CGCCACCGGAAGTTGAGT 20

## RESULT 4

ADN36741

ID ADN36741 standard; DNA; 21 BP.

XX AC ADN36741;

XX DT 15-JUL-2004 (first entry)

XX DE West Nile virus detection-related oligonucleotide probe SeqID63.

XX KW hybridisation assay probe; nucleic acid detection;

XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;

XX KW RNA virus; infection; meningitis; encephalitis;

XX KW high throughput screening; probe; ss.

XX OS West Nile virus.

XX PN WO2004036190-A2.

XX PD 29-APR-2004.

XX PF 10-OCT-2003; 2003WO-US033639.

XX PR 16-OCT-2002; 2002US-0418891P.

XX PR 25-NOV-2002; 2002US-0429006P.

XX PR 24-FEB-2003; 2003US-0449810P.

XX PA (GENP-) GEN-PROBE INC.

XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX DR WPI; 2004-389590/36.

XX PT New hybridization assay probe comprising target-complementary sequence of  
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.

XX PS Claim 26; SEQ ID NO 63; 135pp; English.

XX CC This invention relates to a novel hybridisation assay probe, for  
 CC detecting a nucleic acid, which is a probe sequence that comprises a  
 CC target-complementary sequence of bases, and optionally one or more base  
 CC sequences that are not complementary to the nucleic acid that is to be  
 CC detected. The hybridisation assay probes and the kits are useful in  
 CC detecting and amplifying a target nucleic acid sequence, for example  
 CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC birds and culex mosquitoes, with humans and horses serving as incidental  
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
 CC invention may allow for accurate and efficient high throughput screening.  
 CC The present sequence is that of an oligonucleotide probe which is related  
 CC to the invention.

XX SQ Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4.6;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18

DB 3 CGCCACCGGAAGTTGAGT 20

## RESULT 5

ADN36737

ID ADN36737 standard; DNA; 31 BP.

XX AC ADN36737;

XX DT 15-JUL-2004 (first entry)

XX DE West Nile virus detection-related oligonucleotide probe SeqID59.

XX KW hybridisation assay probe; nucleic acid detection;

XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;

XX KW RNA virus; infection; meningitis; encephalitis;

XX KW high throughput screening; probe; ss.

XX OS West Nile virus.

XX PN WO2004036190-A2.

XX PD 29-APR-2004.

XX PF 10-OCT-2003; 2003WO-US033639.

XX PR 16-OCT-2002; 2002US-0418891P.

XX PR 25-NOV-2002; 2002US-0429006P.

XX PR 24-FEB-2003; 2003US-0449810P.

XX PA (GENP-) GEN-PROBE INC.

XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX DR WPI; 2004-389590/36.

XX PT New hybridization assay probe comprising target-complementary sequence of  
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.

XX PS Claim 18; SEQ ID NO 59; 135pp; English.

XX CC This invention relates to a novel hybridisation assay probe, for  
 CC detecting a nucleic acid, which is a probe sequence that comprises a  
 CC target-complementary sequence of bases, and optionally one or more base  
 CC sequences that are not complementary to the nucleic acid that is to be  
 CC detected. The hybridisation assay probes and the kits are useful in  
 CC detecting and amplifying a target nucleic acid sequence, for example  
 CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC birds and culex mosquitoes, with humans and horses serving as incidental  
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
 CC invention may allow for accurate and efficient high throughput screening.  
 CC The present sequence is that of an oligonucleotide probe which is related  
 CC to the invention.

XX SQ Sequence 31 BP; 6 A; 8 C; 11 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 4.8;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18

DB 3 CGCCACCGGAAGTTGAGT 20

## RESULT 6

ADR32078

ID ADR32078 standard; DNA; 10945 BP.

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XX AC ADR32078;
XX DT 18-NOV-2004 (first entry)
XX DE Genomic DNA of a West Nile virus.
XX KW analysis; target; real time PCR; ds; genomic.
XX OS West Nile virus.
XX PN WO2004072230-A2.
XX PD 26-AUG-2004.
XX PF 10-FEB-2004; 2004WO-US002012.
XX PR 10-FEB-2003; 2003US-00361004.
XX PA (CLEA-) CLEARANT INC.
XX PI Mckenney K, Gillmeister L, Marlowe K, Armistead D;
XX WPI; 2004-625843/60.
XX
XX PT Analyzing a target nucleic acid sequence in a biological material by real
XX time PCR using nucleic acid primers that are separated by at least 750
XX nucleic acid residues in the target sequence.
XX
XX PS Disclosure; SEQ ID NO 5; 96pp; English.
XX
XX CC The invention relates to a novel method for analysing a target nucleic
XX acid sequence in a biological material. The method comprises adding at
XX least two nucleic acid primers that hybridise under stringent conditions
XX to predetermined nucleic acid sequences of the target nucleic acid
XX sequence that are separated by at least 750 nucleic acid residues,
XX amplifying the target nucleic acid sequence by PCR, and detecting and
XX quantifying the target nucleic acid sequence. The methods and
XX compositions of the present invention are useful for analysing a target
XX nucleic acid sequence in a biological material by real time PCR using
XX nucleic acid primers that are separated by at least 750 nucleic acid
XX residues in the target sequence. This polynucleotide sequence represents
XX the genomic DNA of a West Nile virus used in the target analysis method
XX of the invention.
XX
XX SQ Sequence 10945 BP; 2999 A; 2457 C; 3143 G; 2346 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 13; Length 10945;
XX Best Local Similarity 100.0%; Pred. No. 10;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CGCCACCGGAGTTGAGT 18
XX Db 10482 CGCCACCGGAGTTGAGT 10499
XX
XX RESULT 7
XX ADR67768
XX ID ADR67768 standard; DNA; 10945 BP.
XX AC ADR67768;
XX
XX DT 18-NOV-2004 (first entry)
XX DE West Nile virus DNA detected by novel detection method.
XX OS ds; detection; pathogen.
XX KW West Nile virus.
XX OS WO2004072231-A2.
XX PN 26-AUG-2004.
XX PD
XX
XX PF 10-FEB-2004; 2004WO-US002013.
XX PR 10-FEB-2003; 2003US-00361002.
XX PA (CLEA-) CLEARANT INC.
XX PI Mckenney K, Gillmeister L, Marlowe K, Armistead D;
XX WPI; 2004-625844/60.
XX
XX PT Determining level of potentially active biological pathogens in
XX biological material, by adding nucleic acid primer pairs to biological
XX material, amplifying target nucleic acid by PCR, detecting and
XX quantifying target nucleic acid.
XX
XX PS Disclosure; SEQ ID NO 5; 11pp; English.
XX
XX CC The invention relates to a method of determining (M1) level of
XX potentially active biological pathogens in biological material, involves
XX adding at least two nucleic acid primer pairs to biological material,
XX amplifying target nucleic acid sequences by PCR, and detecting and
XX quantifying target nucleic acid sequences, where quantity of the nucleic
XX acid sequences is proportional to number of biological pathogens in
XX biological material. (M1) is useful for determining level of potentially
XX active biological pathogens in a biological material such as cells,
XX tissues, blood or blood components, proteins, enzymes, immunoglobulins,
XX botanicals, food, ligaments, tendons, nerves, bone, teeth, skin grafts,
XX bone marrow, heart valves, cartilage, corneas, arteries, veins, organs,
XX lipids, carbohydrates, collagen, chitin and its derivatives, forensic
XX samples, mummified material, human or animal remains, stem cells, islet
XX of Langerhans cells, cells for transplantation, red blood cells, white
XX blood cells or platelets. The biological pathogen is chosen from
XX bacteria, viruses, fungi and single cell parasites. The biological
XX pathogen is chosen from Aspergillus, Candida, Histoplasma,
XX Saccharomyces, Clostridioides, Cryptococcus, Escherichia, Bacillus,
XX Campylobacter, Helicobacter, Listeria, Clostridium, Streptococcus,
XX Enterococcus, Staphylococcus, Brucella, Haemophilus, Salmonella,
XX Yersinia, Pseudomonas, Serratia, Enterobacter, Klebsiella, Proteus,
XX Citrobacter, Corynebacterium, Propionibacterium and Coxiella. The
XX biological pathogen is chosen from Adeno-associated virus (AAV),
XX California encephalitis virus, Coronavirus, Coxsackievirus-A,
XX Coxsackievirus-B, Eastern equine encephalitis virus (EVEV), Hepatitis
XX Hantavirus, Hepatitis A virus (HAV), Hepatitis C virus (HCV), Hepatitis
XX delta virus (HDV), Hepatitis E virus (HEV), Hepatitis G virus (HGV), HIV,
XX Human T-lymphotropic virus (HTLV), Influenza virus (Flu virus), Measles
XX virus (Rubella), Mumps virus, Norwalk virus, Parainfluenza virus, Polio
XX virus, Rabies virus, Respiratory Syncytial virus, Rhinovirus, Rubella
XX virus, Saint Louis encephalitis virus, Western equine encephalitis virus
XX (WEEV), Yellow fever virus, Adenovirus, Cytomegalovirus (CMV), Epstein-
XX Barr virus (EBV), Hepatitis B virus (HBV), Herpes simplex virus 1, Herpes
XX simplex virus 2, Molluscum contagiosum, Papilloma virus (HPV), Smallpox
XX virus (Variola), Vaccinia virus, Venezuelan equine encephalitis virus
XX (VEEV), Ebola virus, West Nile virus, Human Parvovirus B19 and Rotavirus.
XX (M1) is useful for determining the effectiveness of a sterilization
XX process applied to a biological material. (M1) is useful in determining
XX whether the biological pathogen is inactive or active. (M1) enables
XX determination of whether the particular biological pathogen is present in
XX a biological material as shown by amplification of first target sequence
XX and whether the biological pathogen is inactive or active. (M1) enables
XX evaluation of the effectiveness of sterilization processes, and
XX determination of both the original level and the residual level of
XX potentially active biological pathogens. This sequence corresponds to a
XX West Nile virus DNA detected by the method of the invention.
XX
XX SQ Sequence 10945 BP; 2999 A; 2457 C; 3143 G; 2346 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 13; Length 10945;
XX Best Local Similarity 100.0%; Pred. No. 10;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY -1 CGCCACCGGAGTTGAGT 18
XX ||||||||||||||||

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Db      10482 CGCCACCGGAGTTGAGT 10499

RESULT 8
ADN98022
ID      ADN98022 standard; DNA; 10975 BP.
XX
AC      ADN98022;
XX
DT      29-JUL-2004 (first entry)
XX
DE      West Nile Virus isolate 2741 complete genome sequence.
XX
ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;
KW      Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.
XX
OS      West Nile virus.
XX
PN      WO2004040263-A2.
XX
13-MAY-2004.
XX
31-OCT-2003; 2003WO-US034823.
XX
31-OCT-2002; 2002US-0422755P.
PR      06-JUN-2003; 2003US-0476513P.
XX
(HEAL-) HEALTH RES INC.
XX
Wong SJ, Pei-Yong S;
XX
WPI; 2004-400223/37.
DR      GENBANK; AF206518.
XX
New diagnostic kit comprising West Nile Virus (WNV) envelope protein
PT      reactive with antibody against WNV and cross-reactive with antibody
PT      against a flavivirus, useful in diagnosing flavivirus infection caused by
PT      DENV, WNV, JEV or SLEV.
XX
Disclosure; Fig 37; 212pp; English.
XX
The invention relates to a diagnostic kit comprising at least one
CC      isolated and purified polypeptide comprising a West Nile Virus (WNV)
CC      envelope (E) protein or its immunogenic fragment having a native
CC      conformation or non-denatured structure and that is reactive with a
CC      antibodies against WNV and cross-reactive with antibodies against a
CC      flavivirus. The diagnostic kit is useful in diagnosing flavivirus
CC      infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to
CC      the complete nucleotide sequence of the WNV isolate 2741.
XX
SQ      Sequence 10975 BP; 3007 A; 2460 C; 3149 G; 2359 T; 0 U; 0 Other;
        Query Match      100.0%; Score 18; DB 12; Length 10975;
        Best Local Similarity 100.0%; Pred. No. 10;
        Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 CGCCACCGGAGTTGAGT 18
        |||||
Db      10506 CGCCACCGGAGTTGAGT 10523

RESULT 9
ABZ68481
ID      ABZ68481 standard; DNA; 11029 BP.
XX
AC      ABZ68481;
XX
22-APR-2003 (first entry)
XX
Nucleotide sequence of the genome of West Nile virus IS-98-ST1.
DE
WNV; IS-98-ST1; Flavivirus; infection; encephalitis; gene; ss.
XX

Db      10482 CGCCACCGGAGTTGAGT 10499

OS      West Nile virus.
XX
Key      Location/Qualifiers
FH      CDS
FT      97..10397
FT      /*tag= a
FT      /product= "polyprotein"
XX
PN      WO200281511-A1.
XX
17-OCT-2002.
XX
04-APR-2002; 2002WO-FR001168.
XX
04-APR-2001; 2001FR-00004599.
PR      06-SEP-2001; 2001FR-00011525.
XX
(INSP ) INST PASTEUR.
PA      (KIMR-) KIMRON VETERINARY INST.
XX
Despres P, Deubel V, Guenet J, Drouet M, Malkinson M, Banet C;
PI      Frenkiel M, Courageot M, Coulibaly F, Catteau A, Flament M, Weber P;
PI      Ceccaldi P;
XX
WPI; 2003-058498/05.
DR      P-PSDB; ABP70647.
XX
New neurovirulent strain of West Nile virus, useful in diagnosis and
PT      screening for antiviral agents, also related nucleic acids, proteins and
PT      antibodies.
XX
Claim 1; Page 34-49; 68pp; French.
XX
The present sequence represents the genome of a strain of West Nile virus
CC      (WNV), designated IS-98-ST1. This strain is a neuroinvasive and
CC      neurovirulent strain of WNV. Polynucleotides and polypeptides derived
CC      from the IS-98-ST1 genome are useful for diagnosis and prognosis of
CC      Flavivirus infection, specifically WNV-mediated encephalitis. They are
CC      also useful to raise specific antibodies, for recombinant expression of
CC      WNV proteins or peptides (for diagnosis, production of antibodies and
CC      identification of specific binding partners in cells), for identifying
CC      cellular genes implicated in resistance to viral infection, and for
CC      screening for anti-Flavivirus agents
XX
SQ      Sequence 11029 BP; 3019 A; 2471 C; 3167 G; 2372 T; 0 U; 0 Other;
        Query Match      100.0%; Score 18; DB 8; Length 11029;
        Best Local Similarity 100.0%; Pred. No. 10;
        Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 CGCCACCGGAGTTGAGT 18
        |||||
Db      10524 CGCCACCGGAGTTGAGT 10541

RESULT 10
ABV74821
ID      ABV74821 standard; DNA; 11029 BP.
XX
AC      ABV74821;
XX
28-MAR-2003 (first entry)
XX
West Nile virus strain NY99-flamingo 382-99 complete genome.
DE
Virucide; hepatotropic; antiinflammatory; antiviral; OAS;
KW      2'-5'-oligoadenylate synthase; Flavivirus infection; gene; ss.
XX
West Nile Virus.
XX
Key      Location/Qualifiers
FH      CDS
FT      97..10398
FT      /*tag= a
FT      /product= "West Nile Virus protein"
XX

```

XX WO200281741-A2.  
 XX 17-OCT-2002.  
 XX 04-APR-2002; 2002WO-FR001169.  
 XX 04-APR-2001; 2001FR-00004598.  
 XX (INSP ) INST PASTEUR.  
 XX (CNRS ) CNRS CENT NAT RECH SCI.  
 XX Guenet J, Mashimo T, Simon-Chazottes D, Montagutelli X;  
 PI Frenkiel M, Despres P, Deubel V, Bonhomme F, Lucas M;  
 XX WPI; 2003-058566/05.  
 DR P-PSDB; ABB98821.  
 XX  
 XX Identifying stimulators of oligoadenylate synthase family genes, useful  
 PT as antiviral agents against Flavivirus, also mutated genes responsible  
 PT for sensitivity to virus.  
 XX  
 XX Example 1; Page 52-67; 93pp; -French.  
 XX  
 CC The present invention relates to a method for identifying compounds (I)  
 CC that can stimulate a gene of the OAS (2'-5'-oligoadenylate synthase)  
 CC family. The method comprises: (a) inducing expression of the OAS gene in  
 CC a culture of cells from a non-human mammal (Flvr/Flvr or Flvr/Flvs;  
 CC indicating resistance or sensitivity to Flavivirus infection); (b)  
 CC treating cells with test compound; and (c) measuring activity of OAS gene  
 CC relative to a control. (I) are potentially useful as antiviral agents for  
 CC treating infections by Flaviviruses (e.g. hepatitis C; dengue; yellow  
 CC fever and various forms of encephalitis). Genomic OAS DNA and derived  
 CC cDNA, also the encoded proteins, are useful: (a) for treating Flavivirus  
 CC infection; (b) in screening for anti-Flavivirus agents, and (c) for  
 CC evaluating sensitivity of subjects to Flavivirus infection and their  
 CC likely response to interferon treatment, e.g. to identify patients at  
 CC risk of developing severe forms of such infections. The present sequence  
 CC is West Nile Virus strain NY99-flamingo 382-99 (IS-98-STI) complete  
 CC genome, which was used in an example from the invention. West Nile Virus  
 CC is one such Flavivirus  
 XX  
 SQ Sequence 11029 BP; 3019 A; 2471 C; 3167 G; 2372 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 10; Length 11029;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18  
 |||||  
 DB 10524 CGCCACCGGAGTTGAGT 10541

RESULT 11  
 ADN98023  
 ID ADN98023 standard; DNA; 11029 BP.  
 AC ADN98023;  
 XX 29-JUL-2004 (first entry)  
 DT  
 XX West Nile Virus isolate 3356 complete genome sequence.  
 DE  
 XX ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;  
 KW Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.  
 KW  
 XX West Nile virus.  
 OS  
 XX WO2004040263-A2.  
 EN  
 XX 13-MAY-2004.  
 PD  
 XX 31-OCT-2003; 2003WO-US034823.  
 PF

XX 31-OCT-2002; 2002US-0422755P.  
 PR 06-JUN-2003; 2003US-0476513P.  
 XX (HEAL-) HEALTH RES INC.  
 PA  
 XX Wong SJ, Pei-Yong S;  
 PI WPI; 2004-400223/37.  
 DR GENBANK; AF040756.  
 XX  
 XX New diagnostic kit comprising West Nile Virus (WNV) envelope protein  
 PT reactive with antibody against WNV and cross-reactive with antibody  
 PT against a flavivirus, useful in diagnosing flavivirus infection caused by  
 PT DENV, WNV, JEV or SLEV.  
 XX  
 XX Disclosure; Fig 38; 212pp; English.  
 XX  
 CC The invention relates to a diagnostic kit comprising at least one  
 CC isolated and purified polypeptide comprising a West Nile Virus (WNV)  
 CC envelope (E) protein or its immunogenic fragment having a native  
 CC conformation or non-denatured structure and that is reactive with  
 CC antibodies against WNV and cross-reactive with antibodies against a  
 CC flavivirus. The diagnostic kit is useful in diagnosing flavivirus  
 CC infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to  
 CC the complete nucleotide sequence of the WNV isolate 3356.  
 XX  
 SQ Sequence 11029 BP; 3017 A; 2466 C; 3172 G; 2374 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 12; Length 11029;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18  
 |||||  
 DB 10524 CGCCACCGGAGTTGAGT 10541

RESULT 12  
 ACN07291  
 ID ACN07291 standard; RNA; 17 BP.  
 XX  
 AC ACN07291;  
 XX 22-APR-2004 (first entry)  
 DT  
 XX WNV Amberzyme substrate SEQ ID NO 7294.  
 DE  
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX  
 OS West Nile Virus.  
 XX  
 XX WO200268637-A2.  
 EN  
 XX 06-SEP-2002.  
 PD  
 XX 19-OCT-2001; 2001WO-US048350.  
 PF  
 XX 20-OCT-2000; 2000US-0242411P.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX  
 XX Blatt L, Mcswiggen JA;  
 PI  
 XX WPI; 2002-706994/76.  
 DR  
 XX New nucleic acid molecule that modulates replication of West Nile Virus

PT (MNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX  
 PS Claim 23; SEQ ID NO 7294; 495pp; English.  
 XX  
 CC The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (MNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, myocarditis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention  
 XX  
 SQ Sequence 17 BP; 4 A; 5 C; 6 G; 0 T; 2 U; 0 Other;  
 Query Match 94.4%; Score 17; DB 6; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 16;  
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGCCACCGGAGTTGAG 17  
 |||||  
 Db 1 CGCCACCGGAGTTGAG 17  
 |||||  
 RESULT 13  
 ACN07465/c  
 ID ACN07465 standard; RNA; 17 BP.  
 XX  
 AC ACN07465;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7468.  
 XX  
 KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme; Amberzyme; Zinzyme; ss.  
 XX  
 OS West Nile Virus.  
 XX  
 PN WO200268637-A2.  
 XX  
 PD 06-SEP-2002.  
 XX  
 PF 19-OCT-2001; 2001WO-US048350.  
 XX  
 PR 20-OCT-2000; 2000US-0242411P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX  
 PI Blatt L, Mcswiggen JA;  
 XX  
 DR WPI; 2002-706994/76.  
 XX  
 CC New nucleic acid molecule that modulates replication of West Nile Virus (MNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 PT  
 PS Claim 23; SEQ ID NO 7468; 495pp; English.  
 XX  
 CC The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (MNV). The nucleic acid molecules are useful for

CC treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention  
 XX  
 SQ Sequence 17 BP; 2 A; 6 C; 5 G; 0 T; 4 U; 0 Other;  
 Query Match 94.4%; Score 17; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGCCACCGGAGTTGAG 17  
 |||||  
 Db 17 CGCCACCGGAGTTGAG 1  
 |||||  
 RESULT 14  
 ACN07464/c  
 ID ACN07464 standard; RNA; 17 BP.  
 XX  
 AC ACN07464;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE WNV minus strand Hammerhead Ribozyme substrate' SEQ ID NO 7467.  
 XX  
 KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme; Amberzyme; Zinzyme; ss.  
 XX  
 OS West Nile Virus.  
 XX  
 PN WO200268637-A2.  
 XX  
 PD 06-SEP-2002.  
 XX  
 PF 19-OCT-2001; 2001WO-US048350.  
 XX  
 PR 20-OCT-2000; 2000US-0242411P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX  
 PI Blatt L, Mcswiggen JA;  
 XX  
 DR WPI; 2002-706994/76.  
 XX  
 CC New nucleic acid molecule that modulates replication of West Nile Virus (MNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 PT  
 PS Claim 23; SEQ ID NO 7467; 495pp; English.  
 XX  
 CC The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (MNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at

CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

XX SQ Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;  
 Query Match 94.4%; Score 17; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18  
 Db 17 GCCACCGGAAGTTGAGT 1

## RESULT 15

ADN36743  
 ID ADN36743 standard; DNA; 18 BP.

XX AC ADN36743;

XX DT 15-JUL-2004 (first entry)

XX DE West Nile virus detection-related oligonucleotide probe SeqID65.

XX KW hybridisation assay probe; nucleic acid detection;

XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;

XX KW RNA virus; infection; meningitis; encephalitis;

XX KW high throughput screening; probe; ss.

XX OS West Nile virus.

XX FH Key Location/Qualifiers

FT modified\_base 1 /\*tag= a

FT /mod\_base= i

XX WO2004036190-A2.

XX PD 29-APR-2004.

XX PF 10-OCT-2003; 2003WO-US033639.

XX PR 16-OCT-2002; 2002US-0418891P.

XX PR 25-NOV-2002; 2002US-0429006P.

XX PR 24-FEB-2003; 2003US-0449810P.

XX PA (GENP-) GEN-PROBE INC.

XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX DR WPI; 2004-389590/36.

XX PT New hybridization assay probe comprising target-complementary sequence of  
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.

XX PS Claim 26; SEQ ID NO 65; 135pp; English.

XX CC This invention relates to a novel hybridisation assay probe, for  
 CC detecting a nucleic acid, which is a probe sequence that comprises a  
 CC target-complementary sequence of bases, and optionally one or more base  
 CC sequences that are not complementary to the nucleic acid that is to be  
 CC detected. The hybridisation assay probes and the kits are useful in  
 CC detecting and amplifying a target nucleic acid sequence, for example  
 CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC birds and culex mosquitoes, with humans and horses serving as incidental  
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
 CC invention may allow for accurate and efficient high throughput screening.  
 CC The present sequence is that of an oligonucleotide probe which is related  
 CC to the invention.

XX SQ Sequence 18 BP; 4 A; 4 C; 6 G; 3 T; 0 U; 1 Other;  
 Query Match 94.4%; Score 17; DB 12; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18

Db 2 GCCACCGGAAGTTGAGT 18

## RESULT 16

ADN36739  
 ID ADN36739 standard; DNA; 19 BP.

XX AC ADN36739;

XX DT 15-JUL-2004 (first entry)

XX DE West Nile virus detection-related oligonucleotide probe SeqID61.

XX KW hybridisation assay probe; nucleic acid detection;

XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;

XX KW RNA virus; infection; meningitis; encephalitis;

XX KW high throughput screening; probe; ss.

XX OS West Nile virus.

XX FH Key Location/Qualifiers

FT modified\_base 1 /\*tag= a

FT /mod\_base= i

XX WO2004036190-A2.

XX PD 29-APR-2004.

XX PF 10-OCT-2003; 2003WO-US033639.

XX PR 16-OCT-2002; 2002US-0418891P.

XX PR 25-NOV-2002; 2002US-0429006P.

XX PR 24-FEB-2003; 2003US-0449810P.

XX PA (GENP-) GEN-PROBE INC.

XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX DR WPI; 2004-389590/36.

XX PT New hybridization assay probe comprising target-complementary sequence of  
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.

XX PS Disclosure; SEQ ID NO 61; 135pp; English.

XX CC This invention relates to a novel hybridisation assay probe, for  
 CC detecting a nucleic acid, which is a probe sequence that comprises a  
 CC target-complementary sequence of bases, and optionally one or more base  
 CC sequences that are not complementary to the nucleic acid that is to be  
 CC detected. The hybridisation assay probes and the kits are useful in  
 CC detecting and amplifying a target nucleic acid sequence, for example  
 CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC birds and culex mosquitoes, with humans and horses serving as incidental  
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
 CC invention may allow for accurate and efficient high throughput screening.  
 CC The present sequence is that of an oligonucleotide probe which is related  
 CC to the invention.

XX SQ Sequence 19 BP; 4 A; 6 C; 6 G; 2 T; 0 U; 1 Other;

Query Match 94.4%; Score 17; DB 12; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 17;





KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyne; ss.

OS West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 9631; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

XX Sequence 17 BP; 2 A; 5 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 88.9%; Score 16; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGA 16

Db 16 CGCCACCGGAGTTGA 1

RESULT 20

ACN07290

ID ACN07290 standard; RNA; 17 BP.

AC ACN07290;

XX 22-APR-2004 (first entry)

XX WNV Amberzyme substrate SEQ ID NO 7293.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyne; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 7293; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

XX Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;

Query Match 88.9%; Score 16; DB 6; Length 17;  
 Best Local Similarity 87.5%; Pred. No. 61;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGA 16

Db 2 CGCCACCGGAGTTGA 17

RESULT 21

ACN09627/c

ID ACN09627 standard; RNA; 17 BP.

XX ACN09627;

XX 22-APR-2004 (first entry)

XX WNV minus strand Inozyme substrate SEQ ID NO 9630.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyne; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.



CC method involves providing an unknown nucleotide or polypeptide sequences,  
 CC and comparing it to a number of sequences along with at least one  
 CC algorithm capable of analysing a functional relationship between  
 CC nucleotide and polypeptide sequences. The method is useful for  
 CC characterising the function of nucleic acids and polypeptides that may be  
 CC useful as a target for a drug or essential for the growth or viability of  
 CC an organism

XX SQ Sequence 1326 BP; 229 A; 416 C; 451 G; 230 T; 0 U; 0 Other;

Query Match 88.9%; Score 16; DB 4; Length 1326;  
 Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0;

QY 2 GCCACCGGAAGTTGAG 17  
 |||||  
 DB 1037 GCCACCGGAAGTTGAG 1022

RESULT 24  
 ABL28588/c  
 ID ABL28588 standard; DNA; 31068 BP.

XX ABL28588;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 37237.

XX Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ds.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEKE ) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions.

XX Claim 1; SEQ ID NO 37237; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
 CC ABB72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 31068 BP; 8424 A; 6977 C; 7023 G; 8644 T; 0 U; 0 Other;

Query Match 88.9%; Score 16; DB 4; Length 31068;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0;

QY 1 CGCCACCGGAAGTTGA 16

DB 2641 CGCCACCGGAAGTTGA 2626  
 |||||

RESULT 25  
 AAI99682\_14/c

Continuation (15 of 45) of AAI99682 from base 1400001 (Mycobacterium tuberculosis strain  
 WP Sequence split into 45 fragments LOCUS AAI99682 Accession Aai99682

WP Fragment Name Begin End

WP AAI99682\_00 1 110000

WP AAI99682\_01 100001 210000

WP AAI99682\_02 200001 310000

WP AAI99682\_03 300001 410000

WP AAI99682\_04 400001 510000

WP AAI99682\_05 500001 610000

WP AAI99682\_06 600001 710000

WP AAI99682\_07 700001 810000

WP AAI99682\_08 800001 910000

WP AAI99682\_09 900001 1010000

WP AAI99682\_10 1000001 1110000

WP AAI99682\_11 1100001 1210000

WP AAI99682\_12 1200001 1310000

WP AAI99682\_13 1300001 1410000

WP AAI99682\_14 1400001 1510000

WP AAI99682\_15 1500001 1610000

WP AAI99682\_16 1600001 1710000

WP AAI99682\_17 1700001 1810000

WP AAI99682\_18 1800001 1910000

WP AAI99682\_19 1900001 2010000

WP AAI99682\_20 2000001 2110000

WP AAI99682\_21 2100001 2210000

WP AAI99682\_22 2200001 2310000

WP AAI99682\_23 2300001 2410000

WP AAI99682\_24 2400001 2510000

WP AAI99682\_25 2500001 2610000

WP AAI99682\_26 2600001 2710000

WP AAI99682\_27 2700001 2810000

WP AAI99682\_28 2800001 2910000

WP AAI99682\_29 2900001 3010000

WP AAI99682\_30 3000001 3110000

WP AAI99682\_31 3100001 3210000

WP AAI99682\_32 3200001 3310000

WP AAI99682\_33 3300001 3410000

WP AAI99682\_34 3400001 3510000

WP AAI99682\_35 3500001 3610000

WP AAI99682\_36 3600001 3710000

WP AAI99682\_37 3700001 3810000

WP AAI99682\_38 3800001 3910000

WP AAI99682\_39 3900001 4010000

WP AAI99682\_40 4000001 4110000

WP AAI99682\_41 4100001 4210000

WP AAI99682\_42 4200001 4310000

WP AAI99682\_43 4300001 4410000

WP AAI99682\_44 4400001 4411529

Query Match 88.9%; Score 16; DB 4; Length 110000;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17  
 |||||

DB 50409 GCCACCGGAAGTTGAG 50394

RESULT 26

AAI99683\_14/c

Continuation (15 of 44) of AAI99683 from base 1400001 (Mycobacterium tuberculosis strain  
 WP Sequence split into 44 fragments LOCUS AAI99683 Accession Aai99683

WP Fragment Name Begin End

WP AAI99683\_00 1 110000

WP AAI99683\_01 100001 210000

WP AAI99683\_02 200001 310000

WP AAI99683\_03 300001 410000

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WP AAI99683_04 400001 510000
WP AAI99683_05 500001 610000
WP AAI99683_06 600001 710000
WP AAI99683_07 700001 810000
WP AAI99683_08 800001 910000
WP AAI99683_09 900001 1010000
WP AAI99683_10 1000001 1110000
WP AAI99683_11 1100001 1210000
WP AAI99683_12 1200001 1310000
WP AAI99683_13 1300001 1410000
WP AAI99683_14 1400001 1510000
WP AAI99683_15 1500001 1610000
WP AAI99683_16 1600001 1710000
WP AAI99683_17 1700001 1810000
WP AAI99683_18 1800001 1910000
WP AAI99683_19 1900001 2010000
WP AAI99683_20 2000001 2110000
WP AAI99683_21 2100001 2210000
WP AAI99683_22 2200001 2310000
WP AAI99683_23 2300001 2410000
WP AAI99683_24 2400001 2510000
WP AAI99683_25 2500001 2610000
WP AAI99683_26 2600001 2710000
WP AAI99683_27 2700001 2810000
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WP AAI99683_29 2900001 3010000
WP AAI99683_30 3000001 3110000
WP AAI99683_31 3100001 3210000
WP AAI99683_32 3200001 3310000
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WP AAI99683_34 3400001 3510000
WP AAI99683_35 3500001 3610000
WP AAI99683_36 3600001 3710000
WP AAI99683_37 3700001 3810000
WP AAI99683_38 3800001 3910000
WP AAI99683_39 3900001 4010000
WP AAI99683_40 4000001 4110000
WP AAI99683_41 4100001 4210000
WP AAI99683_42 4200001 4310000
WP AAI99683_43 4300001 4403765

Query Match 88.9%; Score 16; DB 4; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17
    |||||
Db 49933 GCCACCGGAAGTTGAG 49918

RESULT 27
ID ADO21519
AC ADO21519 standard; DNA; 21 BP.
XX
XX ADO21519;
XX
DT 12-AUG-2004 (first entry)
XX
DE West Nile virus forward RT-PCR primer WNV 1, SEQ ID NO:1.
XX
KW West Nile virus; WNV; recombinant host cell; adenovirus E1A protein;
KW whole-inactivated; large-scale production; antiviral; vaccine;
KW West Nile disease; reverse transcription-PCR; RT-PCR; primer; ss.
XX
OS West Nile virus.
XX
PN WO2004042042-A1.
XX
XX 21-MAY-2004.
XX
XX 07-NOV-2003; 2003WO-EP050806.
XX
XX 08-NOV-2002; 2002WO-NL000718.
XX
PR

PR 28-APR-2003; 2003WO-EP050129.
XX
XX (CRUC-) CRUCELL HOLLAND BV.
XX
XX Uytdehaag AGCM, Schouten GJ, Goudsmit J;
XX
XX WPI; 2004-419706/39.
XX
XX Producing West Nile virus useful as vaccine against West Nile virus
XX infection, involves infecting cell, or culture of cell with West Nile
XX virus and culturing cells.
XX
XX Example 2; SEQ ID NO 1; 81pp; English.
XX
XX The invention relates to a method of producing West Nile viruses (WNVs)
XX by infecting a cell (preferably a human cell) which expresses an
XX adenovirus E1A protein with West Nile virus, or by transforming the cell
XX with the West Nile virus genome. The invention also relates to a West
XX Nile virus produced by the method of the invention; vaccine compositions
XX containing such viruses, or containing a whole-inactivated lineage II
XX West Nile virus; and human cells, named PER.C6 cells and deposited under
XX ECACC number 96022940, having at least an adenovirus E1A gene integrated
XX into its genome and which comprises a nucleic acid coding for a West Nile
XX virus. The method and cells of the invention produce high titres of West
XX Nile virus, enabling the large scale production of whole-inactivated West
XX Nile virus. Such viruses can be used in vaccines for the prophylaxis,
XX therapy and/or diagnosis of West Nile disease. These vaccines are also
XX useful for cross-vaccination against viruses that are highly similar to
XX West Nile virus. Sequences ADO21519-ADO21520 represent reverse
XX transcription-PCR (RT-PCR) primers used to detect West Nile virus RNA in
XX samples from infected human cells.
XX
XX Sequence 21 BP; 5 A; 5 C; 7 G; 3 T; 0 U; 1 Other;

Query Match 86.7%; Score 15.6; DB 12; Length 21;
Best Local Similarity 93.8%; Pred. No. 1e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAGT 18
    |||||
Db 1 CCACCGGAAGTTGAGT 16

RESULT 28
ADN73634/c
ID ADN73634 standard; cDNA; 741 BP.
XX
XX AC ADN73634;
XX
XX 15-JUL-2004 (first entry)
XX
XX Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 1529.
DE
XX
XX gene; ss; plant; transgenic; E2Fa/Dpa transcription factor;
XX growth regulator; animal feed product; thale cress;
XX cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
XX
XX Arabidopsis thaliana.
XX
XX WO2004035798-A2.
XX
XX 29-APR-2004.
XX
XX 20-OCT-2003; 2003WO-EP011658.
XX
XX 18-OCT-2002; 2002EP-00079408.
XX
XX (CROP-) CROPDESIGN NV.
XX
XX Inze D, De Veylder L, Vlieghe K;
XX
XX WPI; 2004-348466/32.
XX
XX P-PSDB; ADN73635.
XX
XX

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XX Altering plant characteristics, useful for producing plants for enzyme or  
PT pharmaceutical production comprises modifying in a plant, expression of  
PT one or more nucleic acids and/or modifying level or activity of one or  
PT more proteins.  
XX  
PS Claim 1; SEQ ID NO 1529; 134pp; English.  
XX  
CC This invention relates to a novel method for altering one or more plant  
CC characteristics. Specifically, it refers to identifying genes that are up  
CC - or down-regulated in transgenic plants overexpressing the heterodimeric  
CC E2Fa/DPA transcription factor of Arabidopsis and using these sequences to  
CC alter plant characteristics accordingly. The present invention describes  
CC generating transgenic plants for the production of growth regulators,  
CC enzymes, therapeutics, pharmaceuticals and animal feed products, where  
CC the altered plant characteristics are selected from increased yield or  
CC biomass, enhanced survival capacity, stress tolerance, plant architecture  
CC or physiology, altered endoreduplication, biochemistry, signal  
CC transduction, storage lipid mobilisation and/or altered photosynthesis,  
CC each relative to the corresponding wild type plants. Accordingly, these  
CC sequences can also be useful as positive or negative selectable markers  
CC during transformation of cells or tissues. The identified genes play a  
CC role in a variety of biological processes such as DNA replication, cell  
CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as  
CC transcription factors. This polynucleotide sequence is thale cDNA  
CC repressed 1.3 fold or more in plants overexpressing the E2Fa/DPA  
CC transcription factor, given in an exemplification of the invention.  
XX  
SQ Sequence 741 BP; 190 A; 203 C; 144 G; 204 T; 0 U; 0 Other;  
  
Query Match 85.6%; Score 15.4; DB 12; Length 741;  
Best Local Similarity 94.1%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 CGCCACCGGAGCTGAG 17  
Db 628 CGCCACCGGAGCTGAG 612  
  
RESULT 29  
AAC48174/c  
ID AAC48174 standard; DNA; 879 BP.  
XX  
AC AAC48174;  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 56529.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN BP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0128845P.  
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PR 21-APR-1999; 99US-0130449P.  
  
PR 23-APR-1999; 99US-0130510P.  
PR 28-APR-1999; 99US-0130891P.  
PR 30-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 04-MAY-1999; 99US-0132407P.  
PR 05-MAY-1999; 99US-0132484P.  
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PR 11-MAY-1999; 99US-0132863P.  
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PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
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PR 20-JUL-1999; 99US-0144352P.

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PR 20-JUL-1999; 99US-0144632P.
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PR 27-AUG-1999; 99US-0151080P.
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PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match      85.6%; Score 15.4; DB 3; Length 879;
Best Local Similarity 94.1%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
   |||||
Db 645 CGCCACCGGAAGTTGAG 629

RESULT 30
AAC35195/c
ID AAC35195 standard; DNA; 882 BP.
XX
AC AAC35195;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 9329.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW Protein identification; signal transduction pathway; metabolic pathway;
KW Promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
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PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
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PR 06-MAY-1999; 99US-0132486P.  
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PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
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PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
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PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
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PR 12-JUL-1999; 99US-0142877P.  
PR 13-JUL-1999; 99US-0143342P.  
PR 14-JUL-1999; 99US-0143624P.  
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PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
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PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144684P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
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PR 27-JUL-1999; 99US-0145951P.  
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PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
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PR 09-AUG-1999; 99US-0147935P.  
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PR 11-AUG-1999; 99US-0148319P.  
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PR 13-AUG-1999; 99US-0148684P.  
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PR 20-AUG-1999; 99US-0149929P.  
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PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
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PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154799P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157533P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
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PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 18-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.





XX PN WO2004058146-A2.  
 XX XX 15-JUL-2004.  
 XX PF 15-DEC-2003; 2003WO-US040081.  
 XX PR 17-DEC-2002; 2002US-00322281.  
 XX XX (SAGR-) SAGRES DISCOVERY INC.  
 XX XX Morris DW, Malandro MS;  
 XX PI WPI; 2004-499109/47.  
 XX DR P-PSDB; ABO84820.  
 XX XX  
 PT Novel human cancer associated protein encoded within open reading frame  
 PT of cancer associated gene, useful as targets for diagnosing cancer.  
 XX  
 PS Claim 1; SEQ ID NO 208; 182pp; English.  
 XX  
 CC The invention relates to cancer-associated proteins (CAP) and the cancer-  
 CC associated (CA) nucleic acids encoding them. The invention also relates  
 CC to a method for treating cancers involving administering to a patient an  
 CC inhibitor of CAP, and a method of screening for anticancer activity in a  
 CC potential drug involving providing a cell that expresses a CA gene,  
 CC contacting a tissue sample derived from a cancer cell with an anticancer  
 CC drug candidate and monitoring the effect of the anticancer drug candidate  
 CC on expression of the CA gene. The CAP proteins are useful for detecting  
 CC cancer associated with expression of a CAP protein in a test cell sample  
 CC and for screening for a bioactive agent capable of modulating the  
 CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing  
 CC cancer, involving determining the expression of a CA nucleic acid in a  
 CC tissue. This sequence represents human CA cDNA of the invention. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 64721 BP; 12849 A; 15676 C; 15599 G; 15316 T; 0 U; 5281 Other;  
 Query Match 85.6%; Score 15.4; DB 13; Length 64721;  
 Best Local Similarity 94.1%; Pred. No. 3.7e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 GCCACCGGAAGTTGAGT 18  
 DB 68 GCCACCGGAAGTTGAGT 84  
 RESULT 34  
 ACN14228/c  
 ID ACN14228 standard; RNA; 17 BP.  
 XX  
 AC ACN14228;  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX WNV minus strand Amberzyme substrate SEQ ID NO 14231.  
 DE  
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyme; ss.  
 XX  
 OS West Nile Virus.  
 XX  
 XX WO200268637-A2.  
 PN  
 XX 06-SEP-2002.  
 PD  
 XX 19-OCT-2001; 2001WO-US048350.  
 XX  
 XX

PR 20-OCT-2000; 2000US-0242411P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX  
 PI Blatt L, Mcswiggen JA;  
 XX WPI; 2002-706994/76.  
 XX  
 PT New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX  
 PS Claim 23; SEQ ID NO 14231; 495pp; English.  
 XX  
 CC The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX  
 SQ Sequence 17 BP; 2 A; 5 C; 7 G; 0 T; 3 U; 0 Other;  
 Query Match 83.3%; Score 15; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGCCACCGGAAGTTG 15  
 DB 15 CGCCACCGGAAGTTG 1  
 RESULT 35  
 ACN03350  
 ID ACN03350 standard; RNA; 17 BP.  
 XX  
 AC ACN03350;  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX WNV Inozyme substrate SEQ ID NO 3353.  
 DE  
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyme; ss.  
 XX  
 OS West Nile Virus.  
 XX  
 XX WO200268637-A2.  
 PN  
 XX 06-SEP-2002.  
 PD  
 XX 19-OCT-2001; 2001WO-US048350.  
 XX  
 XX 20-OCT-2000; 2000US-0242411P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX  
 PI Blatt L, Mcswiggen JA;  
 XX

XX DR WPI; 2002-706994/76.  
 XX CC New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX PS Claim 23; SEQ ID NO 3353; 495pp; English.  
 XX CC The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX SQ Sequence 17 BP; 3 A; 7 C; 5 G; 0 T; 2 U; 0 Other;  
 Query Match 83.3%; Score 15; DB 6; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 2.2e+02;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGCCACCGGAAGTTG 15  
 DB 3 CGCCACCGGAAGUUG 17  
 RESULT 36  
 ACN04649  
 ID ACN04649 standard; RNA; 17 BP.  
 XX AC ACN04649;  
 XX DT 22-APR-2004 (first entry)  
 XX DE WNV Zinzyme substrate SEQ ID NO 4652.  
 XX KW WNV; West Nile Virus; antiinflammatory; cytosolic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyme; ss.  
 XX OS West Nile Virus.  
 XX PN WO200268637-A2.  
 XX PD 06-SEP-2002.  
 XX PF 19-OCT-2001; 2001WO-US048350.  
 XX PR 20-OCT-2000; 2000US-024241P.  
 XX PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX PI Blatt L, Mcswiggen JA;  
 XX WPI; 2002-706994/76.  
 XX CC New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX

PS Claim 23; SEQ ID NO 4652; 495pp; English.  
 XX CC The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX SQ Sequence 17 BP; 5 A; 3 C; 6 G; 0 T; 3 U; 0 Other;  
 Query Match 83.3%; Score 15; DB 6; Length 17;  
 Best Local Similarity 80.0%; Pred. No. 2.2e+02;  
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 CACCGGAAGTTGAGT 18  
 DB 1 CACCGGAAGUUGAGU 15  
 RESULT 37  
 AC127596  
 ID AC127596 standard; DNA; 25 BP.  
 XX AC AC127596;  
 XX DT 13-OCT-2003 (first entry)  
 XX DE Human microarray DNA oligonucleotide SEQ ID NO 27587.  
 XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 KW Genetic variation; diallelic marker; polymorphism; human;  
 KW cross-species comparison.  
 XX OS Homo sapiens.  
 XX PN US2003104410-A1.  
 XX PD 05-JUN-2003.  
 XX PF 15-MAR-2002; 2002US-00098263.  
 XX PR 16-MAR-2001; 2001US-0276759P.  
 XX PA (AFFY-) AFFYMETRIX INC.  
 XX PI Mittmann MP;  
 XX WPI; 2003-567953/53.  
 XX DR New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.  
 XX PS Claim 1; SEQ ID NO 27587; 9pp; English.  
 XX CC The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library,  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more

CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying allelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
 XX  
 XX  
 SQ Sequence 25 BP; 7 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACCGGAAGTTGAGT 18  
 Db 2 CACCGGAAGTTGAGT 16  
 |||||

RESULT 38  
 ACH03748/C  
 ID ACH03748 standard; cDNA; 436 BP.  
 XX  
 AC ACH03748;  
 DT 26-SEP-2003 (first entry)  
 XX  
 DE Wheat steroid 22-alpha hydroxylase #1 cDNA.

XX Steroid 22-alpha hydroxylase; transgenic; plant; sterol biosynthesis;  
 KW plant breeding; ss; Gene.  
 KW  
 XX Triticum aestivum.  
 OS  
 XX US6545200-B1.  
 XX  
 PD 08-APR-2003.  
 XX  
 PF 15-DEC-1999; 99US-00464535.  
 XX  
 PR 16-DEC-1998; 98US-0112555P.  
 XX  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX  
 PI Cahoon RE, Famodu OO, Mcgonigle B, Rafalski JA, Sakai H;

XX WPI; 2003-553970/52.  
 DR P-PSDB; ABO44365.  
 XX  
 DR Novel isolated polynucleotide encoding a polypeptide comprising C-8,7  
 PT sterol isomerase activity, useful in the production of a transformed host  
 PT cell and in the production of a transgenic plant.  
 XX  
 PS Disclosure; Col 41-42; 42pp; English.  
 XX  
 CC The invention relates to an isolated polynucleotide comprising a sequence  
 CC encoding a polypeptide having C-8,7 sterol isomerase activity. The  
 CC polynucleotide is useful for transforming a cell and producing a  
 CC transgenic plant. The polynucleotide is useful in the production of  
 CC altered levels of sterol biosynthetic enzyme in a transformed host cell.  
 CC Nucleic acid fragments of the polynucleotide are useful to create  
 CC transgenic plants in which sterol biosynthetic enzymes are present at  
 CC higher or lower levels than normal or in cell types or developmental  
 CC stages in which they are not normally found. The nucleic acid fragments  
 CC are also useful as probes for genetically and physically mapping the  
 CC genes that they are a portion of and as markers for traits linked to

CC those genes. Such information is useful in plant breeding to develop  
 CC lines with desired phenotypes. The nucleic acid fragments are also useful  
 CC as restriction fragment length polymorphism (RFLP) markers, for physical  
 CC mapping and in direct fluorescence in situ hybridisation (FISH) mapping.  
 CC The present sequence represents cDNA encoding a plant steroid 22-alpha  
 CC hydroxylase  
 XX  
 SQ Sequence 436 BP; 102 A; 109 C; 127 G; 98 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 9; Length 436;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAG 17  
 Db 157 CCACCGGAAGTTGAG 143  
 |||||

RESULT 39  
 ACH03761/C  
 ID ACH03761 standard; cDNA; 600 BP.  
 XX  
 AC ACH03761;  
 XX  
 DT 26-SEP-2003 (first entry)  
 XX  
 DE Wheat steroid 22-alpha hydroxylase #2 cDNA.  
 XX  
 KW Steroid 22-alpha hydroxylase; transgenic; plant; sterol biosynthesis;  
 KW plant breeding; ss; Gene.  
 XX  
 OS Triticum aestivum.  
 XX  
 PN US6545200-B1.  
 XX  
 PD 08-APR-2003.  
 XX  
 PF 15-DEC-1999; 99US-00464535.  
 XX  
 PR 16-DEC-1998; 98US-0112555P.  
 XX  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX  
 PI Cahoon RE, Famodu OO, Mcgonigle B, Rafalski JA, Sakai H;

XX WPI; 2003-553970/52.  
 DR P-PSDB; ABO44378.  
 XX  
 DR Novel isolated polynucleotide encoding a polypeptide comprising C-8,7  
 PT sterol isomerase activity, useful in the production of a transformed host  
 PT cell and in the production of a transgenic plant.  
 XX  
 PS Disclosure; Col 71-74; 42pp; English.  
 XX  
 CC The invention relates to an isolated polynucleotide comprising a sequence  
 CC encoding a polypeptide having C-8,7 sterol isomerase activity. The  
 CC polynucleotide is useful for transforming a cell and producing a  
 CC transgenic plant. The polynucleotide is useful in the production of  
 CC altered levels of sterol biosynthetic enzyme in a transformed host cell.  
 CC Nucleic acid fragments of the polynucleotide are useful to create  
 CC transgenic plants in which sterol biosynthetic enzymes are present at  
 CC higher or lower levels than normal or in cell types or developmental  
 CC stages in which they are not normally found. The nucleic acid fragments  
 CC are also useful as probes for genetically and physically mapping the  
 CC genes that they are a portion of and as markers for traits linked to  
 CC those genes. Such information is useful in plant breeding to develop  
 CC lines with desired phenotypes. The nucleic acid fragments are also useful  
 CC as restriction fragment length polymorphism (RFLP) markers, for physical  
 CC mapping and in direct fluorescence in situ hybridisation (FISH) mapping.  
 CC The present sequence represents cDNA encoding a plant steroid 22-alpha  
 CC hydroxylase  
 XX  
 SQ Sequence 600 BP; 147 A; 148 C; 163 G; 142 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 9; Length 600;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAG 17  
|||||  
DB 164 CCACCGGAAGTTGAG 150

RESULT 40  
ACH03758/c  
ID ACH03758 standard; cDNA; 616 BP.  
XX AC ACH03758;  
XX DT 26-SEP-2003 (first entry)  
XX DE Corn steroid 22-alpha hydroxylase #4 cDNA.  
XX KW Steroid 22-alpha hydroxylase; transgenic; plant; sterol biosynthesis;  
XX KW plant breeding; ss; gene.  
XX OS Zea mays.  
XX PN US6545200-B1.  
XX PD 08-APR-2003.  
XX PF 15-DEC-1999; 99US-00464535.  
XX PR 16-DEC-1998; 98US-0112555P.  
XX PA (DUPO) DU PONT DE NEMOURS & CO E I.  
XX PI Cahoon RE, Famodu OO, Mcgonigle B, Rafalski JA, Sakai H;  
XX DR WPI; 2003-553970/52.  
XX DR P-PSDB; ABO44375.  
XX XX  
XX Novel isolated polynucleotide encoding a polypeptide comprising C-8,7  
PT sterol isomerase activity, useful in the production of a transformed host  
PT cell and in the production of a transgenic plant.  
XX PS Disclosure; Col 63-64; 42pp; English.  
XX CC The invention relates to an isolated polynucleotide comprising a sequence  
CC encoding a polypeptide having C-8,7 sterol isomerase activity. The  
CC polynucleotide is useful for transforming a cell and producing a  
CC transgenic plant. The polynucleotide is useful in the production of  
CC altered levels of sterol biosynthetic enzyme in a transformed host cell.  
CC Nucleic acid fragments of the polynucleotide are useful to create  
CC transgenic plants in which sterol biosynthetic enzymes are present at  
CC higher or lower levels than normal or in cell types or developmental  
CC stages in which they are not normally found. The nucleic acid fragments  
CC are also useful as probes for genetically and physically mapping the  
CC genes that they are a portion of and as markers for traits linked to  
CC those genes. Such information is useful in plant breeding to develop  
CC lines with desired phenotypes. The nucleic acid fragments are also useful  
CC as restriction fragment length polymorphism (RFLP) markers, for physical  
CC mapping and in direct fluorescence in situ hybridisation (FISH) mapping.  
CC The present sequence represents cDNA encoding a plant steroid 22-alpha  
CC hydroxylase  
XX SQ Sequence 616 BP; 149 A; 148 C; 180 G; 125 T; 0 U; 14 Other;

Query Match 83.3%; Score 15; DB 9; Length 616;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAG 17  
|||||  
DB 376 CCACCGGAAGTTGAG 362

RESULT 41  
ACH03757/c  
ID ACH03757 standard; cDNA; 673 BP.  
XX AC ACH03757;  
XX DT 26-SEP-2003 (first entry)  
XX DE Corn steroid 22-alpha hydroxylase #3 cDNA.

XX KW Steroid 22-alpha hydroxylase; transgenic; plant; sterol biosynthesis;  
XX KW plant breeding; ss; gene.  
XX OS Zea mays.  
XX PN US6545200-B1.  
XX PD 08-APR-2003.  
XX PF 15-DEC-1999; 99US-00464535.  
XX PR 16-DEC-1998; 98US-0112555P.  
XX PA (DUPO) DU PONT DE NEMOURS & CO E I.  
XX PI Cahoon RE, Famodu OO, Mcgonigle B, Rafalski JA, Sakai H;  
XX DR WPI; 2003-553970/52.  
XX DR P-PSDB; ABO44374.  
XX PT Novel isolated polynucleotide encoding a polypeptide comprising C-8,7  
PT sterol isomerase activity, useful in the production of a transformed host  
PT cell and in the production of a transgenic plant.  
XX PS Disclosure; Col 61-62; 42pp; English.  
XX CC The invention relates to an isolated polynucleotide comprising a sequence  
CC encoding a polypeptide having C-8,7 sterol isomerase activity. The  
CC polynucleotide is useful for transforming a cell and producing a  
CC transgenic plant. The polynucleotide is useful in the production of  
CC altered levels of sterol biosynthetic enzyme in a transformed host cell.  
CC Nucleic acid fragments of the polynucleotide are useful to create  
CC transgenic plants in which sterol biosynthetic enzymes are present at  
CC higher or lower levels than normal or in cell types or developmental  
CC stages in which they are not normally found. The nucleic acid fragments  
CC are also useful as probes for genetically and physically mapping the  
CC genes that they are a portion of and as markers for traits linked to  
CC those genes. Such information is useful in plant breeding to develop  
CC lines with desired phenotypes. The nucleic acid fragments are also useful  
CC as restriction fragment length polymorphism (RFLP) markers, for physical  
CC mapping and in direct fluorescence in situ hybridisation (FISH) mapping.  
CC The present sequence represents cDNA encoding a plant steroid 22-alpha  
CC hydroxylase  
XX SQ Sequence 673 BP; 160 A; 164 C; 197 G; 135 T; 0 U; 17 Other;

Query Match 83.3%; Score 15; DB 9; Length 673;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAG 17  
|||||  
DB 362 CCACCGGAAGTTGAG 348

RESULT 42  
AAH65402/c  
ID AAH65402 standard; DNA; 1863 BP.

XX AC AAH65402;  
XX XX

DT 26-SEP-2001 (first entry)  
XX C glutamicum coding sequence fragment SEQ ID NO: 437.  
DE Coryneform bacterium; amino acid synthesis; vitamin; saccharide;  
XX organic acid synthesis; ds.  
KW Corynebacterium glutamicum.  
XX EP1108790-A2.  
XX 20-JUN-2001.  
XX 18-DEC-2000; 2000EP-00127688.  
XX 16-DEC-1999; 99JP-00377484.  
PR 07-APR-2000; 2000JP-00159162.  
PR 03-AUG-2000; 2000JP-00280988.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;  
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;  
XX WPI; 2001-376931/40.  
DR P-PSDB; AAG90183.  
XX Novel polynucleotides derived from Coryneform bacteria, for identifying  
PT mutation point of a gene, measuring expression of a gene, analyzing  
PT expression profile or pattern of a gene and identifying homologous gene.  
XX Claim 8; SEQ ID NO 437; 246pp + Sequence Listing; English.  
XX The present invention provides a number of nucleotide and protein  
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These  
CC are useful for identifying the mutation point of a gene derived from a  
CC mutant of coryneform bacterium, measuring expression amount and analysing  
CC the expression profile or expression pattern of a gene derived from  
CC Coryneform bacterium, and identifying a homologue of a gene derived from  
CC coryneform bacterium. Coryneform bacteria are useful for producing amino  
CC acids, nucleic acids, vitamins, saccharides and organic acids,  
CC particularly L-lysine. The present sequence is a nucleic acid described  
CC in the exemplification of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from the European Patent Office  
XX SQ Sequence 1863 BP; 411 A; 632 C; 455 G; 365 T; 0 U; 0 Other;  
Query Match 83.3%; Score 15; DB 5; Length 1863;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 CCACCGGAGTTGAG 17  
DB 734 CCACCGGAGTTGAG 720  
RESULT 43  
ADL65984/c  
ID ADL65984 standard; DNA; 1969 BP.  
XX AC ADL65984;  
XX- 20-MAY-2004 (first entry)  
XX C. glutamicum RXA-associated DNA #171.  
DE fine chemical production; lysine production; nucleotide; nucleoside;  
XX lipid; fatty acid; diol; carbohydrate; aromatic compound; vitamin;  
KW co-factor; enzyme; food; animal feed; cosmetic; pharmaceutical; gene; ds.  
XX Corynebacterium glutamicum.

PN DE10154177-A1.  
XX 08-MAY-2003.  
XX 05-NOV-2001; 2001DE-01054177.  
XX 05-NOV-2001; 2001DE-01054177.  
XX (BADI ) BASF AG.  
XX Zelder O, Pompejus M, Schroeder H, Kroeger B, Klopprogge C;  
PI Habershauer G;  
XX WPI; 2003-431900/41.  
DR P-PSDB; ADL65985.  
XX New nucleic acid encoding variant forms of marker and fine chemical -  
PT production proteins, useful for production of fine chemicals,  
PT specifically lysine, in microorganisms.  
XX Claim 1; Page; 20pp; German.  
XX This invention describes novel polynucleotides that encode protein  
CC markers and fine chemical-production proteins from Corynebacterium  
CC glutamicum. The polynucleotides are isolated from a nucleic acid library  
CC of C. glutamicum then mutated at the specified positions, cloned and  
CC expressed by standard methods. Cells, especially Corynebacterium  
CC glutamicum, containing vectors that express the polynucleotides are used  
CC for production of fine chemicals, preferably amino acids and specifically  
CC lysine, but more generally nucleotides, nucleosides, lipids, fatty acids,  
CC diols, carbohydrates, aromatic compounds, vitamins, co-factors and  
CC enzymes. These are useful in the food, animal feed, cosmetics and  
CC pharmaceutical industries. The polynucleotides, optionally as primers and  
CC probes, can also be used for identification and classification of C.  
CC glutamicum and related species, e.g. for diagnosis, for genomic mapping,  
CC functional or evolutionary studies, gene manipulation and modulation of  
CC metabolic activity. Cells that containing the polynucleotides of the  
CC invention may produce fine chemicals in better yields, with higher  
CC productivity and/or more efficiently. NOTE: This sequence is not  
CC represented in the printed specification but is available in electronic  
CC format. The sequence represented in this record has been obtained from  
CC WO2003046123.  
XX SQ Sequence 1969 BP; 438 A; 659 C; 477 G; 395 T; 0 U; 0 Other;  
Query Match 83.3%; Score 15; DB 11; Length 1969;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 CCACCGGAGTTGAG 17  
DB 810 CCACCGGAGTTGAG 796  
RESULT 44  
ABL04952/c  
ID ABL04952 standard; cDNA; 52872 BP.  
XX AC ABL04952;  
XX 26-MAR-2002 (first entry)  
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 9338.  
XX Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical; gene; ss.  
XX Drosophila melanogaster.  
OS WO200171042-A2.  
XX PN 27-SEP-2001.  
XX PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US009231.  
 XX  
 PR 23-MAR-2000; 2000US-0191637P.  
 PR 11-JUL-2000; 2000US-00614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 DR WPI; 2001-656860/75.  
 DR P-PSDB; ABB60849.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signaling and cell-cell  
 PT interactions.  
 XX  
 PS Claim 1; SEQ ID NO 9338; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
 CC ABB72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pat\_sequences  
 XX  
 SQ Sequence 52872 BP; 15532 A; 11487 C; 10803 G; 15050 T; 0 U; 0 Other;  
 Query Match 83.3%; Score 15; DB 4; Length 52872;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 CACCGGAAGTTGAGT 18  
 DB 19409 CACCGGAAGTTGAGT 19395  
 RESULT 45  
 AAH68525/C  
 ID AAH68525 standard; DNA; 349980 BP.  
 AC AAH68525;  
 XX  
 DT 26-SEP-2001 (first entry)  
 XX  
 DE C Glutamicum coding sequence fragment SEQ ID NO: 7060.  
 XX  
 KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;  
 KW organic acid synthesis; ds.  
 XX  
 OS Corynebacterium glutamicum.  
 XX  
 PN EP1108790-A2.  
 XX  
 PD 20-JUN-2001.  
 XX  
 PF 18-DEC-2000; 2000EP-00127688.  
 XX  
 PR 16-DEC-1999; 95JP-00377484.  
 PR 07-APR-2000; 2000JP-00159162.  
 PR 03-AUG-2000; 2000JP-00280988.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;  
 PI Tateishi N, Senoh A, Ikeda M, Ozaki A;  
 XX  
 WPI; 2001-376931/40.  
 XX  
 PT Novel polynucleotides derived from Coryneform bacteria, for identifying

PT mutation point of a gene, measuring expression of a gene, analyzing  
 PT expression profile or pattern of a gene and identifying homologous gene.  
 XX  
 PS Disclosure; SEQ ID NO 7060; 246pp + Sequence Listing; English.  
 XX  
 CC The present invention provides a number of nucleotide and protein  
 CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These  
 CC are useful for identifying the mutation point of a gene derived from a  
 CC mutant of coryneform bacterium, measuring expression amount and analysing  
 CC the expression profile or expression pattern of a gene derived from  
 CC Coryneform bacterium, and identifying a homologue of a gene derived from  
 CC coryneform bacterium. Coryneform bacteria are useful for producing amino  
 CC acids, nucleic acids, vitamins, saccharides and organic acids,  
 CC particularly L-lysine. The present sequence is a nucleic acid described  
 CC in the exemplification of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from the European Patent Office  
 XX  
 SQ Sequence 349980 BP; 80289 A; 91081 C; 97378 G; 81232 T; 0 U; 0 Other;  
 Query Match 83.3%; Score 15; DB 5; Length 349980;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 CCACCGGAAGTTGAG 17  
 DB 111416 CCACCGGAAGTTGAG 111402  
 RESULT 46  
 ACD72382/C  
 ID ACD72382 standard; DNA; 100 BP.  
 XX  
 AC ACD72382;  
 XX  
 DT 18-SEP-2003 (first entry)  
 XX  
 DE E. coli K12 MG1655 biochip probe SEQ ID 3652.  
 XX  
 KW Biochip; gene expression; gut; diagnostic; detection; probe; ss.  
 XX  
 OS Escherichia coli.  
 XX  
 PN EP1260592-A1.  
 XX  
 PD 27-NOV-2002.  
 XX  
 PF 17-MAY-2001; 2001EP-00112179.  
 XX  
 PR 17-MAY-2001; 2001EP-00112179.  
 XX  
 PA (MWGB-) MWG-BIOFTECH AG.  
 XX  
 PI Donner H, Drescher B, Huber A, Weber J;  
 XX  
 DR WPI; 2003-241155/24.  
 XX  
 PT Biochip containing probes complementary with open reading frames in  
 PT Escherichia coli K12, useful for detecting gene expression and expression  
 PT patterns.  
 XX  
 PS Claim 3; Page 576; 2004pp; German.  
 XX  
 CC This invention describes a novel biochip comprising probe spots, each  
 CC containing many identical probes. The probes are nucleotide sequences of  
 CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at  
 CC least one includes a segment of at least 20 bases identical with, or  
 CC complementary to, a segment of an open reading frame (orf) of Escherichia  
 CC coli K12. The biochip is used for specific detection of gene expression  
 CC in K12 and for determining the gene expression pattern, e.g. for  
 CC diagnostic determination of which E. coli strains are present in the gut,  
 CC and to determine the effects of e.g. growth media on gene expression. The  
 CC biochip provides as comprehensive as possible detection of the K12

CC genome, with simultaneous analysis of many different genes with a single  
 CC device, and comparison of gene expression between K12 and its mutants or  
 CC other *E. coli* strains in a single experiment. Apart from qualitative and  
 CC quantitative information about gene expression, it also allows  
 CC measurements of population densities for the various strains. The use of  
 CC synthetic oligonucleotides for preparation of probes allows free  
 CC variation in probe length and ensures high purity (and thus selectivity,  
 CC reactivity and reproducibility); also synthetic probes are generally  
 CC shorter than probes prepared by polymerase chain reaction. ACD68731 to  
 CC ACD81540 represent oligonucleotide probes used with the biochip described  
 CC in the invention

SQ Sequence 100 BP; 23 A; 29 C; 26 G; 22 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 8; Length 100;

Best Local Similarity 88.9%; Pred. No. 3.6e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18

DB 58 CGGCACCGGAGATGAGT 41

RESULT 47

ACD72383/c

ID ACD72383 standard; DNA; 100 BP.

XX

AC ACD72383;

XX

DT 18-SEP-2003 (first entry)

XX

DE *E. coli* K12 MG1655 biochip probe SEQ ID 3653.

XX

KW Biochip; gene expression; gut; diagnostic; detection; probe; ss.

XX

OS *Escherichia coli*.

XX

FN EP1260592-A1.

XX

PD 27-NOV-2002.

XX

PF 17-MAY-2001; 2001EP-00112179.

XX

PR 17-MAY-2001; 2001EP-00112179.

XX

PA (MWGE-) MWG-BIOTECH AG.

XX

PI Donner H, Drescher B, Huber A, Weber J;

XX

DR WPI; 2003-241155/24.

XX

PT Biochip containing probes complementary with open reading frames in  
 PT *Escherichia coli* K12, useful for detecting gene expression and expression  
 PT patterns.

XX

PS Claim 3; Page 576; 2004pp; German.

XX

CC This invention describes a novel biochip comprising probe spots, each  
 CC containing many identical probes. The probes are nucleotide sequences of  
 CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at  
 CC least one includes a segment of at least 20 bases identical with, or  
 CC complementary to, a segment of an open reading frame (orf) of *Escherichia*  
 CC *coli* K12. The biochip is used for specific detection of gene expression  
 CC in K12 and for determining the gene expression pattern, e.g. for  
 CC diagnostic determination of which *E. coli* strains are present in the gut,  
 CC and to determine the effects of e.g. growth media on gene expression. The  
 CC biochip provides as comprehensive as possible detection of the K12  
 CC genome, with simultaneous analysis of many different genes with a single  
 CC device, and comparison of gene expression between K12 and its mutants or  
 CC other *E. coli* strains in a single experiment. Apart from qualitative and  
 CC quantitative information about gene expression, it also allows  
 CC measurements of population densities for the various strains. The use of  
 CC synthetic oligonucleotides for preparation of probes allows free

CC variation in probe length and ensures high purity (and thus selectivity,  
 CC reactivity and reproducibility); also synthetic probes are generally  
 CC shorter than probes prepared by polymerase chain reaction. ACD68731 to  
 CC ACD81540 represent oligonucleotide probes used with the biochip described  
 CC in the invention

SQ Sequence 100 BP; 23 A; 29 C; 26 G; 22 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 8; Length 100;

Best Local Similarity 88.9%; Pred. No. 3.6e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18

DB 58 CGGCACCGGAGATGAGT 41

RESULT 48

ADQ16356/c

ID ADQ16356 standard; DNA; 363 BP.

XX

AC ADQ16356;

XX

DT 09-SEP-2004 (first entry)

XX

DE Nucleotide sequence of a *Bordetella* variable 16S rRNA gene region.

XX

KW fragmentation-based method; mass spectrometric method;

XX

KW nucleic acid polymorphism; nucleic acid mutation; genetic disease;

XX

KW chromosome abnormality; obesity; atherosclerosis; cancer; haplotype; ss;

XX

OS *Bordetella* sp.; strain SHA-1.

XX

PN WO2004050839-A2.

XX

PD 17-JUN-2004.

XX

PF 26-NOV-2003; 2003WO-US037931.

XX

PR 27-NOV-2002; 2002US-0429895P.

XX

PA (SEQU-) SEQUENOM INC.

XX

PI Van Den Boom D, Becker S;

XX

DR WPI; 2004-487567/46.

XX

PT Use of fragmentation-based methods and systems, e.g. mass spectrometric  
 PT methods for the analysis of sequence variations including nucleic acid  
 PT polymorphisms and mutations.

XX

PS Example 4; SEQ ID NO 33; 199pp; English.

XX

CC The specification describes the use of fragmentation-based methods and  
 CC systems including mass spectrometric methods for the analysis of sequence  
 CC variations including nucleic acid polymorphisms and mutations. The  
 CC fragmentation-based methods and systems of the invention are useful for  
 CC the analysis of sequence variations including nucleic acid polymorphisms  
 CC and mutations. The methods are useful for identifying a genetic disease  
 CC or chromosome abnormality; identifying a predisposition to a disease or  
 CC condition including obesity, atherosclerosis, or cancer; identifying an  
 CC infection by an infectious agent; providing information relating to  
 CC identity, heredity, or histocompatibility; identifying pathogens; or  
 CC determining haplotypes. ADQ16353-ADQ16361 represent *Bordetella* variable  
 CC 16S rRNA gene regions. Amplicons from this region were used to demonstrate  
 CC the invention. They were used to demonstrate a method for bacterial  
 CC typing by base-specific fragmentation.

SQ Sequence 363 BP; 86 A; 92 C; 119 G; 66 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 12; Length 363;

Best Local Similarity 88.9%; Pred. No. 4.2e+02;





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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 10:41:57 ; Search time 1341 Seconds  
(without alignments)  
510.930 Million cell updates/sec

Title: US-10-688-489-64

Perfect score: 18  
Sequence: 1 cgcaccggaagttagt 18

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : EST.\*

- 1: gb\_est1.\*
- 2: gb\_est2.\*
- 3: gb\_hic.\*
- 4: gb\_est3.\*
- 5: gb\_est4.\*
- 6: gb\_est5.\*
- 7: gb\_est6.\*
- 8: gb\_gsa1.\*
- 9: gb\_gsa2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description         |
|------------|-------|-------------|--------|----|---------------------|
| C 1        | 17    | 94.4        | 737    | 8  | BH794414 ME MBa000  |
| C 2        | 17    | 94.4        | 895    | 7  | CF824029 EST701411  |
| C 3        | 16.4  | 91.1        | 514    | 8  | AQ492895 HS 5126 A  |
| C 4        | 16.4  | 91.1        | 576    | 2  | BE994137            |
| C 5        | 16.4  | 91.1        | 698    | 5  | BP117402            |
| C 6        | 16.4  | 91.1        | 1331   | 3  | CR665917            |
| C 7        | 16    | 88.9        | 480    | 5  | BQ559427 H4058B07-  |
| C 8        | 16    | 88.9        | 539    | 6  | CA542435 C0618H12-  |
| C 9        | 16    | 88.9        | 587    | 7  | CF895091 A0143H02-  |
| C 10       | 16    | 88.9        | 602    | 2  | AW338466 xw78H03.x  |
| C 11       | 16    | 88.9        | 604    | 8  | AQ447015 mgxb00002M |
| C 12       | 16    | 88.9        | 607    | 7  | CO430950 UI-M-HX0-  |
| C 13       | 16    | 88.9        | 612    | 2  | AW173515 xj08A06.x  |
| C 14       | 16    | 88.9        | 614    | 2  | AW173560 xj08G06.x  |
| C 15       | 16    | 88.9        | 626    | 2  | AW168911 xj15B06.x  |
| C 16       | 16    | 88.9        | 627    | 2  | AW172834 xj04D03.x  |
| C 17       | 16    | 88.9        | 697    | 1  | AI871886 wms3A05.x  |
| C 18       | 16    | 88.9        | 707    | 1  | AI884543 wms3A04.x  |
| C 19       | 16    | 88.9        | 736    | 6  | CB244514 UI-M-FY0-  |
| C 20       | 16    | 88.9        | 823    | 9  | CNS0088X            |
| C 21       | 16    | 88.9        | 897    | 9  | CNS00C0Q            |
| C 22       | 16    | 88.9        | 4339   | 3  | AK040525 Mus muscu  |
| C 23       | 15.4  | 85.6        | 83     | 9  | CG474564 OST2570 M  |
| C 24       | 15.4  | 85.6        | 138    | 9  | CW510696 Cot678_D1  |



|       |      |      |      |   |           |            |           |            |       |      |      |      |   |           |            |
|-------|------|------|------|---|-----------|------------|-----------|------------|-------|------|------|------|---|-----------|------------|
| C 244 | 14.8 | 82.2 | 752  | 7 | CO434442  | UI-M-HX0-  | CO434442  | UI-M-HX0-  | C 317 | 14.8 | 82.2 | 1256 | 3 | CR671014  | Tetraodon  |
| C 245 | 14.8 | 82.2 | 761  | 2 | BE739840  | 601593122  | BE739840  | 601593122  | C 318 | 14.8 | 82.2 | 1257 | 3 | CR669602  | Tetraodon  |
| C 246 | 14.8 | 82.2 | 767  | 8 | BZ571409  | msh2_1872  | BZ571409  | msh2_1872  | C 319 | 14.8 | 82.2 | 1260 | 3 | CR659741  | Tetraodon  |
| C 247 | 14.8 | 82.2 | 769  | 7 | CF710150  | CCAG053TF  | CF710150  | CCAG053TF  | C 320 | 14.8 | 82.2 | 1262 | 3 | CR665207  | Tetraodon  |
| C 248 | 14.8 | 82.2 | 770  | 9 | CL658179  | PR10130C   | CL658179  | PR10130C   | C 321 | 14.8 | 82.2 | 1262 | 3 | CR674922  | Tetraodon  |
| C 249 | 14.8 | 82.2 | 771  | 7 | CF818659  | EST696041  | CF818659  | EST696041  | C 322 | 14.8 | 82.2 | 1263 | 3 | CR671585  | Tetraodon  |
| C 250 | 14.8 | 82.2 | 772  | 2 | BF538276  | 602053757  | BF538276  | 602053757  | C 323 | 14.8 | 82.2 | 1264 | 3 | CR664109  | Tetraodon  |
| C 251 | 14.8 | 82.2 | 774  | 5 | BW464150  | BW464150   | BW464150  | BW464150   | C 324 | 14.8 | 82.2 | 1270 | 3 | CR668244  | Tetraodon  |
| C 252 | 14.8 | 82.2 | 780  | 5 | BW390264  | BW390264   | BW390264  | BW390264   | C 325 | 14.8 | 82.2 | 1270 | 3 | CR670804  | Tetraodon  |
| C 253 | 14.8 | 82.2 | 780  | 8 | BZ070063  | 1kf64c03   | BZ070063  | 1kf64c03   | C 326 | 14.8 | 82.2 | 1270 | 3 | CR699010  | Tetraodon  |
| C 254 | 14.8 | 82.2 | 783  | 6 | CA216701  | SCC8T3C1   | CA216701  | SCC8T3C1   | C 327 | 14.8 | 82.2 | 1270 | 3 | CR679976  | Tetraodon  |
| C 255 | 14.8 | 82.2 | 795  | 7 | CO110027  | GR_EB004   | CO110027  | GR_EB004   | C 328 | 14.8 | 82.2 | 1279 | 3 | CR678540  | Tetraodon  |
| C 256 | 14.8 | 82.2 | 800  | 4 | BI666056  | 603287225  | BI666056  | 603287225  | C 329 | 14.8 | 82.2 | 1282 | 3 | CR668717  | Tetraodon  |
| C 257 | 14.8 | 82.2 | 801  | 6 | CB246377  | UI-M-HNO-  | CB246377  | UI-M-HNO-  | C 330 | 14.8 | 82.2 | 1288 | 3 | CR667596  | Tetraodon  |
| C 258 | 14.8 | 82.2 | 803  | 7 | CN455488  | UI-M-HNO-  | CN455488  | UI-M-HNO-  | C 331 | 14.8 | 82.2 | 1289 | 3 | CR678123  | Tetraodon  |
| C 259 | 14.8 | 82.2 | 808  | 7 | CF682852  | CCAGU4ATF  | CF682852  | CCAGU4ATF  | C 332 | 14.8 | 82.2 | 1289 | 3 | CR661996  | Tetraodon  |
| C 260 | 14.8 | 82.2 | 811  | 7 | CO028051  | EST906435  | CO028051  | EST906435  | C 333 | 14.8 | 82.2 | 1294 | 3 | CR669151  | Tetraodon  |
| C 261 | 14.8 | 82.2 | 822  | 7 | CV125676  | OSTF30043  | CV125676  | OSTF30043  | C 334 | 14.8 | 82.2 | 1297 | 3 | CR677752  | Tetraodon  |
| C 262 | 14.8 | 82.2 | 827  | 7 | CN526319  | UI-M-HNO-  | CN526319  | UI-M-HNO-  | C 335 | 14.8 | 82.2 | 1300 | 3 | CR675285  | Tetraodon  |
| C 263 | 14.8 | 82.2 | 845  | 9 | CG126505  | PUIJBV73TB | CG126505  | PUIJBV73TB | C 336 | 14.8 | 82.2 | 1301 | 3 | CR666747  | Tetraodon  |
| C 264 | 14.8 | 82.2 | 845  | 9 | CG126506  | PUIJBV73TD | CG126506  | PUIJBV73TD | C 337 | 14.8 | 82.2 | 1302 | 3 | CR678826  | Tetraodon  |
| C 265 | 14.8 | 82.2 | 872  | 2 | BE905758  | 601495778  | BE905758  | 601495778  | C 338 | 14.8 | 82.2 | 1304 | 3 | CR679580  | Tetraodon  |
| C 266 | 14.8 | 82.2 | 873  | 8 | BZ5711354 | msh2_1848  | BZ5711354 | msh2_1848  | C 339 | 14.8 | 82.2 | 1304 | 3 | CR659664  | Tetraodon  |
| C 267 | 14.8 | 82.2 | 875  | 8 | BZ578064  | msh2_5704  | BZ578064  | msh2_5704  | C 340 | 14.8 | 82.2 | 1311 | 3 | CR660552  | Tetraodon  |
| C 268 | 14.8 | 82.2 | 875  | 9 | CR169876  | Reverse s  | CR169876  | Reverse s  | C 341 | 14.8 | 82.2 | 1317 | 3 | CR677639  | Tetraodon  |
| C 269 | 14.8 | 82.2 | 882  | 4 | BI598367  | 603250067  | BI598367  | 603250067  | C 342 | 14.8 | 82.2 | 1317 | 3 | CR677639  | Tetraodon  |
| C 270 | 14.8 | 82.2 | 888  | 6 | CD251956  | AGENCOURT  | CD251956  | AGENCOURT  | C 343 | 14.8 | 82.2 | 1326 | 3 | CR678383  | Tetraodon  |
| C 271 | 14.8 | 82.2 | 900  | 2 | BF104921  | 601822654  | BF104921  | 601822654  | C 344 | 14.8 | 82.2 | 1332 | 3 | CR677618  | Tetraodon  |
| C 272 | 14.8 | 82.2 | 909  | 7 | CF721573  | CCAE714TO  | CF721573  | CCAE714TO  | C 345 | 14.8 | 82.2 | 1339 | 3 | CNS0A633  | Arabidops  |
| C 273 | 14.8 | 82.2 | 930  | 4 | BG331325  | 602432061  | BG331325  | 602432061  | C 346 | 14.8 | 82.2 | 1339 | 3 | CR674011  | Tetraodon  |
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| C 275 | 14.8 | 82.2 | 932  | 9 | CG165928  | PUIGH91TD  | CG165928  | PUIGH91TD  | C 348 | 14.8 | 82.2 | 1346 | 3 | CR657169  | Tetraodon  |
| C 276 | 14.8 | 82.2 | 942  | 4 | CNS06X1W  | T7 end of  | CNS06X1W  | T7 end of  | C 349 | 14.8 | 82.2 | 1357 | 8 | BZ580189  | msh2_982   |
| C 277 | 14.8 | 82.2 | 946  | 4 | BG106647  | 602290476  | BG106647  | 602290476  | C 350 | 14.8 | 82.2 | 1371 | 3 | CNS0A50B  | Arabidops  |
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| C 279 | 14.8 | 82.2 | 958  | 7 | CF822320  | EST700302  | CF822320  | EST700302  | C 352 | 14.8 | 82.2 | 1390 | 3 | CNS0A4PE  | Arabidops  |
| C 280 | 14.8 | 82.2 | 984  | 2 | BF793038  | 602254004  | BF793038  | 602254004  | C 353 | 14.8 | 82.2 | 1390 | 3 | CNS0A5XQ  | Arabidops  |
| C 281 | 14.8 | 82.2 | 991  | 9 | CNS06XST  | T7 end of  | CNS06XST  | T7 end of  | C 354 | 14.8 | 82.2 | 1390 | 3 | CR662153  | Tetraodon  |
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| C 284 | 14.8 | 82.2 | 1007 | 8 | CD245614  | CH261-84D  | CD245614  | CH261-84D  | C 357 | 14.8 | 82.2 | 5739 | 9 | AV412184  | Mus muscu  |
| C 285 | 14.8 | 82.2 | 1012 | 7 | CF680690  | CCACK95TO  | CF680690  | CCACK95TO  | C 358 | 14.4 | 80.0 | 176  | 9 | AW101948  | sd81b05.y  |
| C 286 | 14.8 | 82.2 | 1013 | 4 | BM469895  | AGENCOURT  | BM469895  | AGENCOURT  | C 359 | 14.4 | 80.0 | 179  | 9 | BX9495975 | Arabidops  |
| C 287 | 14.8 | 82.2 | 1018 | 8 | BZ563083  | pacs2-164  | BZ563083  | pacs2-164  | C 360 | 14.4 | 80.0 | 213  | 8 | AZ311450  | 1M0026H20  |
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| C 293 | 14.8 | 82.2 | 1098 | 8 | CL237118  | ZMBBb058   | CL237118  | ZMBBb058   | C 366 | 14.4 | 80.0 | 249  | 7 | CV415924  | RC3-CT041  |
| C 294 | 14.8 | 82.2 | 1101 | 8 | BZ563108  | pacs2-164  | BZ563108  | pacs2-164  | C 367 | 14.4 | 80.0 | 257  | 7 | CO756234  | Mdfrt3046  |
| C 295 | 14.8 | 82.2 | 1107 | 3 | CR667312  | Tetraodon  | CR667312  | Tetraodon  | C 368 | 14.4 | 80.0 | 265  | 1 | AV238596  | AV238596   |
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| C 298 | 14.8 | 82.2 | 1196 | 8 | BZ569607  | pacs2-164  | BZ569607  | pacs2-164  | C 371 | 14.4 | 80.0 | 285  | 2 | BB370666  | BB370666   |
| C 299 | 14.8 | 82.2 | 1200 | 3 | CR659993  | Tetraodon  | CR659993  | Tetraodon  | C 372 | 14.4 | 80.0 | 289  | 2 | BB721062  | BB721062   |
| C 300 | 14.8 | 82.2 | 1202 | 3 | CR729671  | Tetraodon  | CR729671  | Tetraodon  | C 373 | 14.4 | 80.0 | 290  | 9 | AL937634  | Arabidops  |
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| C 302 | 14.8 | 82.2 | 1209 | 3 | CR726698  | Tetraodon  | CR726698  | Tetraodon  | C 375 | 14.4 | 80.0 | 294  | 2 | BB310902  | BB310902   |
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| C 306 | 14.8 | 82.2 | 1221 | 3 | CR730718  | Tetraodon  | CR730718  | Tetraodon  | C 379 | 14.4 | 80.0 | 306  | 6 | BY654785  | BY654785   |
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| C 309 | 14.8 | 82.2 | 1237 | 3 | CR678259  | Tetraodon  | CR678259  | Tetraodon  | C 382 | 14.4 | 80.0 | 312  | 1 | AV101708  | AV101708   |
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| C 314 | 14.8 | 82.2 | 1252 | 3 | CR658850  | Tetraodon  | CR658850  | Tetraodon  | C 387 | 14.4 | 80.0 | 321  | 1 | BF013532  | ro14h08.y  |
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## ALIGNMENTS

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RESULT 1
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LOCUS BH794414.1 ME MBA0002N14r Manihot esculenta Manihot esculenta genomic clone
DEFINITION ME MBA0002N14r, genomic survey sequence.
ACCESSION BH794414.1 GI:19892462
VERSION BH794414.1
KEYWORDS GSS
SOURCE Manihot esculenta (cassava)
ORGANISM Manihot esculenta
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
Manihoteae; Manihot.
1 (bases 1 to 737)
Tomkins,J.P., Fregene,M., Main,D., Goicoechea,J.L., Blackmon,B.,
Atkins,M., Tohme,J. and Wing,R.A.
New Genomic Resources for Cassava (Manihot esculenta): Development
of a Deep-Coverage BAC Library and Preliminary STC Analysis
Unpublished (2002)
JOURNAL Contact: Tomkins J
COMMENT Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634, USA
Tel: 864 656 6419
Fax: 864 656 4293
Email: jtmkns@clemson.edu
Total High Quality bases = 383
Seq primer: TAATACGACTCATATAGG
Class: BAC ends

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High quality sequence start: 130  
High quality sequence stop: 737.  
Location/Qualifiers

## FEATURES

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For more details on library preparation and sequence  
analysis see  
http://www.genome.clemson.edu/projects/stc/cassava/ME\_MBA  
To order clones from this library see  
http://www.genome.clemson.edu/orders "

## ORIGIN

Query Match 94.4%; Score 17; DB 8; Length 737;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
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QY 1 GCCACCGGAAGTTGAG 17

Db 254 CGCCACCGGAAGTTGAG 238

## RESULT 2

CF824029

LOCUS

DEFINITION EST701411 Coccidioides posadasii saprobic phase cDNA library, 2 to 4 kb Coccidioides posadasii cDNA clone CIDAP04 5' end, mRNA

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Analysis of gene expression in Coccidioides posadasii mycelia and spherules via expressed sequence tags

Unpublished (2003)

Other\_ESTS: EST701410

Contact: Gardner MJ

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301 838 3519

Fax: 301 838 0208

Email: gardner@tigr.org

Seq primer: M13 Reverse.

Location/Qualifiers

1. .895

/organism="Coccidioides posadasii"

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/clone\_lib="Coccidioides posadasii saprobic phase cDNA library, 2 to 4 kb"

/note="Vector: pExpress 1; Site 1: Not I; Site 2: EcoRV;

Coccidioides posadasii saprobic phase cDNA library, size

fractionated cDNA 2 to 4 kb"

## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches

QY

Db

2 GCCACCGGAAGTTGAGT 18

829 GCCACCGGAAGTTGAGT 845

RESULT 3

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

10449764

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htec.washington.edu

Plate: 702 row: E column: 12

Seq primer: T7

Class: BAC ends

High quality sequence stop: 514.

Location/Qualifiers

1. 514

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/clone="plate=702 Col=12 Row=E"

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/note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;

Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and

EcoRI Methylase. Size selected DNA was cloned into the

pBACE3.6 vector at EcoRI sites"

ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 514;

Best Local Similarity 94.4%; Pred. No. 6.5e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCACCGGAAGTTGAGT 18

298 CGCCACCGGAAGTTGAGT 281

RESULT 4

LOCUS

DEFINITION

BE994137

UI-M-CG0p-bih-d-02-0-UI.s1 NIH\_BMAP\_Ret4\_s2 Mus musculus cDNA clone

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 BE994137  
 VERSION BE994137.1 GI:10677076  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 576)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PubMed 8889548  
 COMMENT Contact: Chin, H  
 National Institute of Mental Health  
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
 20892-9643, USA  
 Tel: 301 443 1706  
 Fax: 301 443 9890  
 Email: mEST@mail.nih.gov  
 Oligo-dt track not found, Not I site shown in beginning of sequence  
 is likely internal to the message. cDNA Library Preparation: M.B.  
 Soares Lab Clone distribution: Researchers may obtain BMAP cDNA  
 clones from RESEARCH GENETICS. It should be noted that Bento Soares  
 is generating a small number of additional specialized  
 non-redundant arrays of BMAP cDNAs whose availability will be  
 considered under appropriate and limited collaborative arrangements  
 The tissue for this library was contributed by Dr. Xin-Yuan Fu,  
 Yale University School of Medicine  
 Seq primer: M13 Forward  
 POLYA=No.

## FEATURES

source

1..576

/organism="Mus musculus"

/mol\_type="mRNA"

/strains="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UI-M-CG0p-bih-d-02-0-UI"

/lab\_host="DH10B (life technologies)"

/clone\_lib="NIH BMAP Ret4 S2"

/note="Vector: pRT73D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; The

NIH BMAP Ret4 S2 library is a subtracted library,

ultimately derived from mouse retina tissue libraries at

various stages of development. For a detailed description

of the library from which this clone was derived, please

visit our web site at brainest.eng.uiowa.edu. The tissue

for this library was contributed by Dr. Xin-Yuan Fu, Yale

University School of Medicine

TAG\_SEQ=None found"

location/Qualifiers

1..576

/organism="Mus musculus"

/mol\_type="mRNA"

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/db\_xref="taxon:10090"

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/lab\_host="DH10B (life technologies)"

/clone\_lib="NIH BMAP Ret4 S2"

/note="Vector: pRT73D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; The

NIH BMAP Ret4 S2 library is a subtracted library,

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University School of Medicine

TAG\_SEQ=None found"

location/Qualifiers

1..576

/organism="Mus musculus"

/mol\_type="mRNA"

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/db\_xref="taxon:10090"

/clone="UI-M-CG0p-bih-d-02-0-UI"

/lab\_host="DH10B (life technologies)"

/clone\_lib="NIH BMAP Ret4 S2"

/note="Vector: pRT73D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; The

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visit our web site at brainest.eng.uiowa.edu. The tissue

for this library was contributed by Dr. Xin-Yuan Fu, Yale

University School of Medicine

TAG\_SEQ=None found"

location/Qualifiers

1..576

/organism="Mus musculus"

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/clone="UI-M-CG0p-bih-d-02-0-UI"

/lab\_host="DH10B (life technologies)"

/clone\_lib="NIH BMAP Ret4 S2"

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NIH BMAP Ret4 S2 library is a subtracted library,

ultimately derived from mouse retina tissue libraries at

various stages of development. For a detailed description

Query Match 91.1%; Score 16.4; DB 2; Length 576;  
 Best Local Similarity 94.4%; Pred. No. 6.5e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CGCCACCGGAGTTGAGT 18  
 |||||  
 Db 163 CGCCACCGGAGTTGAGT 146  
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## FEATURES

source

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/organism="Mus musculus"

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/lab\_host="DH10B (life technologies)"

/clone\_lib="NIH BMAP Ret4 S2"

/note="Vector: pRT73D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; The

NIH BMAP Ret4 S2 library is a subtracted library,

ultimately derived from mouse retina tissue libraries at

various stages of development. For a detailed description

of the library from which this clone was derived, please

visit our web site at brainest.eng.uiowa.edu. The tissue

for this library was contributed by Dr. Xin-Yuan Fu, Yale

University School of Medicine

TAG\_SEQ=None found"

location/Qualifiers

1..576

/organism="Mus musculus"

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/db\_xref="taxon:10090"

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/lab\_host="DH10B (life technologies)"

/clone\_lib="NIH BMAP Ret4 S2"

/note="Vector: pRT73D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; The

NIH BMAP Ret4 S2 library is a subtracted library,

ultimately derived from mouse retina tissue libraries at

various stages of development. For a detailed description

of the library from which this clone was derived, please

visit our web site at brainest.eng.uiowa.edu. The tissue

for this library was contributed by Dr. Xin-Yuan Fu, Yale

University School of Medicine

TAG\_SEQ=None found"

location/Qualifiers

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/lab\_host="DH10B (life technologies)"

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polylinker; Site 1: Not I; Site 2: Eco RI; The

NIH BMAP Ret4 S2 library is a subtracted library,

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various stages of development. For a detailed description

of the library from which this clone was derived, please

visit our web site at brainest.eng.uiowa.edu. The tissue

for this library was contributed by Dr. Xin-Yuan Fu, Yale

University School of Medicine

TAG\_SEQ=None found"

location/Qualifiers

1..576

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/strains="C57BL/6J"

/db\_xref="taxon:10090"

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/lab\_host="DH10B (life technologies)"

/clone\_lib="NIH BMAP Ret4 S2"

/note="Vector: pRT73D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; The

NIH BMAP Ret4 S2 library is a subtracted library,

ultimately derived from mouse retina tissue libraries at

various stages of development. For a detailed description

Query Match 91.1%; Score 16.4; DB 3; Length 1331;  
 Best Local Similarity 94.4%; Pred. No. 6.7e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CGCCACCGGAGTTGAGT 18  
 |||||  
 Db 685 CGCCACCGGAGTTGAGT 668  
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## FEATURES

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/tissue\_type="compound eye"

/clone\_lib="ce--"

/note="mixed stages from 5th instar larva to pupa"

location/Qualifiers

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/note="mixed stages from 5th instar larva to pupa"

location/Qualifiers

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/organism="Bombyx mori"

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/tissue\_type="compound eye"

/clone\_lib="ce--"

/note="mixed stages from 5th instar larva to pupa"

location/Qualifiers

1..698

/organism="Bombyx mori"

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/db\_xref="taxon:7091"

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/clone\_lib="ce--"

/note="mixed stages from 5th instar larva to pupa"

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location/Qualifiers

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location/Qualifiers

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Query Match 91.1%; Score 16.4; DB 3; Length 1331;  
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 QY 1 CGCCACCGGAGTTGAGT 18  
 |||||  
 Db 685 CGCCACCGGAGTTGAGT 668  
 |||||

## FEATURES

source

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/clone\_lib="ce--"

/note="mixed stages from 5th instar larva to pupa"

location/Qualifiers

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/mol\_type="mRNA"

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/clone="ce--0261"

/tissue\_type="compound eye"

/clone\_lib="ce--"

/note="mixed stages from 5th instar larva to pupa"

location/Qualifiers

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/organism="Bombyx mori"

/mol\_type="mRNA"

/db\_xref="taxon:7091"

/clone="ce--0261"

/tissue\_type="compound eye"

/clone\_lib="ce--"

/note="mixed stages from 5th instar larva to pupa"

BQ559427/c  
 LOCUS  
 DEFINITION H4058B07-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone  
 H4058B07 5', mRNA sequence.  
 ACCESSION BQ559427  
 VERSION BQ559427.1 GI:21460312  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 480)  
 VanBuren,V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G.,  
 Martin,P.R., Scagg,C.A., Basseu,U., Aiba,K., Hanatani,T.,  
 Kargul,G.J., Luo,A.G., Kalso,J., Hide,W. and Ko,M.S.H.  
 Assembly, verification, and initial annotation of NIA 7.4K mouse  
 cDNA clone set  
 Genome Res. 12 (12), 1999-2003 (2002)  
 22354164  
 12466305  
 Other ESTs: H4058B07-3  
 Contact: Yong Qian  
 Laboratory of Genetics  
 National Institute on Aging/National Institutes of Health  
 333 Casseil Drive, Suite 3000, Baltimore, MD 21224-6820, USA  
 Email: cdna@igsun.grc.nia.nih.gov  
 This clone set has been freely distributed to the community. Please  
 visit http://igsun.grc.nia.nih.gov/cDNA/NIA\_7\_4k.html for details.  
 Plate: H4058 row: B column: 07  
 Seq primer: -21M13 Reverse  
 High quality sequence stop: 480  
 POLYA=NO.

FEATURES  
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 Location/Qualifiers  
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 /organism="Mus musculus"  
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 /db\_xref="niaEST:H4058B07-5"  
 /db\_xref="taxon:10090"  
 /clone="H4058B07"  
 /sex="mixed"  
 /dev\_stage="mixed"  
 /lab\_host="DH10B"  
 /clone\_lib="NIA Mouse 7.4K cDNA Clone Set"  
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This clone is among a rearranged set of 7,407 clones from more than 20 cDNA libraries."

ORIGIN  
 Query Match 88.9%; Score 16; DB 5; Length 480;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GCCACCGGAAGTTGAG 17  
 |||||  
 Db 440 GCCACCGGAAGTTGAG 425

RESULT 8  
 CA542435/c  
 LOCUS  
 DEFINITION C0618H12-5N NIA Mouse Trophoblast Stem Cell cDNA Library (Long) Mus  
 musculus cDNA clone NIA:C0618H12 IMAGE:30021983 5', mRNA sequence.  
 ACCESSION CA542435  
 VERSION CA542435.1 GI:25085016  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 539)  
 Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Luo,A.,  
 Tanaka,T., Kunath,T., Rossant,J. and Ko,M.S.H.

Systematic Analyses of NIA Mouse Trophoblast Stem Cell cDNA Library  
 (Long)  
 Unpublished (2001)  
 Other ESTs: C0618H12-3  
 Contact: Dawood B. Dudekula  
 Laboratory of Genetics  
 National Institute on Aging/National Institutes of Health  
 333 Casseil Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
 Email: cdna@igsun.grc.nia.nih.gov  
 Plate: C0618 row: H column: 12  
 Seq primer: M13 Reverse  
 High quality sequence stop: 539  
 POLYA=NO.

FEATURES  
 source  
 Location/Qualifiers  
 1..539  
 /organism="Mus musculus"  
 /mol\_type="cDNA"  
 /strain="B5/EGFP transgenic ICR mice"  
 /db\_xref="niaEST:C0618H12-5N"  
 /db\_xref="taxon:10090"  
 /clone="NIA:C0618H12 IMAGE:30021983"  
 /tissue\_type="Trophoblast stem cell"  
 /dev\_stage="3.5-dpc"  
 /lab\_host="DH10B"  
 /clone\_lib="NIA Mouse Trophoblast Stem Cell cDNA Library (Long)"  
 /note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 1154199]). Total RNAs were obtained from Dr. Janet Rossant and Tilo Kunath (Samuel Lunenfeld Research Institute, Canada). Double-stranded cDNAs were synthesized with an Oligo(dT) primer  
 [Invitrogen:  
 5'-pGACTAGTTCTAGATCGGAGCGCGCCCTTTT-3'] from 4 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.6 kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN  
 Query Match 88.9%; Score 16; DB 6; Length 539;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GCCACCGGAAGTTGAG 17  
 |||||  
 Db 440 GCCACCGGAAGTTGAG 425

RESULT 9  
 CF895091/c  
 LOCUS  
 DEFINITION A0143H02-5 NIA Mouse Undifferentiated ES Cell cDNA Library (Long 1)  
 Mus musculus cDNA clone NIA:A0143H02 IMAGE:30727765 5', mRNA  
 sequence.  
 ACCESSION CF895091  
 VERSION CF895091.1 GI:38162140  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



REFERENCE  
AUTHORS  
TITLE  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 587)  
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.  
Construction of long-transcript enriched cDNA libraries from  
submicrogram amounts of total RNAs by a universal PCR amplification  
method  
Genome Res. 11 (9), 1553-1558 (2001)  
21429098  
11544199  
Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@lgsun.grc.nia.nih.gov  
Plate: A0143 row: H column: 02  
Seq primer: M13 Reverse  
High quality sequence stop: 587  
POLYA=No.

FEATURES  
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1. 587  
Location/Qualifiers  
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/mol\_type="mRNA"  
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/db\_xref="taxon:10090"  
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/dev\_stage="E1 ES cells"  
/lab\_host="DH10B"  
/clone\_lib="NIA Mouse Undifferentiated ES Cell cDNA  
Library (long 1)"  
/notes="Vector: pCMV-SPORT6 (Invitrogen); Site 1: Sali;  
Site 2: NotI; Mouse cDNA project by the Laboratory of  
Genetics, National Institute on Aging (NIA), Intramural  
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).  
This is a long-transcript enriched cDNA library (Ref.  
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total  
RNAs were obtained from Dr. Kenneth R. Boheler (National  
Institute on Aging, USA). ES cells were cultured without  
feeder cells in the presence of LIF and BRL-conditioned  
media. Double-stranded cDNAs were synthesized with an  
Oligo(dT) primer [Invitrogen:  
5'-pGACTAGTCTAGATCGAGCGCGCCCTTTT-3'] from  
14.2 ug of total RNA, treated with T4 DNA polymerase, and  
purified by ethanol-precipitation. The cDNAs were ligated  
to Loxe-linker IL-Sal4, purified by phenol/chloroform, and  
separated from free linkers by Centricon 100. Then, the  
cDNAs were amplified by long-range high fidelity PCR using  
Ex Taq polymerase (Takara) with a primer Sal4-S. The  
products were purified by phenol/chloroform and Centricon  
100. The cDNAs were digested with Sali and NotI enzymes  
and cloned into Sali/NotI site of pCMV-SPORT6 plasmid  
vector. The DH10B E. coli host was transformed with the  
ligation mixture by the standard chemical method. The  
average insert size is about 2.4 kb. The library was  
constructed by Yulan Piao."

ORIGIN  
Query Match 88.9%; Score 16; DB 7; Length 587;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17  
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Db 214 GCCACCGGAAGTTGAG 199

RESULT 10  
AW338466/c  
LOCUS  
DEFINITION  
xw78h03.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2834165 3'  
similar to SW:ACDV HUMAN P49748 ACYL-COA DEHYDROGENASE,  
VERY-LONG-CHAIN SPECIFIC PRECURSOR ;contains Alu repetitive  
element;; mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AW338466  
AW338466.1 GI:6835092  
EST.  
Homo sapiens (human)  
Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 602)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Life Technologies catalog #: 11548-013  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: -40UP from Gibco  
High quality sequence stop: 359.

FEATURES  
source

1. 602  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2834165"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B"  
/clone\_lib="NCI-CGAP\_Pan1"  
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Sali;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.72 kb. Life Technologies catalog #:  
11548-013"

ORIGIN

Query Match 88.9%; Score 16; DB 2; Length 602;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAGT 18  
|||||  
Db 564 CCACCGGAAGTTGAGT 549

RESULT 11  
AQ447015/c  
LOCUS  
DEFINITION  
mgxb0002M12f CUGI Rice Blast BAC Library Magnaporthe grisea genomic  
clone mgxb0002M12f, genomic survey sequence.  
ACCESSION  
AQ447015  
VERSION  
AQ447015.1 GI:4576152  
KEYWORDS  
SOURCE  
ORGANISM  
Magnaporthe grisea (anamorph: Pyricularia grisea)  
Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.  
1 (bases 1 to 604)  
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,  
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.  
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea  
Genome  
Unpublished (1998)  
Contact: Dean RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson University, Clemson, SC 29634  
Tel: 864 656 5737  
Fax: 864 656 4293  
Email: rdean@clemson.edu  
Seq primer: TAATACGACTCACTATAGG  
Class: BAC ends  
High quality sequence start: 61



High quality sequence stop: 455.

#### FEATURES source

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  /issue_type="Protoplasts"
  /lab_host="E. coli DH10B"
  /clone_lib="CUGI Rice Blast BAC Library"
  /note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."
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#### ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAGT 18
  |||||
Db 558 CCACCGGAAGTTGAGT 543
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#### RESULT 12 LOCUS

```
CO430950/c
DEFINITION      607 bp mRNA linear EST 06-JUL-2004
IMAGE:30685069 5', mRNA sequence.
ACCESSION      CO430950
VERSION        CO430950.1 GI:49677244
KEYWORDS      EST.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      1 (bases 1 to 607)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
                Email: cgabbs-r@mail.nih.gov
                Tissue Procurement: Dr. James Lin University of Iowa
                CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
                DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
                Clone Distribution: Distribution information can be found at
                http://genome.uiowa.edu/distribution/mousefl.html
                This clone was contributed by the Brain Molecular Anatomy Project
                (BMAP)
```

#### FEATURES source

```
Seq primer: pYX-5,
  /location/Qualifiers
  1. .607
  /organism="Mus musculus"
  /mol_type="mRNA"
  /strain="C57BL/6"
  /db_xref="taxon:10090"
  /clone="IMAGE:30685069"
  /issue_type="whole eye"
  /dev_stage="newborn (1, 5, 15 days) and embryonic (15, 16,
17, 18 dpc)"
  /lab_host="DH10B (T1 phage resistant)"
  /clone_lib="NIH BMAP HX0"
  /note="Organ: Eye; Vector: pYX-Asc; Site_1: EcoR I;
```

Site\_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag is AATAATTACG. This library was created for the polyA tail Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

#### ORIGIN

```
Query Match      88.9%; Score 16; DB 7; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCACCGGAAGTTGAG 17
  |||||
Db 101 GCACCGGAAGTTGAG 86
```

#### RESULT 13 LOCUS

```
AW173515/c
DEFINITION      612 bp mRNA linear EST 16-NOV-1999
IMAGE:2656594 3', mRNA sequence.
ACCESSION      AW173515
VERSION        AW173515.1 GI:6439463
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 612)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                Tumor Gene Index
                Unpublished (1997)
                Contact: Robert Strausberg, Ph.D.
                Email: cgabbs-r@mail.nih.gov
                Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                Emmert-Buck, M.D., Ph.D.
                CDNA Library Preparation: Life Technologies, Inc.
                CDNA Library Arrayed by: Greg Lennon, Ph.D.
                DNA Sequencing by: Washington University Genome Sequencing Center
                Clone Distribution: NCI-CGAP clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                www-bio.llnl.gov/bbrp/image/image.html
                Seq primer: -40UP from Gibco
                High quality sequence stop: 416.
```

#### FEATURES source

```
Location/Qualifiers
  1. .612
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:2656594"
  /tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
  /lab_host="DH10B"
  /clone_lib="NCI CGAP Ut2"
  /note="Organ: Uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
```

#### ORIGIN

```
Query Match      88.9%; Score 16; DB 2; Length 612;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      3 CCACCGGAAGTTGAGT 18
Db      571 CCACCGGAAGTTGAGT 556

RESULT 14
AW173560/c
LOCUS   xj08906.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2656666 3,
DEFINITION VERY-LONG-CHAIN SPECIFIC PRECURSOR i, mRNA sequence.
ACCESSION AW173560
VERSION   AW173560.1 GI:6439508
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 614)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
          Emmert-Buck, M.D., Ph.D.
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html
          Seq primer: -40UP from Gibco
          High quality sequence stop: 415.
          Location/Qualifiers
          1..614
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:2656666"
             /tissue_type="moderately-differentiated endometrial
             adenocarcinoma, 3 pooled tumors"
             /lab_host="DH10B"
             /clone_lib="NCI CGAP Ut2"
             /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
             Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
             Average insert size 1.85 kb. Life Technologies catalog #:
             11539-012"

FEATURES
          source
          1..614
             Query Match      88.9%; Score 16; DB 2; Length 614;
             Best Local Similarity 100.0%; Pred. No. 1.1e+03;
             Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 CCACCGGAAGTTGAGT 18
Db      570 CCACCGGAAGTTGAGT 555

RESULT 15
AW168911/c
LOCUS   xj15b06.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2657267 3,
DEFINITION similar to SW:ACDV HUMAN P49748 ACYL-COA DEHYDROGENASE,
          VERY-LONG-CHAIN SPECIFIC PRECURSOR i, mRNA sequence.
ACCESSION AW168911
VERSION   AW168911.1 GI:6400436
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

REFERENCE 1 (bases 1 to 626)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
          Emmert-Buck, M.D., Ph.D.
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html
          Seq primer: -40UP from Gibco
          High quality sequence stop: 425.
          Location/Qualifiers
          1..626
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:2657267"
             /tissue_type="moderately-differentiated endometrial
             adenocarcinoma, 3 pooled tumors"
             /lab_host="DH10B"
             /clone_lib="NCI CGAP Ut2"
             /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
             Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
             Average insert size 1.85 kb. Life Technologies catalog #:
             11539-012"

ORIGIN
          Query Match      88.9%; Score 16; DB 2; Length 626;
          Best Local Similarity 100.0%; Pred. No. 1.1e+03;
          Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 CCACCGGAAGTTGAGT 18
Db      565 CCACCGGAAGTTGAGT 550

RESULT 16
AW172834/c
LOCUS   xj04d03.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2656229 3,
DEFINITION similar to SW:ACDV HUMAN P49748 ACYL-COA DEHYDROGENASE,
          VERY-LONG-CHAIN SPECIFIC PRECURSOR i, mRNA sequence.
ACCESSION AW172834
VERSION   AW172834.1 GI:6438782
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 627)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
          Emmert-Buck, M.D., Ph.D.
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html
          Seq primer: -40UP from Gibco
          High quality sequence stop: 401.

```

```

FEATURES
source
  Location/Qualifiers
    1. .627
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:2656229"
      /tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
      /lab_host="DH10B"
      /clone_lib="NCI CGAP Ut2"
      /notes="Organ: uterus; Vector: pCMV-SPORT6; Site 1: Sali;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"

ORIGIN
Query Match      88.9%; Score 16; DB 2; Length 627;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAGT 18
|||||
Db 562 CCACCGGAAGTTGAGT 547

RESULT 17
AI871886/c
LOCUS
DEFINITION
  AI871886 697 bp mRNA linear EST 07-MAR-2000
  wm53a05.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2439632 3'
  similar to SW:ACDV_HUMAN P49748 ACYL-COA DEHYDROGENASE,
  VERY-LONG-CHAIN SPECIFIC PRECURSOR ;, mRNA sequence.
ACCESSION
  AI871886
VERSION
  AI871886.1 GI:5545935
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 697)
AUTHORS
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
JOURNAL
  Unpublished (1997)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
  Emmert-Buck, M.D., Ph.D.
  cDNA Library Preparation: Life Technologies, Inc.
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html
  Insert Length: 1198 Std Error: 0.00
  Seq primer: -40UP from Gibco
  High quality sequence stop: 414.
  Location/Qualifiers
    1. .697
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:2439632"
      /tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
      /lab_host="DH10B"
      /clone_lib="NCI CGAP Ut2"
      /notes="Organ: uterus; Vector: pCMV-SPORT6; Site 1: Sali;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"

ORIGIN
Query Match      88.9%; Score 16; DB 1; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES
source
  Location/Qualifiers
    1. .627
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:2656229"
      /tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
      /lab_host="DH10B"
      /clone_lib="NCI CGAP Ut2"
      /notes="Organ: uterus; Vector: pCMV-SPORT6; Site 1: Sali;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"

ORIGIN
Query Match      88.9%; Score 16; DB 1; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAGT 18
|||||
Db 564 CCACCGGAAGTTGAGT 549

RESULT 18
AI884543/c
LOCUS
DEFINITION
  AI884543 707 bp mRNA linear EST 07-MAR-2000
  wm34a04.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2437806 3'
  similar to SW:ACDV_HUMAN P49748 ACYL-COA DEHYDROGENASE,
  VERY-LONG-CHAIN SPECIFIC PRECURSOR ;, mRNA sequence.
ACCESSION
  AI884543
VERSION
  AI884543.1 GI:5589707
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 707)
AUTHORS
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
JOURNAL
  Unpublished (1997)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
  Emmert-Buck, M.D., Ph.D.
  cDNA Library Preparation: Life Technologies, Inc.
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html
  Insert Length: 1252 Std Error: 0.00
  Seq primer: -40UP from Gibco
  High quality sequence stop: 410.
  Location/Qualifiers
    1. .707
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:2437806"
      /tissue_type="serous papillary carcinoma, high grade, 2
pooled tumors"
      /lab_host="DH10B"
      /clone_lib="NCI CGAP Ut4"
      /notes="Organ: uterus; Vector: pCMV-SPORT6; Site 1: Sali;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"

ORIGIN
Query Match      88.9%; Score 16; DB 1; Length 707;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAGT 18
|||||
Db 568 CCACCGGAAGTTGAGT 553

RESULT 19
CB244514/c
LOCUS
DEFINITION
  CB244514 736 bp mRNA linear EST 09-JUL-2003
  UI-M-FYO-cdq-1-20-0-UI.r1 NIH BMAP_FYO Mus musculus cDNA clone
  IMAGE:6833085 5', mRNA sequence.
ACCESSION
  CB244514
VERSION
  CB244514.1 GI:28366158
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)

```

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 736)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Straubeberg, Ph.D.  
Email: [gsapbs@email.nih.gov](mailto:gsapbs@email.nih.gov)  
Tissue Procurement: Dr. Jim Lin, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>  
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)  
Seq primer: pYX-5.

FEATURES  
source Location/Qualifiers  
1..736

/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:6833085"  
/tissue\_type="whole brain"  
/dev\_stage="embryo 13.5,14.5,16.5,17.5dpc"  
/lab\_host="DH10B (TI phage resistant)"  
/clone\_lib="NIH BMAP\_FY0"  
/notes="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaïdo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGACACG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

## ORIGIN

Query Match 88.9%; Score 16; DB 6; Length 736;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GCCACCGGAAGTTGAG 17  
|||||  
Db 438 GCCACCGGAAGTTGAG 423

RESULT 20  
CNS0088X/c  
LOCUS  
DEFINITION  
Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR16G18 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Drosophila melanogaster (fruit fly)  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 823)  
Genoscope.  
Direct Submission

## JOURNAL

## COMMENT

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : [secref@genoscope.cns.fr](mailto:secref@genoscope.cns.fr))  
- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammose in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

source

1..823  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACR16G18"  
/clone\_lib="RPCI-98"  
/note="end : TET3"

## ORIGIN

Query Match 88.9%; Score 16; DB 9; Length 823;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGCCACCGGAAGTTGA 16  
|||||  
Db 418 CGCCACCGGAAGTTGA 403

## RESULT 21

CNS00CQ0

LOCUS

DEFINITION

Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR24G05 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Drosophila melanogaster (fruit fly)  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

## REFERENCE

AUTHORS

TITLE

JOURNAL

## COMMENT

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : [secref@genoscope.cns.fr](mailto:secref@genoscope.cns.fr))  
- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammose in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

Location/Qualifiers

```

source
1. .897
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR24G05"
/clone_lib="RPCL-98"
/notes="end : TET3"

ORIGIN
Query Match      88.9%; Score 16; DB 9; Length 897;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGA 16
Db 372 CGCCACCGGAAGTTGA 387

RESULT 22
AK040525/c
LOCUS
DEFINITION
Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
library, clone:A430105D10 product:hypothetical protein, full insert
sequence.
AK040525
AK040525.1 GI:26087907
VERSION
HTC; CAP trapper.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kusunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 695-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4639)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Oheato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
FEATURES
source
1. .4639
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:A430105D10"
/db_xref="taxon:10090"
/clone="A430105D10"
/tissue_type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
1. .4639
/notes="hypothetical protein (evidence: rscds)"
ORIGIN
Query Match      88.9%; Score 16; DB 3; Length 4639;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17
Db 830 GCCACCGGAAGTTGAG 815

RESULT 23
CG474564/c
LOCUS
DEFINITION
Mus musculus 129Sv/Ev Mus musculus cDNA clone OST2570, mRNA
sequence.
CG474564
CG474564.1 GI:37225453
VERSION
GSS.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 83)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Friedle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP

```

OmniBank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: materials@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
Class: Gene Trap.

## FEATURES

source  
1. .83  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone="OST2570"  
/cell\_type="embryonic stem cell"  
/clone\_lib="Mus musculus 129Sv/Ev"

## ORIGIN

Query Match 85.6%; Score 15.4; DB 9; Length 83;  
Best Local Similarity 94.1%; Pred. No. 2.2e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17  
||| ||||| ||||| |||||  
Db 36 CGTCACCGGAAGTTGAG 20

## RESULT 24

CW510696 138 bp DNA linear GSS 06-OCT-2004  
LOCUS Cot678.D17.077.g1.Ta001 Triticum aestivum High-cot Triticum  
DEFINITION aestivum genomic, genomic survey sequence.

ACCESSION CW510696  
VERSION CW510696.1 GI:53840202  
KEYWORDS GSS.

## SOURCE

Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.

## REFERENCE

AUTHORS Gao, W. and Bennetzen, J.L.  
TITLE High Cot sequence analysis of the wheat genome  
JOURNAL Unpublished (2004)  
COMMENT Contact: Bennetzen JL  
Department of Genetics  
University of Georgia  
1057 Green Street, Athens, GA 30602, USA  
Tel: 706 542 9729  
Fax: 706 583 0972  
Email: maize@uga.edu  
Class: High-Cot.

## FEATURES

source  
1. .138  
Location/Qualifiers  
/organism="Triticum aestivum"  
/mol\_type="genomic DNA"  
/cultivar="Chinese Spring"  
/db\_xref="taxon:4565"  
/clone\_lib="Triticum aestivum High-cot"

/note="Organ: Seedling; Vector: PCR4-TOPO; Wheat genomic DNA was Sheared to fragments averaging about 1.8 kb, denatured and then reassociated in phosphate buffer at 650C. After a given Cot value was reached, aliquots were run through a hydroxyapatite (HAP) column in order to separate single stranded DNA from double stranded DNA. The single stranded DNA was then converted to a double stranded form with one round of Klenow DNA polymerase treatment with random 6-mer primers. The double-stranded fragments were then further size-selected through a column and cloned into the PCR4-TOPO vector"

## ORIGIN

Query Match 85.6%; Score 15.4; DB 9; Length 138;

Best Local Similarity 94.1%; Pred. No. 2.2e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17  
||| ||||| ||||| |||||  
Db 21 CGCCACCGGAAGTTGAG 37

## RESULT 25

CW510353 140 bp DNA linear GSS 06-OCT-2004  
LOCUS Cot678.D17.077.b1.Ta001 Triticum aestivum High-cot Triticum  
DEFINITION aestivum genomic, genomic survey sequence.

ACCESSION CW510353  
VERSION CW510353.1 GI:53839859  
KEYWORDS GSS.

## SOURCE

Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 140)  
AUTHORS Gao, W. and Bennetzen, J.L.  
TITLE High Cot sequence analysis of the wheat genome  
JOURNAL Unpublished (2004)  
COMMENT Contact: Bennetzen JL  
Department of Genetics  
University of Georgia  
1057 Green Street, Athens, GA 30602, USA  
Tel: 706 542 9729  
Fax: 706 583 0972  
Email: maize@uga.edu  
Class: High-Cot.

## FEATURES

source  
1. .140  
Location/Qualifiers  
/organism="Triticum aestivum"  
/mol\_type="genomic DNA"  
/cultivar="Chinese Spring"  
/db\_xref="taxon:4565"  
/clone\_lib="Triticum aestivum High-cot"

/note="Organ: Seedling; Vector: PCR4-TOPO; Wheat genomic DNA was Sheared to fragments averaging about 1.8 kb, denatured and then reassociated in phosphate buffer at 650C. After a given Cot value was reached, aliquots were run through a hydroxyapatite (HAP) column in order to separate single stranded DNA from double stranded DNA. The single stranded DNA was then converted to a double stranded form with one round of Klenow DNA polymerase treatment with random 6-mer primers. The double-stranded fragments were then further size-selected through a column and cloned into the PCR4-TOPO vector"

## ORIGIN

Query Match 85.6%; Score 15.4; DB 9; Length 140;  
Best Local Similarity 94.1%; Pred. No. 2.2e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17  
||| ||||| ||||| |||||  
Db 106 CGCCACCGGAAGTTGAG 90

## RESULT 26

BW540688/c 258 bp mRNA linear EST 31-AUG-2004  
LOCUS BW540688 Yutaka Satou unpublished cDNA library (cstb) Ciona  
DEFINITION savignyi cDNA clone cstb013k24 5', mRNA sequence.

ACCESSION BW540688  
VERSION BW540688.1 GI:51720539  
KEYWORDS EST.

## SOURCE

Ciona savignyi  
ORGANISM Ciona savignyi  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

```

REFERENCE
1 (bases 1 to 258)
LOCUS
Phlebobranchia; Cionidae; Ciona.
AUTHORS
Satou, Y. and Satoh, N.
TITLE
Expressed genes in Ciona savignyi
JOURNAL
Unpublished (2004)
COMMENT
Contact: Yutaka Satou
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-705-1113
Email: yutaka@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source
Location/Qualifiers
1..258
/organism="Ciona savignyi"
/mol_type="mRNA"
/db_xref="taxon:51511"
/clone="cstb013k24"
/dev_stage="tailbud stage"
/clone_lib="Yutaka Satou unpublished cDNA library (cstb)"

ORIGIN
Query Match 85.6%; Score 15.4; DB 5; Length 258;
Best Local Similarity 94.1%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
|||||
Db 203 CGCCACCGGAAGTTGAG 187

RESULT 27
BM500789
LOCUS
332 bp mRNA linear EST 14-FEB-2002
DEFINITION
PAC000000000174 Pioneer AF-1 array Zea mays cDNA, mRNA sequence.
ACCESSION
BM500789
VERSION
BM500789.1 GI:18660297
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 332)
Hunter, B.G., Beatty, M., Singletary, G., Hamaker, B., Larkins, B.A. and
Jung, R.

TITLE
Maize opaque endosperm mutations create extensive changes in
patterns of gene expression
JOURNAL
Unpublished (2002)
COMMENT
Contact: Jung R
Trait and Technology Development, Food and Feed Research
Pioneer Hi-Bred International, Inc.
7300 NW 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA
Tel: 515 270 5934
Fax: 515 254 2619
Email: rudolf.jung@pioneer.com.

FEATURES
source
Location/Qualifiers
1..332
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/clone_lib="Pioneer AF-1 array"

ORIGIN
Query Match 85.6%; Score 15.4; DB 4; Length 332;
Best Local Similarity 94.1%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
|||||
Db 279 CGCCACCGGAAGTTGAG 295

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RESULT 28  
BY660181/c  
LOCUS

DEFINITION  
Rathke's pouches Mus musculus cDNA clone K720001K04 3', mRNA  
sequence.

ACCESSION  
BY660181  
VERSION  
EST.  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 357)

REFERENCE  
AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,  
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,  
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,  
Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,  
Fletcher, C.P., Forrest, A., Frazer, K.S., Gaasterland, T.,  
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,  
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,  
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,  
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,  
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,  
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,  
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,  
Ravasi, T., Reed, J.C., Reid, J., Reid, J., Ring, B.Z., Ringwald, M.,  
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,  
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,  
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,  
Wells, C., Wilming, L.G., Wyshaw-Boris, A., Yanagisawa, M., Yang, I.,  
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,  
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,  
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Ishii, Y.,  
Aizawa, K., Akimura, T., Arakawa, T., Arakawa, T., Carninci, P., Fukuda, S.,  
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,  
Rogers, J., Birney, E. and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
22354683  
12456851

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

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Laboratory for Genome Exploration Research Group, RIKEN Genomic  
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The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,  
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,  
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,  
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,  
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and  
Hayashizaki, Y. Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken



Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Tissues were provided by Michelle Brinkmeier and Sally Camper (Dept. Human Genetics University of Michigan Medical School 4301 MSRB 3 1500 W. Medical Center Dr. Ann Arbor, MI 48109-0638 USA) whose assistance we gratefully acknowledge.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

## FEATURES

source  
Location/Qualifiers  
1. .357  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="K72000LK04"  
/tissue\_type="Rathke's pouches"  
/dev\_stage="14.5 days embryo RP+/+"  
/clone\_lib="RIKEN full-length enriched, 14.5 days embryo RP+/+ Rathke's pouches"

## ORIGIN

Query Match 85.6%; Score 15.4; DB 6; Length 357;  
Best Local Similarity 94.1%; Pred. No. 2.2e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAG 17

Db 138 CGCCACTGGAGTTGAG 122

## RESULT 29

D69844 360 bp mRNA linear EST 07-DEC-1995  
LOCUS CELK09209F Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA  
DEFINITION clone yk9299 5', mRNA sequence.

ACCESSION D69844

VERSION D69844.1

KEYWORDS GI:1105806

SOURCE EST.

ORGANISM Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 360)

AUTHORS Kohara.Y., Mitsuiki.H., Nishigaki.A., Motohashi.T., Sugimoto.A. and

Tabara.H.

Toward an expression map of the C.elegans genome

Unpublished (1994)

CONTACT Yuji Kohara

Genome Biology Lab.

National Institute of Genetics

Yata 1111, Mishima, Shizuoka 411, Japan

Tel: 81-559-81-6854

Fax: 81-559-81-6855

Email: ykohara@lab.nig.ac.jp.

Location/Qualifiers

1. .360

/organism="Caenorhabditis elegans"

/mol\_type="mRNA"

/strain="CB1489 him-8(e1489)"

/db\_xref="taxon:6239"

/clone="yk9299"

/sex="hermaphrodite, male"

/tissue\_type="whole animal"

/dev\_stage="varied"

/clone\_lib="Yuji Kohara unpublished cDNA"

ORIGIN

Query Match 85.6%; Score 15.4; DB 7; Length 360;  
Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18

|||||

## Db

323 CGCCACCGGAGCTGAGT 340

## RESULT 30

LOCUS CK119645/c

DEFINITION

5-PRIME, mRNA sequence.

CK119645

CK119645.1

GI:47829961

EST.

Arabidopsis thaliana (chale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 371)

AUTHORS Feilner,T., Immink,R.G.H., Cahill,D.J. and Kersten,B.

Generation of a cDNA expression library from Arabidopsis

inflorescence meristem

Unpublished (2003)

CONTACT Birgit Kersten

Plant Protein Chip Group, Department Lehrach

Max-Planck-Institute for Molecular Genetics

Imnestr. 73 D-14195 Berlin, Germany

Tel: +49(0)30/84131648

Fax: +49(0)30/84131128

Email: Kersten@molgen.mpg.de

Insert Length: 371 Std Error: 0.00

Plate: 211 row: F column: 22

Seq primer: POE65

Location/Qualifiers

1. .371

/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/ecotype="Columbia"

/db\_xref="GABI:953887"

/db\_xref="taxon:3702"

/clone="MPMGp2011P22211"

/tissue\_type="inflorescence meristem"

/dev\_stage="about one week after bolting"

/lab\_host="E. coli SCS-1/pSE111"

/clone\_lib="AtCM1"

/note="Vector: POE-3ONAST-attB (AY386205); Site\_1: SalI;

Site\_2: NotI; About 1 week after bolting, cDNA synthesis

using SuperscriptTM-System (Invitrogen) with an

oligo(dT)-primer containing NotI restriction site and a

SalI adapter. The main library (plate numbers begin with

1) of 38,000 clones was rearrayed into the sublibrary

(plate numbers begin with 201) containing 5,000 putative

expression clones. Average insert size is 1 kb. Note: The

rearrayed sublibrary (plate numbers begin with 201) was

sequenced. Library generation and sequencing was granted

in context of GABI-LAPP; data are also accessible at

<https://gabi.rzpd.de>"

ORIGIN

Query Match 85.6%; Score 15.4; DB 7; Length 371;

Best Local Similarity 94.1%; Pred. No. 2.2e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAG 17

|||||

Db 189 CGCCACCGGAGCTGAG 173

## RESULT 31

LOCUS BY612625/c

DEFINITION

BY612625 RIKEN full-length enriched, visual cortex Mus musculus

cDNA clone K230333P10 3', mRNA sequence.

BY612625

ACCESSION

BY612625

VERSION

BY612625.1

GI:26947807



## KEYWORDS

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Oato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, B.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

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Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Michela Fagioli and Takao K. Hensch (Laboratory for Neuronal Circuit Development Brain Science Institute RIKEN 2-1 Hiroswa, Wako-shi, Saitama 351-0198 Japan) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for

## FEATURES

## source

Location/Qualifiers

1..388

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="K23033P10"

/tissue\_type="visual cortex"

/clone\_lib="RIKEN full-length enriched, visual cortex"

## ORIGIN

Query Match 85.6%; Score 15.4; DB 6; Length 388;

Best Local Similarity 94.1%; Pred. NO. 2.2e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## QY

1 CGCCACCGAAGTTGAG 17

## DB

172 CGCCACTCGAAGTTGAG 156

## RESULT 32

CV240627/c

## LOCUS

CV240627 WS0251.B21\_O12 PT-MB-N-A-15 Populus balsamifera subsp. trichocarpa

CDNA clone WS0251\_O12 3', mRNA sequence.

## ACCESSION

CV240627

## VERSION

CV240627.1 GI:52493602

## KEYWORDS

EST.

## SOURCE

Populus balsamifera subsp. trichocarpa (Populus trichocarpa)

Populus balsamifera subsp. trichocarpa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Malpighiales; Salicaceae; Populus.

## REFERENCE

## AUTHORS

1 (bases 1 to 392)

Ralph, S., Cooper, D., Kolosova, N., Oddy, C., Butterfield, Y., Kirkpatrick, R., Liu, J., Palmquist, D., Scott, J., Barber, S., Yang, G., Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A., Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddiqui, A., Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and Bohlmann, J.

The poplar transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries

Unpublished (2004)

## JOURNAL

## COMMENT

Contact: Joerg Bohlmann

Genome BC forest Genomics program

University of British Columbia

UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237,

Vancouver, British Columbia, Canada, V6T 1Z3

Tel: 1-604-822-0282

Fax: 1-604-822-6097

Email: bohlmann@interchange.ubc.ca

Plate: WS0251 row: O column: 12

High quality sequence stop: 392

POLYA=Yes.

## FEATURES

## source

Location/Qualifiers

1..392

/organism="Populus balsamifera subsp. trichocarpa"

/mol\_type="mRNA"

/cultivar="Wild clone"

/sub\_species="trichocarpa"

/db\_xref="taxon:3694"

/clone="WS0251\_O12"

/sex="Male"

/lab\_host="E. coli DH10B T1 phage resistant cells"

/clone\_lib="PT-MB-N-A-15"

/note=vector: pBluescript II SK (+) XR; Site 1: EcoRI (5' end of cDNA); Site 2: XhoI (3' end of cDNA); Terminal

vegetative buds from 20 year old trees harvested near Corvallis, Oregon on September 19th, 2001. cDNA was prepared from 5 micrograms of mRNA and directionally ligated into the pBluescript II SK (+) XR vector using the pBluescript II XR cDNA Library Construction Kit according

to manufacturer's instructions with modifications (Stratagene). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation. Normalization was applied according to published methods [Bonaldo M.F. et al. (1996) Genome Research 6(9):791] in order to reduce the abundance of highly expressed transcripts."

ORIGIN

Query Match 85.6%; Score 15.4; DB 7; Length 392;  
 Best Local Similarity 94.1%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGGTTGAG 17  
 |||||  
 Db 355 CGCCACCGGAGGTTGAG 339

RESULT 33  
 CA662270/c

LOCUS  
 DEFINITION wlmk1.pk0013.h6 wlmk1 Triticum aestivum cDNA clone wlmk1.pk0013.h6  
 5' end, mRNA sequence.

ACCESSION CA662270  
 VERSION CA662270.1 GI:25240795  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum

REFERENCE  
 AUTHORS Tingley,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,  
 Miao,G., Caraher,N. and Hanafey,M.K.  
 TITLE DuPont Wheat cDNA Sequence  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Scott V. Tingley  
 Crop Genetics  
 E. I. DuPont de Nemours and Company  
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
 Tel: 302-631-2602  
 Fax: 302-631-2607  
 Email: Scott.V.Tingley@USA.dupont.com  
 Seq primer: M13.

FEATURES  
 Location/Qualifiers  
 1..400  
 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /cultivar="Stephens"  
 /db\_xref="taxon:4565"  
 /clone="wlmk1.pk0013.h6"  
 /tissue\_type="leaf"  
 /clone\_lib="wlmk1"  
 /note="Vector: Lambda Zap; Site 1: EcoRI; Site 2: XhoI;  
 Wheat (Triticum aestivum L.) seedlings 1 hr after  
 inoculation with Erysiphe graminis f. sp tritici and  
 treatment with  
 6-iodo-3-propyl-2-propyloxy-4(3H)-quinazolinone"

ORIGIN

Query Match 85.6%; Score 15.4; DB 6; Length 400;  
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGGTTGAGT 18  
 |||||  
 Db 333 CGCCACCGGAGGTTGAGT 316

RESULT 34  
 AV798486

LOCUS  
 DEFINITION AV798486 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-16-G21 3',

mRNA sequence.

ACCESSION AV798486  
 VERSION AV798486.1 GI:19832469  
 KEYWORDS EST.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana

REFERENCE  
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsi  
 1 (bases 1 to 430)  
 Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,  
 Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Iehi,Y.,  
 Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.  
 and Shinozaki,K.  
 TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Motoaki Seki  
 Plant Functional Genomics Research Group  
 RIKEN Genomic Sciences Center  
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
 Tel: 81-298-36-4359  
 Fax: 81-298-36-9060  
 Email: msekic@rtc.riken.go.jp

FEATURES  
 Location/Qualifiers  
 1..430  
 /organism="Arabidopsis thaliana"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3702"  
 /clone="RAFL09-16-G21"  
 /dev\_stage="plants at various developmental stages from  
 germination to mature seeds"  
 /lab\_host="DH10B"  
 /clone\_lib="RAFL9"  
 /note="Site 1: BamHI; Site 2: SalI; subjected to  
 dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24  
 hr) treatments"

ORIGIN

Query Match 85.6%; Score 15.4; DB 1; Length 430;  
 Best Local Similarity 94.1%; Pred. No. 2.3e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGGTTGAG 17  
 |||||  
 Db 262 CGCCACCGGAGGTTGAG 278

RESULT 35  
 CE271971

LOCUS  
 DEFINITION tigr-gss-dog-17000333558770 Dog Library Canis familiaris genomic,  
 genomic survey sequence.

ACCESSION CE271971  
 VERSION CE271971.1 GI:36006115  
 KEYWORDS GSS.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 1 (bases 1 to 432)  
 Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
 Venter,J.C.  
 TITLE The dog genome: survey sequencing and comparative analysis  
 JOURNAL Science 301 (5641), 1898-1903 (2003)  
 MEDLINE 22875432

14512627  
 COMMENT Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirknes@tigr.org  
 Class: shotgun.

FEATURES  
 source  
 Location/Qualifiers  
 1..432  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /notes="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"

ORIGIN  
 Query Match 85.6%; Score 15.4; DB 9; Length 432;  
 Best Local Similarity 94.1%; Pred. No. 2.3e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17  
 |||||  
 Db 219 CGCCGCGGAAGTTGAG 235

RESULT 36  
 AZ738118/c  
 LOCUS 446 bp DNA linear GSS 25-JAN-2001  
 DEFINITION RPCI-24-102J15.TVB RPCI-24 Mus musculus genomic clone  
 RPCI-24-102J15, genomic survey sequence.

ACCESSION AZ738118  
 VERSION  
 KEYWORDS  
 SOURCE GSS.  
 ORGANISM Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 446)  
 Zhao, S., Nieman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M.,  
 Tsagaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,  
 Russell, D., de Jong, P., and Fraser, C.M.  
 Mouse BAC End Sequences from Library RPCI-24  
 Unpublished (1999)  
 Other\_GSSs: RPCI-24-102J15.TJB  
 Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: szhao@tigr.org  
 Clones are derived from the mouse BAC library RPCI-24. For BAC  
 library availability, please contact Pieter de Jong  
 {pdejong@mail.cho.org}. Clones may be purchased from BACPAC  
 Resources (<http://www.chori.org/bacpac/orderingframe.htm>). BAC end  
 page: [http://www.tigr.org/tdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html)  
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 Seq primer: T7  
 Class: BAC ends.

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 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:10090"  
 /clone="RPCI-24-102J15"  
 /sex="Male"  
 /cell\_type="Spleen/Brain"  
 /clone\_lib="RPCI-24"

ORIGIN  
 Query Match 85.6%; Score 15.4; DB 8; Length 446;  
 Best Local Similarity 94.1%; Pred. No. 2.3e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCACCGGAAGTTGAGT 18  
 |||||  
 Db 333 GCACCTGAAGTTGAGT 317

RESULT 37  
 CD986497/c  
 LOCUS 451 bp mRNA linear EST 16-JUL-2003  
 DEFINITION QAN22e08.Yg QAN Zea mays CDNA clone QAN22e08, mRNA sequence.  
 CD986497  
 ACCESSION  
 VERSION  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 451)  
 Genoplante.  
 AUTHORS  
 TITLE Unpublished (2003)  
 JOURNAL  
 COMMENT Contact: Genoplante  
 Genoplante  
 93 rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
 and <http://genoplante-info.infobiogen.fr>).

FEATURES  
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 /organism="Zea mays"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:4577"  
 /clone="QAN22e08"  
 /tissue\_type="pericarp"  
 /clone\_lib="QAN"

ORIGIN  
 Query Match 85.6%; Score 15.4; DB 6; Length 451;  
 Best Local Similarity 94.1%; Pred. No. 2.3e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17  
 |||||  
 Db 311 CGCCTCCGGAAGTTGAG 295

RESULT 38  
 CD573266  
 LOCUS 453 bp mRNA linear EST 12-JUN-2003  
 DEFINITION 3529 1.119 1.B10.x.1 3529 - 2 mm ear tissue from Schmidt and Hake  
 labs Zea mays CDNA, mRNA sequence.  
 CD573266  
 ACCESSION  
 VERSION  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

/note="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI;  
 RPCI-24 Mouse BAC Library produced by Pieter de Jong. The  
 library was cloned in the pTARBAC1 cloning vector at the  
 BamHI sites using MboI partially digested male C57BL/6J  
 DNA."

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 453)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3529.1.119.1 row: E column: 10.
FEATURES
source
Location/Qualifiers
1..453
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="ear"
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/clone_lib="3529 - 2 mm ear tissue from Schmidt and Hake
labs"
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Query Match 85.6%; Score 15.4; DB 6; Length 453;
Best Local Similarity 94.1%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAG 17
|||||
Db 400 CGCCCCCGGAGTTGAG 416

RESULT 39
BE345714/c
LOCUS
DEFINITION
481 bp mRNA linear EST 17-JUL-2000
946025D07.y2 946 - tassell primordium prepared by Schmidt lab Zea
mays cDNA, mRNA sequence.
ACCESSION
BE345714
VERSION
BE345714.1 GI:9255246
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 481)
Walbot V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946025 row: D column: 07.
FEATURES
source
Location/Qualifiers
1..481
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="OH43"
/db_xref="taxon:4577"
/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to
inflorescence development"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 453)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
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FEATURES
source
Location/Qualifiers
1..453
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/mol_type="mRNA"
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/tissue_type="ear"
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labs"
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Query Match 85.6%; Score 15.4; DB 6; Length 453;
Best Local Similarity 94.1%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAG 17
|||||
Db 400 CGCCCCCGGAGTTGAG 416

RESULT 39
BE345714/c
LOCUS
DEFINITION
481 bp mRNA linear EST 17-JUL-2000
946025D07.y2 946 - tassell primordium prepared by Schmidt lab Zea
mays cDNA, mRNA sequence.
ACCESSION
BE345714
VERSION
BE345714.1 GI:9255246
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 481)
Walbot V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946025 row: D column: 07.
FEATURES
source
Location/Qualifiers
1..481
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="OH43"
/db_xref="taxon:4577"
/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to
inflorescence development"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 453)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
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FEATURES
source
Location/Qualifiers
1..485
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="Ohio43"
/db_xref="taxon:4577"
/tissue_type="nucellar, embryo, and endosperm"
/dev_stage="10-14 days post-pollination"
/clone_lib="605 - Endosperm cDNA library from Schmidt lab"
/clone_host="DH5(alpha)"
/clone_org="Kernel; Vector: PAD-GAL4-2; Site_1: EcoRI;
Site_2: XhoI; Kernel endosperm cDNA library from Schmidt
lab"
ORIGIN
Query Match 85.6%; Score 15.4; DB 1; Length 485;
Best Local Similarity 94.1%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAG 17
|||||
Db 430 CGCCCCCGGAGTTGAG 446

RESULT 41
AV544944
LOCUS
DEFINITION
499 bp mRNA linear EST 20-FEB-2004
Arabidopsis thaliana roots Columbia Arabidopsis thaliana

```

```

/lab_host="XLOLR"
/clone_lib="946 - tassell primordium prepared by Schmidt
lab"
/note="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI;
Site 2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybriZAP. Sample insert size range was 350 bp
to 3 Kb with a 1 Kb average."

```

## ORIGIN

```

Query Match 85.6%; Score 15.4; DB 2; Length 481;
Best Local Similarity 94.1%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```
QY 1 CGCCACCGGAGTTGAG 17
```

```
|||||
Db 180 CGCCCCCGGAGTTGAG 164
```

## RESULT 40

```
AI664820
```

```
LOCUS
```

```
DEFINITION
```

```
AI664820 485 bp mRNA linear EST 02-FEB-2000
```

```
605002A06.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays
```

```
cDNA, mRNA sequence.
```

```
ACCESSION AI664820
```

```
VERSION AI664820.1 GI:4775815
```

```
KEYWORDS EST.
```

```
SOURCE Zea mays
```

```
ORGANISM Zea mays
```

```
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```

```
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
```

```
clade; Panicoideae; Andropogoneae; Zea.
```

```
1 (bases 1 to 485)
```

```
Walbot,V.
```

```
Maize ESTs from various cDNA libraries sequenced at Stanford
```

```
University
```

```
Unpublished (1999)
```

```
Contact: Walbot V
```

```
Department of Biological Sciences
```

```
Stanford University
```

```
855 California Ave, Palo Alto, CA 94304, USA
```

```
Tel: 650 723 2227
```

```
Fax: 650 725 8221
```

```
Email: walbot@stanford.edu
```

```
Plate: 605002 row: A column: 06.
```

```
FEATURES
```

```
source
```

```
Location/Qualifiers
```

```
1..485
```

```
/organism="Zea mays"
```

```
/mol_type="mRNA"
```

```
/cultivar="Ohio43"
```

```
/db_xref="taxon:4577"
```

```
/tissue_type="nucellar, embryo, and endosperm"
```

```
/dev_stage="10-14 days post-pollination"
```

```
/clone_lib="605 - Endosperm cDNA library from Schmidt lab"
```

```
/clone_host="DH5(alpha)"
```

```
/clone_org="Kernel; Vector: PAD-GAL4-2; Site_1: EcoRI;
```

```
Site_2: XhoI; Kernel endosperm cDNA library from Schmidt
```

```
lab"
```

```
ORIGIN
```

```
Query Match 85.6%; Score 15.4; DB 1; Length 485;
```

```
Best Local Similarity 94.1%; Pred. No. 2.3e+03;
```

```
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 CGCCACCGGAGTTGAG 17
```

```
|||||
```

```
Db 430 CGCCCCCGGAGTTGAG 446
```

```
RESULT 41
```

```
AV544944
```

```
LOCUS
```

```
DEFINITION
```

```
499 bp mRNA linear EST 20-FEB-2004
```

```
Arabidopsis thaliana roots Columbia Arabidopsis thaliana
```

```

cDNA clone RZ64h05F 3', mRNA sequence.
AV544944
VERSION AV544944.1 GI:8716358
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 499)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
JOURNAL DNA Res. 7 (3), 175-180 (2000)
MEDLINE 20363093
PUBMED 10907847
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES
    source
        Location/Qualifiers
            1..499
                /organism="Arabidopsis thaliana"
                /mol_type="mRNA"
                /ecotype="Columbia"
                /db_xref="taxon:3702"
                /clone="RZ64h05F"
                /tissue_type="roots"
                /clone_lib="Arabidopsis thaliana roots Columbia"
                /note="Vector: pBluescriptII SK-, Site_1: EcoRI; Site_2:
                XhoI"
ORIGIN
    Query Match      85.6%; Score 15.4; DB 1; Length 499;
    Best Local Similarity 94.1%; Pred. No. 2.3e+03;
    Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CGCCACCGGAGTTGAG 17
    |||||
Db 204 CGCCACCGGAGTTGAG 220
    |||||
RESULT 42
CA148045/c
LOCUS CA148045 512 bp mRNA linear EST 24-SEP-2003
DEFINITION SCEZRZ1016C02.g R21 Saccharum officinarum cDNA clone SCEZRZ1016C02
5', mRNA sequence.
ACCESSION CA148045
VERSION CA148045.1 GI:35048690
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE 1 (bases 1 to 512)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 016 row: C column: 02
cDNA clone RZ64h05F 3', mRNA sequence.
AV544944
VERSION AV544944.1 GI:8716358
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 499)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
JOURNAL DNA Res. 7 (3), 175-180 (2000)
MEDLINE 20363093
PUBMED 10907847
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES
    source
        Location/Qualifiers
            1..512
                /organism="Saccharum officinarum"
                /mol_type="mRNA"
                /db_xref="taxon:4547"
                /clone="SCEZRZ1016C02"
                /lab_host="DH10B"
                /clone_lib="R21"
                /note="Organ: Shoot-root transition zone from young plants
                (large insert library); Vector: pSport1; Site_1: SalI;
                Site_2: NotI; An unidirectional cDNA library generated
                from [Shoot-root transition zone from young plants (large
                insert library)]. cDNA was prepared from poly(A+ mRNA
                using SuperScript Plasmid System Kit (Invitrogen). The
                double-strand cDNAs were fractionated in a sepharose
                CL-2B 40cm-columns and fragments sizing between 0.8 and
                1.5 Kb were directionally cloned into the vector. Details
                of each source of RNA and library construction can be
                obtained at http://sucest.lad.ic.unicamp.br/public"
ORIGIN
    Query Match      85.6%; Score 15.4; DB 6; Length 512;
    Best Local Similarity 94.1%; Pred. No. 2.3e+03;
    Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CGCCACCGGAGTTGAG 17
    |||||
Db 47 CGCCACCGGAGTTGAG 31
    |||||
RESULT 43
BI097902/c
LOCUS BI097902 529 bp mRNA linear EST 26-JUN-2001
DEFINITION IP1_29_E03.g1_A002 Immature pannicle 1 (IP1) Sorghum bicolor cDNA,
mRNA sequence.
ACCESSION BI097902
VERSION BI097902.1 GI:14569484
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 529)
AUTHORS Klein,R.R., Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M. and
Pratt,L.H.
TITLE An EST database from Sorghum: developing preanthesis pannicles
JOURNAL Unpublished (2001)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for high quality sequence is
20. Three-prime sequences, which are obtained with PolyTMix or T7
sequencing primer, are presented as the reverse complement.
Seq primer: T7
High quality sequence start: 125
High quality sequence stop: 529
POLVA=Yes.
FEATURES
    source
        Location/Qualifiers
            1..529
                /organism="Sorghum bicolor"
                /mol_type="mRNA"
                /cultivar="BTx623"
                /db_xref="taxon:4558"
                /clone_lib="Immature pannicle 1 (IP1)"
                /note="Organ: Developing preanthesis pannicles; Vector:
                pBluescript II SK(-) from Lambda Zap II; Site_1: XhoI;

```

Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."

## ORIGIN

Query Match 85.6%; Score 15.4; DB 4; Length 529;  
Best Local Similarity 94.1%; Pred. No. 2.3e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17  
|||||  
Db 62 CGCCCCCGGAAGTTGAG 46

RESULT 44  
BI211550/c

LOCUS BI211550 531 bp mRNA linear EST 11-JUL-2001  
DEFINITION IP1\_59\_A04\_g1\_A002 Immature pannicle 1 (IP1) Sorghum bicolor cDNA, mRNA sequence.

ACCESSION BI211550

VERSION BI211550.1

KEYWORDS GI:14689274

SOURCE Sorghum bicolor (sorghum)

ORGANISM Sorghum bicolor

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

AUTHORS 1 (bases 1 to 531)

TITLE Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and Pratt, L.H.

JOURNAL An EST database from Sorghum: developing preanthesis pannicles

COMMENT Unpublished (2001)

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions

below Phred quality 16. The threshold for high quality sequence is

20. Three-prime sequences, which are obtained with PolyTWix or T7

sequencing primer, are presented as the reverse complement.

Seq primer: T7

High quality sequence start: 5

High quality sequence stop: 531

POLYA=Yes.

## FEATURES

source

1..531 Location/Qualifiers  
/organism="Sorghum bicolor"  
/mol\_type="mRNA"  
/cultivar="BTx623"  
/db\_xref="taxon:4558"  
/clone\_lib="Immature pannicle 1 (IP1)"  
/note="Organ: Developing preanthesis pannicles; Vector: pBluescript II SK(-) from Lambda zap II; Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."

## ORIGIN

Query Match 85.6%; Score 15.4; DB 4; Length 531;  
Best Local Similarity 94.1%; Pred. No. 2.3e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17

|||||

Db 65 CGCCCCCGGAAGTTGAG 49

## RESULT 45

BI2139519/c

LOCUS

BI2139519 533 bp mRNA linear EST 02-NOV-2002

## DEFINITION

BI2139519 Nori Satoh unpublished cDNA library, gastrula and neurula

Ciona intestinalis cDNA clone rcign053a17 3', mRNA sequence.

ACCESSION BI2139519

VERSION BI2139519.1

KEYWORDS GI:24495918

SOURCE EST.

ORGANISM Ciona intestinalis

Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Cloniidae; Ciona.

REFERENCE 1 (bases 1 to 533)

AUTHORS Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.

TITLE Expressed genes in Ciona intestinalis (2002c)

JOURNAL Unpublished (2002)

COMMENT Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@ascidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

1..533

/organism="Ciona intestinalis"

/mol\_type="mRNA"

/db\_xref="taxon:7719"

/clone="rcign053a17"

/tissue\_type="whole body"

/dev\_stages="gastrula and neurula"

/clone\_lib="Nori Satoh unpublished cDNA library, gastrula

and neurula"

ORIGIN

Query Match 85.6%; Score 15.4; DB 5; Length 533;

Best Local Similarity 94.1%; Pred. No. 2.3e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17

|||||

Db 28 CGCCACCGGAAGTTGCG 12

RESULT 46

BI2139519/c

LOCUS

BI2139519 534 bp mRNA linear EST 20-FEB-2001

DEFINITION 1000090D03.x1 1000 - Unigene 1 from Maize Genome Project Zea mays

CDNA, mRNA sequence.

ACCESSION BI2139519

VERSION BI2139519.1

KEYWORDS GI:12969396

SOURCE EST.

ORGANISM Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 534)

AUTHORS Walbot, V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL University

Unpublished (1999)

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 100090 row: D column: 03.

Location/Qualifiers

1..534

/organism="Zea mays"

/mol\_type="mRNA"

/db\_xref="dbEST:606038C11.x1"

/db\_xref="taxon:4577"

/clone\_lib="1000 - Unigene I from Maize Genome Project"  
/notes="This library represents the unique ESTs found in  
the first round of EST sequencing at Stanford University  
for the maize genome project. Sequences are present from  
libraries 486, 487, 496, 603, 605, 606, 614, 618, 660,  
683, 687, 707, and 945. Contigs were assembled using  
TIGR's CAP program and a representative EST from each  
contig was selected for the Unigene set. All singlets were  
also selected."

## ORIGIN

Query Match 85.6%; Score 15.4; DB 4; Length 534;  
Best Local Similarity 94.1%; Pred. No. 2.3e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17  
|||||  
Db 480 CGCCCCCGGAAGTTGAG 496

## RESULT 47

BF145790  
LOCUS  
DEFINITION  
WHE1840\_F12\_L24ZS Secale cereale anther cDNA library Secale cereale  
CDNA clone WHE1840\_F12\_L24, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS

## SOURCE

BF145790.1 GI:11027221  
EST.  
Secale cereale (rye)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Secale.

## REFERENCE

1 (bases 1 to 542)  
Anderson, O.D., Butler, E., Chao, S., Choi, D.W., Close, T.J.,  
Fenton, R.D., Gustafson, J.P., Han, P.S., Hsia, C.C., Kang, Y.,  
Lazo, G.R., Miller, R., Rausch, C.J., Ross, K., Seaton, C.L. and  
Tong, J.C.

The structure and function of the expressed portion of the wheat  
genomes - Anther cDNA library from rye

## JOURNAL

Unpublished (2000)  
Contact: Olin Anderson  
US Department of Agriculture, Agriculture Research Service, Pacific  
West Area, Western Regional Research Center  
800 Buchanan Street, Albany, CA 94710, USA  
Tel: 5105595773  
Fax: 5105595818

Email: oanderson@pv.usda.gov  
Sequence have been trimmed to remove vector sequence and low  
quality sequence with phred score less than 20  
Seq primer: Stratagene SK primer.

## FEATURES

## Source

Location/Qualifiers  
1..542  
/organism="Secale cereale"  
/mol\_type="mRNA"  
/cultivar="Blanco"  
/db\_xref="taxon:4550"  
/clone="WHE1840\_F12\_L24"  
/tissue\_type="Anther"  
/dev\_stage="Adult plant before anthesis"  
/lab\_host="E. coli SOLR"  
/clone\_lib="Secale cereale anther cDNA library"  
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;  
Site 1: EcoRI; Site 2: XhoI; Plants were grown in the  
greenhouse. Anthers were harvested and pooled from early  
meiosis to late meiosis. The tissue, total RNA, and  
poly(A) RNA were prepared (Butler, Ross and Gustafson) at  
University of Missouri, Columbia. A cDNA library was  
made, and the cDNA clones were in vivo excised to give  
phagescript phagemids in the TJ Close lab (Choi, Close,  
Fenton) at the University of California, Riverside.  
Plasmid DNA preparations and DNA sequencing were performed  
in the OD Anderson lab (all other authors)."

## ORIGIN

Query Match 85.6%; Score 15.4; DB 2; Length 542;  
Best Local Similarity 94.1%; Pred. No. 2.3e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17  
|||||  
Db 34 CGCCACCGGAAGATGAG 50

## RESULT 48

BI245760/c  
LOCUS  
DEFINITION  
IP1\_64\_A04\_g1\_A002 Immature pannicle 1 (IP1) Sorghum bicolor cDNA,  
mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS

## SOURCE

BI245760.1 GI:14823471  
EST.  
Sorghum bicolor (sorghum)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Sorghum.

## REFERENCE

1 (bases 1 to 544)  
Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and  
Pratt, L.H.

An EST database from Sorghum: developing preanthesis pannicles  
Unpublished (2001)

## JOURNAL

Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210

Email: mmpratt@uga.edu  
Sequences have been trimmed to exclude PolyA, vector and regions  
below three prime quality 16. The threshold for high quality sequence is  
20. Three prime sequences, which are obtained with PolyTmix or T7  
sequencing primer, are presented as the reverse complement.

Seq primer: T7  
High quality sequence start: 11  
High quality sequence stop: 544  
POLYA=Yes.

## FEATURES

## source

Location/Qualifiers  
1..544  
/organism="Sorghum bicolor"  
/mol\_type="mRNA"  
/cultivar="BTx623"  
/db\_xref="taxon:4558"  
/clone\_lib="Immature pannicle 1 (IP1)"  
/note="Organ: Developing preanthesis pannicles; Vector:  
phagescript II SK(-) from Lambda Zap II; Site 1: XhoI;  
Site 2: EcoRI; The library was made from poly-A RNA in the  
cloning vector lambda ZAP II. Clones to be sequenced were  
prepared by mass excision."

## ORIGIN

Query Match 85.6%; Score 15.4; DB 4; Length 544;  
Best Local Similarity 94.1%; Pred. No. 2.3e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17  
|||||  
Db 77 CGCCCCCGGAAGTTGAG 61

## RESULT 49

BG266709  
LOCUS  
DEFINITION  
1000100E03.x3 1000 - Unigene I from Maize Genome Project Zea mays  
cDNA, mRNA sequence.

## ACCESSION

BG266709

```

VERSION      BG266709.1  GI:12969892
KEYWORDS
SOURCE
ORGANISM     Zea mays

REFERENCE
AUTHORS      Walbot, V.
TITLE        Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL
COMMENT      University
              Contact: Walbot V
              Department of Biological Sciences
              Stanford University
              855 California Ave, Palo Alto, CA 94304, USA
              Tel: 650 723 2227
              Fax: 650 725 8221
              Email: walbot@stanford.edu
              Plate: 100100 row: E column: 03.

FEATURES
  source
    1..547
      Location/Qualifiers
        /organism="Zea mays"
        /mol_type="mRNA"
        /db_xref="dbEST:60502H07.x1"
        /db_xref="taxon:4577"
        /clone_lib="1000 - Unigene 1 from Maize Genome Project"
        /note="This library represents the unique ESTs found in
the first round of EST sequencing at Stanford University
for the maize genome project. Sequences are present from
libraries 486, 487, 496, 603, 605, 606, 614, 618, 660,
683, 687, 707, and 945. Contigs were assembled using
TIGR's CAP program and a representative EST from each
contig was selected for the Unigene set. All singlets were
also selected."

ORIGIN
  Query Match      85.6%; Score 15.4; DB 4; Length 547;
  Best Local Similarity 94.1%; Pred. No. 2.3e+03;
  Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  QY 1 CGCCACCGGAAGTTGAG 17
      ||| ||||| ||||| |||||
  Db 459 CGCCCCCGGAAGTTGAG 475

RESULT 50
BG948081/C
LOCUS
DEFINITION   IP1.9_B08.g1.A002 Immature pannicle 1 (IP1) Sorghum bicolor cDNA,
              mRNA sequence.
ACCESSION   BG948081
VERSION     BG948081.1  GI:14366270
KEYWORDS
SOURCE
ORGANISM     Sorghum bicolor (sorghum)
              Sorghum bicolor
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Sorghum.
              1. (bases 1 to 549)
              Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and
              Pratt, L.H.
              An EST database from Sorghum: developing preanthesis pannicles
              Unpublished (2001)
              Contact: Cordonnier-Pratt MM
              Laboratory for Genomics and Bioinformatics
              The University of Georgia, Department of Plant Biology
              Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
              Tel: 706 542 1860
              Fax: 706 583 0210
              Email: mmpratt@uga.edu
              Sequences have been trimmed to exclude PolyA, vector and regions
              below Phred quality 16. The threshold for high quality sequence is

```

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20. Three-prime sequences, which are obtained with PolyTWix or T7
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prepared by mass excision."

ORIGIN
  Query Match      85.6%; Score 15.4; DB 4; Length 549;
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  Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  QY 1 CGCCACCGGAAGTTGAG 17
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  Db 97 CGCCCCCGGAAGTTGAG 81

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Search completed: March 25, 2005, 12:32:57  
Job time : 1406 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 10:59:21 ; Search time 58.7143 Seconds  
(without alignments)  
501.632 Million cell updates/sec

Title: US-10-688-489-64

Perfect score: 18  
Sequence: 1 cgcaccacgaagtgtgagt 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : Issued Patents NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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| 102   | 13.8 | 76.7 | 51259   | 3 | US-08-781-891-209    | Sequence 209, App  | 175   | 13.2 | 73.3 | 1017 | 4 | US-09-252-991A-819   | Sequence 819, App  |
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| c 106 | 13.8 | 76.7 | 68719   | 4 | US-09-949-016-12799  | Sequence 12799, A  | 179   | 13.2 | 73.3 | 1291 | 1 | US-07-952-755-2      | Sequence 2, Appl   |
| c 107 | 13.8 | 76.7 | 68720   | 4 | US-09-949-016-14296  | Sequence 14296, A  | c 180 | 13.2 | 73.3 | 1291 | 1 | US-08-443-679-2      | Sequence 2, Appl   |
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| c 110 | 13.8 | 76.7 | 323820  | 4 | US-09-949-016-14139  | Sequence 14139, A  | 183   | 13.2 | 73.3 | 1364 | 4 | US-09-949-016-464    | Sequence 464, App  |
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| c 112 | 13.8 | 76.7 | 4411529 | 3 | US-09-103-840A-1     | Sequence 1, Appl   | c 185 | 13.2 | 73.3 | 1426 | 1 | US-08-630-592-6      | Sequence 6, Appl   |
| c 113 | 13.4 | 74.4 | 20      | 3 | US-09-457-474-1      | Sequence 1, Appl   | c 186 | 13.2 | 73.3 | 1426 | 1 | US-08-714-981-6      | Sequence 6, Appl   |
| c 114 | 13.4 | 74.4 | 275     | 4 | US-09-313-294A-4639  | Sequence 4639, App | c 187 | 13.2 | 73.3 | 1426 | 3 | US-09-032-365A-7     | Sequence 7, Appl   |
| c 115 | 13.4 | 74.4 | 224     | 4 | US-09-543-681A-2408  | Sequence 2408, App | 188   | 13.2 | 73.3 | 1431 | 4 | US-09-902-540-7719   | Sequence 7719, App |
| c 116 | 13.4 | 74.4 | 381     | 4 | US-09-489-039A-4498  | Sequence 4498, App | 189   | 13.2 | 73.3 | 1443 | 4 | US-09-252-991A-6853  | Sequence 6853, App |
| c 117 | 13.4 | 74.4 | 456     | 4 | US-09-252-991A-634   | Sequence 634, App  | c 190 | 13.2 | 73.3 | 1482 | 3 | US-08-996-441B-69    | Sequence 69, Appl  |
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| c 124 | 13.4 | 74.4 | 747     | 3 | US-09-727-578-23     | Sequence 23, Appl  | c 197 | 13.2 | 73.3 | 1518 | 3 | US-08-955-918C-11    | Sequence 11, Appl  |
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| c 128 | 13.4 | 74.4 | 1287    | 4 | US-09-573-080A-50    | Sequence 50, Appl  | c 201 | 13.2 | 73.3 | 1622 | 1 | US-08-631-200-13     | Sequence 13, Appl  |
| c 129 | 13.4 | 74.4 | 1374    | 4 | US-09-721-870-25     | Sequence 25, Appl  | c 202 | 13.2 | 73.3 | 1622 | 1 | US-08-829-553-13     | Sequence 13, Appl  |
| c 130 | 13.4 | 74.4 | 1434    | 4 | US-09-252-991A-11085 | Sequence 11085, A  | c 203 | 13.2 | 73.3 | 1622 | 2 | US-08-922-267A-13    | Sequence 13, Appl  |
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| c 137 | 13.4 | 74.4 | 3756    | 4 | US-09-252-991A-692   | Sequence 692, App  | c 210 | 13.2 | 73.3 | 1702 | 4 | US-09-902-540-292    | Sequence 292, App  |
| c 138 | 13.4 | 74.4 | 3774    | 4 | US-09-252-991A-719   | Sequence 719, App  | c 211 | 13.2 | 73.3 | 1722 | 4 | US-09-489-847-93     | Sequence 93, Appl  |
| c 139 | 13.4 | 74.4 | 3804    | 3 | US-09-356-952-14     | Sequence 14, Appl  | c 212 | 13.2 | 73.3 | 1806 | 4 | US-09-902-540-4583   | Sequence 4583, App |
| c 140 | 13.4 | 74.4 | 6885    | 4 | US-09-252-991A-660   | Sequence 660, App  | c 213 | 13.2 | 73.3 | 1890 | 3 | US-09-032-365A-61    | Sequence 61, Appl  |
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| c 145 | 13.4 | 74.4 | 109590  | 4 | US-09-949-016-13525  | Sequence 13525, A  | c 218 | 13.2 | 73.3 | 1946 | 4 | US-08-755-592A-5     | Sequence 5, Appl   |
| c 146 | 13.4 | 74.4 | 147382  | 4 | US-09-949-016-14624  | Sequence 14624, A  | c 219 | 13.2 | 73.3 | 1946 | 4 | US-08-617-923-1      | Sequence 1, Appl   |
| c 147 | 13.4 | 74.4 | 187595  | 4 | US-09-949-016-15546  | Sequence 15546, A  | c 220 | 13.2 | 73.3 | 1953 | 1 | US-08-315-468-5      | Sequence 3, Appl   |
| c 148 | 13.4 | 74.4 | 232547  | 4 | US-09-949-016-16603  | Sequence 16603, A  | c 221 | 13.2 | 73.3 | 1953 | 3 | US-07-941-650A-3     | Sequence 3, Appl   |
| c 149 | 13.2 | 73.3 | 253     | 4 | US-09-513-999C-10336 | Sequence 10336, A  | c 222 | 13.2 | 73.3 | 1956 | 3 | US-08-996-441B-51    | Sequence 51, Appl  |
| c 150 | 13.2 | 73.3 | 418     | 4 | US-09-270-767-30068  | Sequence 30068, A  | c 223 | 13.2 | 73.3 | 1956 | 3 | US-08-996-441B-55    | Sequence 55, Appl  |
| c 151 | 13.2 | 73.3 | 441     | 4 | US-09-710-278-2587   | Sequence 2587, App | c 224 | 13.2 | 73.3 | 1956 | 3 | US-08-996-441B-57    | Sequence 57, Appl  |
| c 152 | 13.2 | 73.3 | 591     | 4 | US-09-252-991A-11344 | Sequence 11344, A  | c 225 | 13.2 | 73.3 | 1956 | 3 | US-08-993-722A-51    | Sequence 51, Appl  |
| c 153 | 13.2 | 73.3 | 601     | 4 | US-09-949-016-21137  | Sequence 21137, A  | c 226 | 13.2 | 73.3 | 1956 | 3 | US-08-993-722A-55    | Sequence 55, Appl  |
| c 154 | 13.2 | 73.3 | 601     | 4 | US-09-949-016-21138  | Sequence 21138, A  | c 227 | 13.2 | 73.3 | 1956 | 3 | US-08-993-722A-57    | Sequence 57, Appl  |
| c 155 | 13.2 | 73.3 | 601     | 4 | US-09-949-016-26966  | Sequence 26966, A  | c 228 | 13.2 | 73.3 | 1956 | 3 | US-08-993-170A-51    | Sequence 51, Appl  |
| c 156 | 13.2 | 73.3 | 601     | 4 | US-09-949-016-47505  | Sequence 47505, A  | c 229 | 13.2 | 73.3 | 1956 | 3 | US-08-993-170A-55    | Sequence 55, Appl  |
| c 157 | 13.2 | 73.3 | 601     | 4 | US-09-949-016-47506  | Sequence 47506, A  | c 230 | 13.2 | 73.3 | 1956 | 3 | US-08-993-170A-57    | Sequence 57, Appl  |
| c 158 | 13.2 | 73.3 | 601     | 4 | US-09-949-016-87133  | Sequence 87133, A  | c 231 | 13.2 | 73.3 | 1956 | 3 | US-08-993-775B-51    | Sequence 51, Appl  |
| c 159 | 13.2 | 73.3 | 601     | 4 | US-09-949-016-204217 | Sequence 204217, A | c 232 | 13.2 | 73.3 | 1956 | 3 | US-08-993-775B-55    | Sequence 55, Appl  |
| c 160 | 13.2 | 73.3 | 601     | 4 | US-09-949-016-204906 | Sequence 204906, A | c 233 | 13.2 | 73.3 | 1956 | 4 | US-09-427-770-51     | Sequence 51, Appl  |
| c 161 | 13.2 | 73.3 | 606     | 4 | US-09-252-991A-6866  | Sequence 6866, App | c 234 | 13.2 | 73.3 | 1956 | 4 | US-09-427-770-55     | Sequence 55, Appl  |
| c 162 | 13.2 | 73.3 | 640     | 4 | US-09-513-999C-829   | Sequence 829, App  | c 235 | 13.2 | 73.3 | 1956 | 4 | US-09-427-770-57     | Sequence 57, Appl  |
| c 163 | 13.2 | 73.3 | 702     | 4 | US-09-902-540-2058   | Sequence 2058, App | c 236 | 13.2 | 73.3 | 1956 | 4 | US-09-427-769-51     | Sequence 51, Appl  |
| c 164 | 13.2 | 73.3 | 708     | 4 | US-09-270-767-11725  | Sequence 11725, A  | c 237 | 13.2 | 73.3 | 1956 | 4 | US-09-427-769-55     | Sequence 55, Appl  |
| c 165 | 13.2 | 73.3 | 753     | 4 | US-09-902-540-2320   | Sequence 2320, App | c 238 | 13.2 | 73.3 | 1956 | 4 | US-09-427-769-57     | Sequence 57, Appl  |
| c 166 | 13.2 | 73.3 | 783     | 4 | US-09-902-540-6140   | Sequence 6140, App | c 239 | 13.2 | 73.3 | 1959 | 3 | US-08-996-441B-1     | Sequence 1, Appl   |
| c 167 | 13.2 | 73.3 | 862     | 4 | US-09-270-767-9860   | Sequence 9860, App | c 240 | 13.2 | 73.3 | 1959 | 3 | US-08-996-441B-3     | Sequence 3, Appl   |
| c 168 | 13.2 | 73.3 | 885     | 4 | US-09-583-110-1079   | Sequence 1079, App | c 241 | 13.2 | 73.3 | 1959 | 3 | US-08-996-441B-5     | Sequence 5, Appl   |
| c 169 | 13.2 | 73.3 | 891     | 4 | US-09-711-164-156    | Sequence 156, App  | c 242 | 13.2 | 73.3 | 1959 | 3 | US-08-996-441B-7     | Sequence 7, Appl   |
| c 170 | 13.2 | 73.3 | 900     | 3 | US-08-961-527-332    | Sequence 332, App  | c 243 | 13.2 | 73.3 | 1959 | 3 | US-08-996-441B-9     | Sequence 9, Appl   |
| c 171 | 13.2 | 73.3 | 900     | 4 | US-09-252-991A-465   | Sequence 465, App  | c 244 | 13.2 | 73.3 | 1959 | 3 | US-08-996-441B-11    | Sequence 11, Appl  |
| c 172 | 13.2 | 73.3 | 948     | 4 | US-09-107-433-518    | Sequence 518, App  | c 245 | 13.2 | 73.3 | 1959 | 3 | US-08-996-441B-13    | Sequence 13, Appl  |
| c 173 | 13.2 | 73.3 | 972     | 4 | US-09-252-991A-404   | Sequence 404, App  | c 246 | 13.2 | 73.3 | 1959 | 3 | US-08-996-441B-13    | Sequence 13, Appl  |





```

RESULT 2
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      88.9%; Score 16; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCACCGGAAGTTGAG 17
DB      1450409 GCACCGGAAGTTGAG 1450394
          |||||
          |||||

RESULT 3
US-09-464-535-13/c
; Sequence 13, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McGonigle, Brian
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB1306 US NA
; CURRENT APPLICATION NUMBER: US/09/464,535
; CURRENT FILING DATE: 1999-12-15
; EARLIER APPLICATION NUMBER: 60/112,555
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-464-535-13

Query Match      83.3%; Score 15; DB 4; Length 436;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 CCACCGGAAGTTGAG 17
DB      157 CCACCGGAAGTTGAG 143
          |||||
          |||||

RESULT 4
US-09-464-535-39/c
; Sequence 39, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.

```

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; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McGonigle, Brian
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB1306 US NA
; CURRENT APPLICATION NUMBER: US/09/464,535
; CURRENT FILING DATE: 1999-12-15
; EARLIER APPLICATION NUMBER: 60/112,555
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 39
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-464-535-39

Query Match      83.3%; Score 15; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 CCACCGGAAGTTGAG 17
DB      164 CCACCGGAAGTTGAG 150
          |||||
          |||||

RESULT 5
US-09-464-535-33/c
; Sequence 33, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McGonigle, Brian
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB1306 US NA
; CURRENT APPLICATION NUMBER: US/09/464,535
; CURRENT FILING DATE: 1999-12-15
; EARLIER APPLICATION NUMBER: 60/112,555
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 33
; LENGTH: 616
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (387)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (415)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (489)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (491)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (544)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (551)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (558)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (562)

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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (567)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (569)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (592)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (600)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (611)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (616)
; US-09-464-535-33

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Query Match 83.3%; Score 15; DB 4; Length 616;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 CCACCGGAAGTTGAG 17
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Db 376 CCACCGGAAGTTGAG 362

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RESULT 6
US-09-464-535-31/c
; Sequence 31, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McGonigle, Brian
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB1306 US NA
; CURRENT APPLICATION NUMBER: US/09/464,535
; EARLIER FILING DATE: 1999-12-15
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 31
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (41)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (95)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (227)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (385)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (388)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (390)
; FEATURE:

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; NAME/KEY: unsure
; LOCATION: (487)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (491)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (554)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (557)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (560)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (626)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (634)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (650)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (664)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (668)
; US-09-464-535-31

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Query Match 83.3%; Score 15; DB 4; Length 673;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 CCACCGGAAGTTGAG 17
    |||||
Db 362 CCACCGGAAGTTGAG 348

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RESULT 7
US-08-976-259-27/c
; Sequence 27, Application US/08976259
; Patent No. 6316609
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Choi, Gil H.
; APPLICANT: Welch, Rodney A.
; TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
; Patent No. 6316609
; NUMBER OF SEQUENCES: 142
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,259
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,626 AND US 60/061,953
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0740002/EKS/CBM

```

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1118 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-976-259-27

Query Match 82.2%; Score 14.8; DB 3; Length 1118;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGGTTGAGT 18  
||||| ||| |||||  
Db 1054 CGCCACGAGGTTGAGT 1037

## RESULT 8

US-09-956-004-27/c  
Sequence 27, Application US/09956004  
Patent No. 6787643  
GENERAL INFORMATION:  
APPLICANT: Patrick J. Dillon et al.  
TITLE OF INVENTION: Nucleotide Sequences of Escherichia coli Pathogenicity Islands  
FILE REFERENCE: PB324D1  
CURRENT APPLICATION NUMBER: US/09/956,004  
CURRENT FILING DATE: 2001-09-20  
PRIOR APPLICATION NUMBER: 08/976,259  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/061,953  
PRIOR FILING DATE: 1997-10-14  
PRIOR APPLICATION NUMBER: 60/031,626  
PRIOR FILING DATE: 1996-11-22  
NUMBER OF SEQ ID NOS: 142  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 27

LENGTH: 1118  
TYPE: DNA  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (142)..(142)  
OTHER INFORMATION: n equals a, t, g, or c  
NAME/KEY: misc feature  
LOCATION: (228)..(228)  
OTHER INFORMATION: n equals a, t, g, or c  
NAME/KEY: misc feature  
LOCATION: (261)..(261)  
OTHER INFORMATION: n equals a, t, g, or c  
NAME/KEY: misc feature  
LOCATION: (693)..(693)  
OTHER INFORMATION: n equals a, t, g, or c  
US-09-956-004-27

Query Match 82.2%; Score 14.8; DB 4; Length 1118;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGGTTGAGT 18  
||||| ||| |||||  
Db 1054 CGCCACGAGGTTGAGT 1037

## RESULT 9

US-09-252-991A-14725  
Sequence 14725, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 14725  
LENGTH: 1203  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14725

Query Match 82.2%; Score 14.8; DB 4; Length 1203;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGGTTGAGT 18  
||||| ||| |||||  
Db 277 CGCCACCGGAGGTTGATT 294

## RESULT 10

US-09-252-991A-14603  
Sequence 14603, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 14603  
LENGTH: 1233  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14603

Query Match 82.2%; Score 14.8; DB 4; Length 1233;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGGTTGAGT 18  
||||| ||| |||||  
Db 266 CGCCACCGGAGGTTGATT 283

## RESULT 11

US-09-252-991A-15026/c  
Sequence 15026, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 15026  
LENGTH: 1329

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; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15026

Query Match      82.2%; Score 14.8; DB 4; Length 1329;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAAGTTGAGT 18
   ||||| ||||| |||||
Db 1005 CGCCACCGGAAGTTGATT 988

RESULT 12
US-09-252-991A-15978/c
; Sequence 15978, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15978
; LENGTH: 1806
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15978

Query Match      82.2%; Score 14.8; DB 4; Length 1806;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAAGTTGAGT 18
   ||||| ||||| |||||
Db 536 CGCCACCGGAAGCCGAGT 519

RESULT 13
US-09-252-991A-16301
; Sequence 16301, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16301
; LENGTH: 2289
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16301

Query Match      82.2%; Score 14.8; DB 4; Length 2289;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAAGTTGAGT 18
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Db 1994 CGCCACCGGAAGCCGAGT 2011
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RESULT 14
US-09-543-681A-3437
; Sequence 3437, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543.681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 3437
; LENGTH: 5151
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-3437

Query Match      82.2%; Score 14.8; DB 4; Length 5151;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAAGTTGAGT 18
   ||||| ||||| |||||
Db 5069 CGCCTCCGCAAGTTGAGT 5086

RESULT 15
US-09-949-016-17417
; Sequence 17417, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17417
; LENGTH: 77772
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(77772)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17417

Query Match      82.2%; Score 14.8; DB 4; Length 77772;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAAGTTGAGT 18
   ||||| ||||| |||||
Db 921 CGCCACCGGAAGTTGAGT 938

RESULT 16
US-09-949-016-12249
; Sequence 12249, Application US/09949016
; Patent No. 6812339
```



GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: CL001307  
 CURRENT APPLICATION NUMBER: US/09/949,016  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 12249  
 LENGTH: 77997  
 TYPE: DNA  
 ORGANISM: Human  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: (1)...(77997)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-949-016-12249

Query Match 82.2%; Score 14.8; DB 4; Length 77997;  
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18  
 DB 925 CGCCACCGGACTTTGAGT 942

RESULT 17  
 US-09-634-238-154  
 Sequence 154, Application US/09634238  
 Patent No. 6544772  
 GENERAL INFORMATION:  
 APPLICANT: Glenn, Matthew  
 APPLICANT: Havukkala, Ilkka J.  
 APPLICANT: Bloksberg, Leonard, N.  
 APPLICANT: Lubbers, Mark W.  
 APPLICANT: Dekker, James  
 APPLICANT: Christensen, Anna C.  
 APPLICANT: Holland, Ross  
 APPLICANT: O'Toole, Paul W.  
 APPLICANT: Reid, Julian R.  
 APPLICANT: Coolbear, Timothy  
 TITLE OF INVENTION: Polynucleotides, materials incorporating  
 them and methods for using them.  
 FILE REFERENCE: 11000.1043U1  
 CURRENT APPLICATION NUMBER: US/09/634,238  
 CURRENT FILING DATE: 2000-08-08  
 NUMBER OF SEQ ID NOS: 422  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 154  
 LENGTH: 435  
 TYPE: DNA  
 ORGANISM: Lactobacillus rhamnosus  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: (1)...(435)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-634-238-154

Query Match 80.0%; Score 14.4; DB 4; Length 435;  
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGA 16  
 DB 420 CGCCACCGGAGTGA 435

RESULT 18  
 US-09-949-016-142247  
 Sequence 142247, Application US/09949016  
 Patent No. 6812339  
 GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: CL001307  
 CURRENT APPLICATION NUMBER: US/09/949,016  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 142247  
 LENGTH: 601  
 TYPE: DNA  
 ORGANISM: Human  
 US-09-949-016-142247

Query Match 80.0%; Score 14.4; DB 4; Length 601;  
 Best Local Similarity 93.8%; Pred. No. 2.5e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17  
 DB 449 GCCACCGGAGTTGAG 464

RESULT 19  
 US-09-549-848B-5/c  
 Sequence 5, Application US/09549848B  
 Patent No. 6541259  
 GENERAL INFORMATION:  
 APPLICANT: Lassner, Michael  
 APPLICANT: Post-Beittenmiller, Dusty  
 APPLICANT: Savidge, Beth  
 APPLICANT: Weiss, James  
 TITLE OF INVENTION: Nucleic Acid Sequences Involved in  
 Tumor Promotion and Tumor Inhibition  
 FILE REFERENCE: 17133/02/US  
 CURRENT APPLICATION NUMBER: US/09/549,848B  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/129,899  
 PRIOR FILING DATE: 1999-04-15  
 PRIOR APPLICATION NUMBER: 60/146,461  
 PRIOR FILING DATE: 1999-07-30  
 NUMBER OF SEQ ID NOS: 94  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 5  
 LENGTH: 1296  
 TYPE: DNA  
 ORGANISM: Arabidopsis sp  
 US-09-549-848B-5

Query Match 80.0%; Score 14.4; DB 4; Length 1296;  
 Best Local Similarity 93.8%; Pred. No. 2.8e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17  
 DB 1238 GCCACCGGAGTTGAG 1223

RESULT 20  
 US-08-704-966-3/c

Fri Mar 25 15:14:16 2005

us-10-688-489-64.rni

```

; Sequence 3, Application US/08704966
; Patent No. 6013523
; GENERAL INFORMATION:
; APPLICANT: Adams, Michael J.
; APPLICANT: Rocheleau, Thomas A.
; APPLICANT: Merlo, Donald
; APPLICANT: Murray, Elizabeth E.
; TITLE OF INVENTION: Synthetic Insecticidal Crystal Protein
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 1000 Legion Place, Suite 1750
; CITY: Orlando
; STATE: Florida
; COUNTRY: USA
; ZIP: 32801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,966
; FILING DATE: 29-AUG-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/369,839
; FILING DATE: 06-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,191
; FILING DATE: 03-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,844
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/242,482
; FILING DATE: 09-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: MPS 8-88AFD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 407-426-7500
; TELEFAX: 407-839-8589
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1833 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-704-966-3

```

```

Query Match      80.0%; Score 14.4; DB 3; Length 1833;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      3 CCACCGGAAGTTGAGT 18
DB      1402 CCAACGGAAGTTGAGT 1387

```

```

RESULT 21
US-08-705-438-3/c
; Sequence 3, Application US/08705438
; Patent No. 6015891
; GENERAL INFORMATION:
; APPLICANT: Adams, Michael J.
; APPLICANT: Rocheleau, Thomas A.
; APPLICANT: Merlo, Donald
; APPLICANT: Murray, Elizabeth E.
; TITLE OF INVENTION: 'Synthetic Insecticidal Crystal Protein

```

```

; TITLE OF INVENTION: Gene
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 1000 Legion Place, Suite 1750
; CITY: Orlando
; STATE: Florida
; COUNTRY: USA
; ZIP: 32801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,438
; FILING DATE: 29-AUG-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/369,839
; FILING DATE: 06-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,191
; FILING DATE: 03-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,844
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/242,482
; FILING DATE: 09-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: MPS 8-88AFD4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 407-426-7500
; TELEFAX: 407-839-8589
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1833 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-705-438-3

```

```

Query Match      80.0%; Score 14.4; DB 3; Length 1833;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      3 CCACCGGAAGTTGAGT 18
DB      1402 CCAACGGAAGTTGAGT 1387

```

```

RESULT 22
US-09-549-848B-93/c
; Sequence 93, Application US/09549848B
; Patent No. 6541259
; GENERAL INFORMATION:
; APPLICANT: Lasener, Michael
; APPLICANT: Post-Beittenmiller, Dusty
; APPLICANT: Savidge, Beth
; APPLICANT: Weiss, James
; TITLE OF INVENTION: Nucleic Acid Sequences Involved in
; FILE REFERENCE: 17133/02/US
; CURRENT APPLICATION NUMBER: US/09/549,848B
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/129,899
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/146,461
; PRIOR FILING DATE: 1999-07-30

```

```
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 2850
; TYPE: DNA
; ORGANISM: Arabidopsis sp
; US-09-549-8488-93

Query Match      80.0%; Score 14.4; DB 4; Length 2850;
Best Local Similarity 93.8%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCACCGGAAGTTGAG 17
Db      2371 GCACCGGAGTTGAG 2356

RESULT 23
US-09-949-016-14257
; Sequence 14257, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14257
; LENGTH: 29321
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-14257

Query Match      80.0%; Score 14.4; DB 4; Length 29321;
Best Local Similarity 93.8%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCACCGGAAGTTGAG 17
Db      9179 GCACCGGAAGTTGAG 9194

RESULT 24
US-09-949-016-14258
; Sequence 14258, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14258
; LENGTH: 29321
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-14258

Query Match      80.0%; Score 14.4; DB 4; Length 29321;
Best Local Similarity 93.8%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCACCGGAAGTTGAG 17
Db      9179 GCACCGGAAGTTGAG 9194

RESULT 25
US-09-949-016-11758
; Sequence 11758, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11758
; LENGTH: 32798
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-11758

Query Match      80.0%; Score 14.4; DB 4; Length 32798;
Best Local Similarity 93.8%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 CCACCGGAAGTTGAGT 18
Db      11464 CCACCGGAAGTAGAGT 11479

RESULT 26
US-09-949-016-17366
; Sequence 17366, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17366
; LENGTH: 32798
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-17366

Query Match      80.0%; Score 14.4; DB 4; Length 32798;
Best Local Similarity 93.8%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 CCACCGGAAGTTGAGT 18
Db      11464 CCACCGGAAGTAGAGT 11479

RESULT 27
US-09-949-016-17367
; Sequence 17367, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17367
; LENGTH: 32798
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-17367

Query Match      80.0%; Score 14.4; DB 4; Length 32798;
Best Local Similarity 93.8%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 CCACCGGAAGTTGAGT 18
Db      11464 CCACCGGAAGTAGAGT 11479
```

```
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAGT 18
Db 11464 CCACCGGAAGTTAGT 11479

RESULT 27
US-09-949-016-11932/c
; Sequence 11932, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11932
; LENGTH: 41522
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11932

Query Match 80.0%; Score 14.4; DB 4; Length 41522;
Best Local Similarity 93.8%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17
Db 4350 GCCACAGGAAGTTGAG 4335

RESULT 28
US-09-949-016-15764/c
; Sequence 15764, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15764
; LENGTH: 41523
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15764

Query Match 80.0%; Score 14.4; DB 4; Length 41523;
Best Local Similarity 93.8%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17
Db 4350 GCCACAGGAAGTTGAG 4335
```

```
RESULT 29
US-09-491-356C-1
; Sequence 1, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Ginns, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491,356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 55298
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (485)..(485)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (838)..(838)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (16728)..(16728)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (22750)..(22750)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (22756)..(22756)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (28519)..(28519)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (44804)..(44804)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (45002)..(45002)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (54049)..(54049)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (54226)..(54226)
; OTHER INFORMATION: n is not determined
US-09-491-356C-1

Query Match 80.0%; Score 14.4; DB 4; Length 55298;
Best Local Similarity 93.8%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17
Db 34613 GCCACCGGAAGTTTCAG 34628

RESULT 30
US-09-949-016-15794
; Sequence 15794, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

```
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15794
; LENGTH: 123513
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(123513)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15794

Query Match      80.0%; Score 14.4; DB 4; Length 123513;
Best Local Similarity 93.8%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 CCACCGGAAGTTGAGT 18
        |||
Db      118414 CCACCGGAAGTTGACT 118429

RESULT 31
US-09-270-767-14483
; Sequence 14483, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14483
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-14483

Query Match      77.8%; Score 14; DB 4; Length 443;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCACCGGAAGTTG 15
        |||
Db      334 GCACCGGAAGTTG 347

RESULT 32
US-09-902-540-8535/c
; Sequence 8535, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 899
; LENGTH: 8518
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-899

Query Match      77.8%; Score 14; DB 4; Length 8518;
```

```
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8535
; LENGTH: 2850
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8535

Query Match      77.8%; Score 14; DB 4; Length 2850;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGCCACCGGAAGTT 14
        |||
Db      1752 CGCCACCGGAAGTT 1739

RESULT 33
US-09-949-016-12296
; Sequence 12296, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12296
; LENGTH: 2913
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12296

Query Match      77.8%; Score 14; DB 4; Length 2913;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGCCACCGGAAGTT 14
        |||
Db      758 CGCCACCGGAAGTT 771

RESULT 34
US-09-902-540-899
; Sequence 899, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 899
; LENGTH: 8518
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-899

Query Match      77.8%; Score 14; DB 4; Length 8518;
```

Best Local Similarity 100.0%; Pred. No. 6.1e+02; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0;

QY 1 GCCACCGGAAGTT 14  
Db 6766 CGCACCGGAAGTT 6779

## RESULT 35

US-09-085-199B-30  
; Sequence 30, Application US/09085199B  
; Patent No. 6235879  
; GENERAL INFORMATION:  
; APPLICANT: Hayden, Michael R.  
; APPLICANT: Hackam, Abigail  
; APPLICANT: Hug, A.H.M. Mahbubul  
; APPLICANT: Chopra, Vikramjit Singh  
; APPLICANT: Kalchman, Michael  
; TITLE OF INVENTION: Apoptosis Modulators That Interact with the  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Oppedahl & Larson  
; STREET: PO Box 5270  
; CITY: Frisco  
; STATE: CO  
; COUNTRY: USA  
; ZIP: 80443-5270  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS DOS 5.0  
; SOFTWARE: WordPerfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/085,199B  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Larson, Marina T.  
; REGISTRATION NUMBER: 32038  
; REFERENCE/DOCKET NUMBER: UBC-P-013US2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (970) 668-2050  
; TELEFAX: (970) 668-2052  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 359  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: genomic DNA  
; HYPOTHETICAL: no  
; ANTI-SENSE: no  
; ORIGINAL SOURCE:  
; ORGANISM: human  
; FEATURE:  
; OTHER INFORMATION: exon 15 of HIP1  
US-09-085-199B-30

Query Match 76.7%; Score 13.8; DB 3; Length 359;  
Best Local Similarity 88.2%; Pred. No. 5.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18  
Db 231 GCCACCGGAAGTTGAGT 247

## RESULT 36

US-09-513-999C-20187/c  
; Sequence 20187, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclet, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59 US2 REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 20187  
; LENGTH: 420  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-513-999C-20187

Query Match 76.7%; Score 13.8; DB 4; Length 420;  
Best Local Similarity 88.2%; Pred. No. 5.2e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18  
Db 111 GCCACCGGAAGTTAGT 95

## RESULT 37

US-09-270-767-4798/c  
; Sequence 4798, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 4798  
; LENGTH: 483  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-4798

Query Match 76.7%; Score 13.8; DB 4; Length 483;  
Best Local Similarity 88.2%; Pred. No. 5.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18  
Db 211 GCCATCGGAAGTTGAGT 195

## RESULT 38

US-09-270-767-20080/c  
; Sequence 20080, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 20080  
; LENGTH: 483  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-20080

Query Match 76.7%; Score 13.8; DB 4; Length 483;

```
Best Local Similarity 88.2%; Pred. No. 5.3e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 2 GCCACCGGAAGTTGAGT 18
    |||||
Db 211 GCCATCGGAAGTTGAGT 195

RESULT 39
US-09-949-016-89710/c
; Sequence 89710, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89710
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-89710

Query Match 76.7%; Score 13.8; DB 4; Length 601;
Best Local Similarity 88.2%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCACCGGAAGTTGAGT 17
    |||||
Db 200 CCCACCGGAAGTTGAGT 184

RESULT 40
US-08-998-416-51
; Sequence 51, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebschuing, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
```

```
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 632 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1013UP
US-08-998-416-51

Query Match 76.7%; Score 13.8; DB 3; Length 632;
Best Local Similarity 88.2%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 17
    |||||
Db 24 CGCCACCGGAAGTTGAGT 40

RESULT 41
US-09-134-000C-32
; Sequence 32, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-32

Query Match 76.7%; Score 13.8; DB 4; Length 720;
Best Local Similarity 88.2%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18
    |||||
Db 141 GCCACCGGAAGTTGAGT 157

RESULT 42
US-09-791-540-5/c
; Sequence 5, Application US/09791540
; Patent No. 6824782
; GENERAL INFORMATION:
; APPLICANT: WHITLOW, MARC
; APPLICANT: SHORR, ROBERT G.L.
; APPLICANT: FILIPULA, DAVID R.
; APPLICANT: LEE, LIHSYNG S.
; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
; POLYPEPTIDES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 NEW YORK AVENUE, SUITE 600  
 CITY: WASHINGTON  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/791,540  
 FILING DATE: 26-Feb-2001

CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/069,842  
 FILING DATE: 1998-04-30

APPLICATION NUMBER: US 60/050,472  
 FILING DATE: 23-JUN-1997

APPLICATION NUMBER: US 60/063,074  
 FILING DATE: 27-OCT-1997

APPLICATION NUMBER: US 60/067,341  
 FILING DATE: 02-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: JORGE A. GOLDSTEIN

REGISTRATION NUMBER: 29,021

REFERENCE/DOCKET NUMBER: 0977.1840002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 723 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

FEATURE:

NAME/KEY: CDS

LOCATION: 1..723

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-791-540-5

Query Match 76.7%; Score 13.8; DB 4; Length 723;

Best Local Similarity 88.2%; Pred. No. 5.6e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17

Db 358 CGCTACCGGAAGTAGAG 342

RESULT 43

US-08-392-338A-12/c

Sequence 12, Application US/08392338A

Patent No. 5869620

GENERAL INFORMATION:

APPLICANT: Whitlow, Marc

APPLICANT: Wood, James F.

APPLICANT: Hardman, Karl

APPLICANT: Bird, Robert

APPLICANT: Filpula, David

TITLE OF INVENTION: Multivalent Antigen-Binding Proteins

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, NW

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/392,338A

FILING DATE: 22-FEB-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/989,846

FILING DATE: 20-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/796,936

FILING DATE: 25-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: Goldstein, Jorge A.

REGISTRATION NUMBER: 29,021

REFERENCE/DOCKET NUMBER: 0977.0030007

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 744 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

FEATURE:

NAME/KEY: CDS

LOCATION: 1..732

US-08-392-338A-12

Query Match 76.7%; Score 13.8; DB 2; Length 744;

Best Local Similarity 88.2%; Pred. No. 5.6e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17

Db 358 CGCTACCGGAAGTAGAG 342

RESULT 44

US-09-166-750-12/c

Sequence 12, Application US/09166750

Patent No. 6025165

GENERAL INFORMATION:

APPLICANT: Whitlow, Marc

APPLICANT: Wood, James F.

APPLICANT: Hardman, Karl

APPLICANT: Bird, Robert

APPLICANT: Filpula, David

APPLICANT: Rollence, Michelle

TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, NW

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/166,750

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/392,338

FILING DATE: 22-FEB-1995



;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/989,846  
;; FILING DATE: 20-NOV-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/796,936  
;; FILING DATE: 25-NOV-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Goldstein, Jorge A.  
;; REGISTRATION NUMBER: 29,021  
;; REFERENCE/DOCKET NUMBER: 0977.003000C  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 371-2600  
;; TELEFAX: (202) 371-2540  
;; INFORMATION FOR SEQ ID NO: 12:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 744 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: both  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 1..732  
US-09-166-750-12

Query Match 76.7%; Score 13.8; DB 3; Length 744;  
Best Local Similarity 88.2%; Pred. No. 5.6e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17  
Db 358 CGCTACCGGAAGTAGAG 342

RESULT 45  
US-09-166-093-12/c  
; Sequence 12, Application US/09166093  
; Patent No. 6027725  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Wood, James F.  
; APPLICANT: Hardman, Karl  
; APPLICANT: Bird, Robert  
; APPLICANT: Filpula, David  
; APPLICANT: Rollence, Michelle  
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, NW  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/166,093  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/392,338  
; FILING DATE: 22-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/989,846  
; FILING DATE: 20-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,936  
; FILING DATE: 25-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.003000C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 744 base pairs  
; TYPE: nucleic acid

;; REGISTRATION NUMBER: 29,021  
;; REFERENCE/DOCKET NUMBER: 0977.003000B  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 371-2600  
;; TELEFAX: (202) 371-2540  
;; INFORMATION FOR SEQ ID NO: 12:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 744 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: both  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 1..732  
US-09-166-093-12

Query Match 76.7%; Score 13.8; DB 3; Length 744;  
Best Local Similarity 88.2%; Pred. No. 5.6e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17  
Db 358 CGCTACCGGAAGTAGAG 342

RESULT 46  
US-09-172-019-12/c  
; Sequence 12, Application US/09172019  
; Patent No. 6103889  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Hardman, Karl  
; APPLICANT: Bird, Robert  
; APPLICANT: Filpula, David  
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain  
; TITLE OF INVENTION: Antigen-Binding Proteins (As Amended)  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, NW  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/172,019  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/392,338  
; FILING DATE: 22-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/989,846  
; FILING DATE: 20-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,936  
; FILING DATE: 25-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.003000D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 744 base pairs  
; TYPE: nucleic acid

STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..732  
US-09-172-019-12

Query Match 76.7%; Score 13.8; DB 3; Length 744;  
Best Local Similarity 88.2%; Pred. No. 5.6e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17  
DB 358 CGCTACCGGAGTAGAG 342

RESULT 47  
US-09-166-094-12/c  
; Sequence 12, Application US/09166094  
; Patent No. 6121424  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Wood, James F.  
; APPLICANT: Hardman, Karl  
; APPLICANT: Bird, Robert  
; APPLICANT: Filpula, David  
; APPLICANT: Rollence, Michelle  
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, NW  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09166,094  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/392,338  
; FILING DATE: 22-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/989,846  
; FILING DATE: 20-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,936  
; FILING DATE: 25-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.003000A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 744 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..732  
US-09-166-094-12

Query Match 76.7%; Score 13.8; DB 3; Length 744;

Best Local Similarity 88.2%; Pred. No. 5.6e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17  
DB 358 CGCTACCGGAGTAGAG 342

RESULT 48  
US-09-443-213-12/c  
; Sequence 12, Application US/09443213  
; Patent No. 6515110  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Wood, James F.  
; APPLICANT: Hardman, Karl  
; APPLICANT: Bird, Robert  
; APPLICANT: Filpula, David  
; APPLICANT: Rollence, Michelle  
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, NW  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09443,213  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/166,094  
; FILING DATE: 05-OCT-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/392,338  
; FILING DATE: 22-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/989,846  
; FILING DATE: 20-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,936  
; FILING DATE: 25-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.003000E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 744 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..732  
US-09-443-213-12

Query Match 76.7%; Score 13.8; DB 4; Length 744;  
Best Local Similarity 88.2%; Pred. No. 5.6e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17  
DB 358 CGCTACCGGAGTAGAG 342

Db 358 CGCTACCGGAGTAGAG 342

## RESULT 49

US-09-069-821-1/c  
; Sequence 1, Application US/09069821  
; Patent No. 6323322  
; GENERAL INFORMATION:  
; APPLICANT: FILPULA, DAVID  
; APPLICANT: WANG, MAOLIANG  
; APPLICANT: SHORR, ROBERT  
; APPLICANT: WHITLOW, MARC  
; APPLICANT: LEE, LIHSYNG S.  
; TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS  
; TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/069,821  
; FILING DATE: 30-APR-1998  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/067,341  
; FILING DATE: 02-DEC-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/063,074  
; FILING DATE: 27-OCT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/050,472  
; FILING DATE: 23-JUN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 0977.2280003  
; REFERENCE/DOCKET NUMBER:  
; TELEPHONE: (202)371-2600  
; TELEFAX: (202)371-2540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 758 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..747  
US-09-069-821-1

Query Match 76.7%; Score 13.8; DB 3; Length 758;  
Best Local Similarity 88.2%; Pred. No. 5.6e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAGTAGAG 17

Db 358 CGCTACCGGAGTAGAG 342

## RESULT 50

US-09-956-086-1/c  
; Sequence 1, Application US/09956086  
; Patent No. 6743896  
; GENERAL INFORMATION:  
; APPLICANT: FILPULA, DAVID  
; APPLICANT: WANG, MAOLIANG  
; APPLICANT: SHORR, ROBERT  
; APPLICANT: WHITLOW, MARC  
; APPLICANT: LEE, LIHSYNG S.  
; TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS  
; TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/956,086  
; FILING DATE: 20-Sep-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/069,821  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 60/063,074  
; FILING DATE: 27-OCT-1997  
; APPLICATION NUMBER: US 60/050,472  
; FILING DATE: 23-JUN-1997  
; APPLICATION NUMBER: US 60/044,449  
; FILING DATE: 30-APR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KIM, JUDITH U.  
; REGISTRATION NUMBER: 40,679  
; REFERENCE/DOCKET NUMBER: 0977.2280003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)371-2600  
; TELEFAX: (202)371-2540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 758 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..747  
US-09-956-086-1

Query Match 76.7%; Score 13.8; DB 4; Length 758;  
Best Local Similarity 88.2%; Pred. No. 5.6e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAGTAGAG 17

Db 358 CGCTACCGGAGTAGAG 342

Search completed: March 25, 2005, 12:34:42  
Job time: 85.2143 secs





|     |      |      |         |    |                      |                    |       |      |      |     |    |                      |                    |
|-----|------|------|---------|----|----------------------|--------------------|-------|------|------|-----|----|----------------------|--------------------|
| 85  | 14.4 | 80.0 | 936     | 15 | US-10-146-772-67     | Sequence 67, Appl  | c 158 | 13.8 | 76.7 | 604 | 17 | US-10-027-632-277475 | Sequence 277475,   |
| 86  | 14.4 | 80.0 | 936     | 17 | US-10-241-742-67     | Sequence 67, Appl  | c 159 | 13.8 | 76.7 | 628 | 9  | US-09-770-149-724    | Sequence 724, App  |
| 87  | 14.4 | 80.0 | 936     | 17 | US-10-440-532-67     | Sequence 67, Appl  | c 160 | 13.8 | 76.7 | 634 | 13 | US-10-027-632-272892 | Sequence 272892,   |
| 88  | 14.4 | 80.0 | 936     | 17 | US-10-440-503-67     | Sequence 67, Appl  | c 161 | 13.8 | 76.7 | 634 | 17 | US-10-027-632-272892 | Sequence 272892,   |
| 89  | 14.4 | 80.0 | 936     | 17 | US-10-461-925-67     | Sequence 67, Appl  | c 162 | 13.8 | 76.7 | 639 | 18 | US-10-425-115-83189  | Sequence 83189, A  |
| 90  | 14.4 | 80.0 | 1296    | 16 | US-10-349-508-5      | Sequence 5, Appl   | c 163 | 13.8 | 76.7 | 666 | 15 | US-10-156-761-136    | Sequence 136, App  |
| 91  | 14.4 | 80.0 | 1296    | 17 | US-10-437-169-5      | Sequence 5, Appl   | c 164 | 13.8 | 76.7 | 681 | 15 | US-10-156-761-4364   | Sequence 4364, Ap  |
| 92  | 14.4 | 80.0 | 1446    | 18 | US-10-437-963-947    | Sequence 947, App  | c 165 | 13.8 | 76.7 | 683 | 18 | US-10-425-115-165802 | Sequence 165802, A |
| 93  | 14.4 | 80.0 | 1819    | 18 | US-10-437-963-948    | Sequence 948, App  | c 166 | 13.8 | 76.7 | 684 | 17 | US-10-369-493-43274  | Sequence 43274, A  |
| 94  | 14.4 | 80.0 | 2067    | 13 | US-10-027-632-174959 | Sequence 174959,   | c 167 | 13.8 | 76.7 | 699 | 18 | US-10-767-701-4456   | Sequence 4456, Ap  |
| 95  | 14.4 | 80.0 | 2067    | 13 | US-10-027-632-174959 | Sequence 174959,   | c 168 | 13.8 | 76.7 | 700 | 18 | US-10-767-701-3290   | Sequence 3290, Ap  |
| 96  | 14.4 | 80.0 | 2379    | 18 | US-10-437-963-7515   | Sequence 7515, Ap  | c 169 | 13.8 | 76.7 | 711 | 9  | US-09-815-242-9769   | Sequence 9769, Ap  |
| 97  | 14.4 | 80.0 | 2850    | 16 | US-10-349-508-93     | Sequence 93, Appl  | c 170 | 13.8 | 76.7 | 711 | 17 | US-10-282-122A-39884 | Sequence 39884, A  |
| 98  | 14.4 | 80.0 | 2850    | 17 | US-10-437-169-93     | Sequence 93, Appl  | c 171 | 13.8 | 76.7 | 712 | 18 | US-10-767-701-8678   | Sequence 8678, Ap  |
| 99  | 14.4 | 80.0 | 3026    | 13 | US-10-027-632-76054  | Sequence 76054, A  | c 172 | 13.8 | 76.7 | 723 | 9  | US-09-791-578-5      | Sequence 5, Appl   |
| 100 | 14.4 | 80.0 | 3026    | 17 | US-10-027-632-76054  | Sequence 76054, A  | c 173 | 13.8 | 76.7 | 723 | 9  | US-09-791-578-5      | Sequence 5, Appl   |
| 101 | 14.4 | 80.0 | 4547    | 9  | US-09-812-471-4      | Sequence 4, Appl   | c 174 | 13.8 | 76.7 | 723 | 19 | US-10-915-069-5      | Sequence 5, Appl   |
| 102 | 14.4 | 80.0 | 4547    | 9  | US-09-812-633-4      | Sequence 4, Appl   | c 175 | 13.8 | 76.7 | 723 | 19 | US-10-909-948-5      | Sequence 5, Appl   |
| 103 | 14.4 | 80.0 | 4547    | 9  | US-09-988-117-4      | Sequence 4, Appl   | c 176 | 13.8 | 76.7 | 758 | 9  | US-09-956-086-1      | Sequence 1, Appl   |
| 104 | 14.4 | 80.0 | 4547    | 19 | US-10-828-815-4      | Sequence 4, Appl   | c 177 | 13.8 | 76.7 | 758 | 9  | US-09-956-087-1      | Sequence 1, Appl   |
| 105 | 14.4 | 80.0 | 618     | 18 | US-10-437-963-37689  | Sequence 37689, A  | c 178 | 13.8 | 76.7 | 769 | 13 | US-10-027-632-167387 | Sequence 167387,   |
| 106 | 14.4 | 80.0 | 9852    | 17 | US-10-152-319A-1440  | Sequence 1440, App | c 179 | 13.8 | 76.7 | 769 | 17 | US-10-027-632-167387 | Sequence 167387,   |
| 107 | 14.4 | 80.0 | 12120   | 10 | US-09-840-743-19     | Sequence 19, Appl  | c 180 | 13.8 | 76.7 | 778 | 18 | US-10-425-115-39327  | Sequence 39327, A  |
| 108 | 14.4 | 80.0 | 138115  | 18 | US-10-322-281-377    | Sequence 377, App  | c 181 | 13.8 | 76.7 | 781 | 13 | US-10-027-632-171021 | Sequence 171021,   |
| 109 | 14.4 | 80.0 | 202251  | 13 | US-10-087-192-385    | Sequence 985, App  | c 182 | 13.8 | 76.7 | 781 | 17 | US-10-027-632-171021 | Sequence 171021,   |
| 110 | 14.4 | 80.0 | 2731748 | 18 | US-10-297-465A-1     | Sequence 1, Appl   | c 183 | 13.8 | 76.7 | 782 | 9  | US-09-791-578-3      | Sequence 3, Appl   |
| 111 | 14   | 77.8 | 469     | 13 | US-10-027-632-175539 | Sequence 175539,   | c 184 | 13.8 | 76.7 | 782 | 9  | US-09-791-540-3      | Sequence 3, Appl   |
| 112 | 14   | 77.8 | 469     | 17 | US-10-027-632-175539 | Sequence 175539,   | c 185 | 13.8 | 76.7 | 782 | 9  | US-09-983-580-1      | Sequence 1, Appl   |
| 113 | 14   | 77.8 | 501     | 13 | US-10-027-632-175560 | Sequence 175560,   | c 186 | 13.8 | 76.7 | 782 | 9  | US-09-985-442-1      | Sequence 1, Appl   |
| 114 | 14   | 77.8 | 501     | 17 | US-10-027-632-175560 | Sequence 175560,   | c 187 | 13.8 | 76.7 | 782 | 19 | US-10-915-069-3      | Sequence 3, Appl   |
| 115 | 14   | 77.8 | 516     | 18 | US-10-021-323-1477   | Sequence 1477, Ap  | c 188 | 13.8 | 76.7 | 782 | 19 | US-10-909-948-3      | Sequence 3, Appl   |
| 116 | 14   | 77.8 | 542     | 17 | US-10-341-961A-74    | Sequence 74, Appl  | c 189 | 13.8 | 76.7 | 783 | 18 | US-10-437-963-99190  | Sequence 99190, A  |
| 117 | 14   | 77.8 | 1185    | 17 | US-10-424-599-1857   | Sequence 1857, Ap  | c 190 | 13.8 | 76.7 | 787 | 18 | US-10-425-115-26871  | Sequence 26871, A  |
| 118 | 14   | 77.8 | 1381    | 17 | US-10-767-701-3537   | Sequence 3537, Ap  | c 191 | 13.8 | 76.7 | 810 | 18 | US-10-425-115-23491  | Sequence 23491, A  |
| 119 | 13.8 | 76.7 | 25      | 15 | US-10-098-263B-35243 | Sequence 35243, A  | c 192 | 13.8 | 76.7 | 813 | 17 | US-10-424-599-66647  | Sequence 66647, A  |
| 120 | 13.8 | 76.7 | 180     | 17 | US-10-424-599-73552  | Sequence 73552, A  | c 193 | 13.8 | 76.7 | 818 | 9  | US-09-983-580-3      | Sequence 3, Appl   |
| 121 | 13.8 | 76.7 | 195     | 9  | US-09-983-965-4177   | Sequence 4177, Ap  | c 194 | 13.8 | 76.7 | 818 | 9  | US-09-985-442-3      | Sequence 3, Appl   |
| 122 | 13.8 | 76.7 | 204     | 18 | US-10-437-963-38527  | Sequence 38527, A  | c 195 | 13.8 | 76.7 | 824 | 9  | US-09-776-874A-12    | Sequence 12, Appl  |
| 123 | 13.8 | 76.7 | 208     | 18 | US-10-425-115-84091  | Sequence 84091, A  | c 196 | 13.8 | 76.7 | 824 | 9  | US-09-988-113-12     | Sequence 12, Appl  |
| 124 | 13.8 | 76.7 | 248     | 18 | US-10-425-115-70979  | Sequence 70979, A  | c 197 | 13.8 | 76.7 | 824 | 16 | US-10-341-582-12     | Sequence 12, Appl  |
| 125 | 13.8 | 76.7 | 255     | 17 | US-10-424-599-70953  | Sequence 70953, A  | c 198 | 13.8 | 76.7 | 824 | 16 | US-10-384-451-12     | Sequence 12, Appl  |
| 126 | 13.8 | 76.7 | 271     | 9  | US-09-923-876-5993   | Sequence 5993, Ap  | c 199 | 13.8 | 76.7 | 824 | 16 | US-10-384-450-12     | Sequence 12, Appl  |
| 127 | 13.8 | 76.7 | 271     | 10 | US-09-923-876-5993   | Sequence 5993, Ap  | c 200 | 13.8 | 76.7 | 824 | 17 | US-10-371-218A-12    | Sequence 12, Appl  |
| 128 | 13.8 | 76.7 | 279     | 18 | US-10-425-115-108956 | Sequence 108956, A | c 201 | 13.8 | 76.7 | 824 | 17 | US-10-456-573-12     | Sequence 12, Appl  |
| 129 | 13.8 | 76.7 | 294     | 18 | US-10-437-963-49607  | Sequence 49607, A  | c 202 | 13.8 | 76.7 | 824 | 18 | US-10-785-116-12     | Sequence 12, Appl  |
| 130 | 13.8 | 76.7 | 318     | 18 | US-10-437-963-5115   | Sequence 5115, Ap  | c 203 | 13.8 | 76.7 | 830 | 18 | US-10-425-115-26868  | Sequence 26868, A  |
| 131 | 13.8 | 76.7 | 328     | 18 | US-10-425-115-160530 | Sequence 160530,   | c 204 | 13.8 | 76.7 | 834 | 15 | US-10-156-761-3300   | Sequence 3300, Ap  |
| 132 | 13.8 | 76.7 | 339     | 17 | US-10-335-977-3847   | Sequence 3847, Ap  | c 205 | 13.8 | 76.7 | 835 | 18 | US-10-437-963-55487  | Sequence 55487, A  |
| 133 | 13.8 | 76.7 | 344     | 17 | US-10-242-535A-43458 | Sequence 43458, A  | c 206 | 13.8 | 76.7 | 855 | 17 | US-10-425-114-4342   | Sequence 4342, Ap  |
| 134 | 13.8 | 76.7 | 344     | 17 | US-10-085-783A-43458 | Sequence 43458, A  | c 207 | 13.8 | 76.7 | 882 | 18 | US-10-437-963-48660  | Sequence 48660, A  |
| 135 | 13.8 | 76.7 | 355     | 18 | US-10-425-115-5212   | Sequence 5212, Ap  | c 208 | 13.8 | 76.7 | 912 | 18 | US-10-425-115-183238 | Sequence 183238,   |
| 136 | 13.8 | 76.7 | 401     | 17 | US-10-424-599-113936 | Sequence 113936,   | c 209 | 13.8 | 76.7 | 973 | 17 | US-10-425-114-12904  | Sequence 12904, A  |
| 137 | 13.8 | 76.7 | 406     | 11 | US-09-987-899-203    | Sequence 203, App  | c 210 | 13.8 | 76.7 | 974 | 17 | US-10-425-114-21001  | Sequence 21001, A  |
| 138 | 13.8 | 76.7 | 412     | 18 | US-10-425-115-103241 | Sequence 103241,   | c 211 | 13.8 | 76.7 | 978 | 14 | US-10-227-884-51     | Sequence 51, Appl  |
| 139 | 13.8 | 76.7 | 420     | 18 | US-10-437-963-39913  | Sequence 39913, A  | c 212 | 13.8 | 76.7 | 978 | 14 | US-10-230-163-51     | Sequence 51, Appl  |
| 140 | 13.8 | 76.7 | 432     | 18 | US-10-425-115-14254  | Sequence 14254, A  | c 213 | 13.8 | 76.7 | 978 | 14 | US-10-230-338-51     | Sequence 51, Appl  |
| 141 | 13.8 | 76.7 | 466     | 10 | US-09-918-995-21738  | Sequence 21738, A  | c 214 | 13.8 | 76.7 | 978 | 14 | US-10-218-631-51     | Sequence 51, Appl  |
| 142 | 13.8 | 76.7 | 483     | 18 | US-10-425-115-56918  | Sequence 56918, A  | c 215 | 13.8 | 76.7 | 978 | 14 | US-10-232-224-51     | Sequence 51, Appl  |
| 143 | 13.8 | 76.7 | 484     | 18 | US-10-767-701-29695  | Sequence 29695, A  | c 216 | 13.8 | 76.7 | 978 | 14 | US-10-218-159A-51    | Sequence 51, Appl  |
| 144 | 13.8 | 76.7 | 512     | 18 | US-10-425-115-107490 | Sequence 107490,   | c 217 | 13.8 | 76.7 | 978 | 14 | US-10-218-849-51     | Sequence 51, Appl  |
| 145 | 13.8 | 76.7 | 524     | 18 | US-10-767-701-26211  | Sequence 26211, A  | c 218 | 13.8 | 76.7 | 978 | 14 | US-10-227-873-51     | Sequence 51, Appl  |
| 146 | 13.8 | 76.7 | 529     | 17 | US-10-437-963-46153  | Sequence 46153, A  | c 219 | 13.8 | 76.7 | 978 | 14 | US-10-227-883-51     | Sequence 51, Appl  |
| 147 | 13.8 | 76.7 | 531     | 17 | US-10-425-114-20853  | Sequence 20853, A  | c 220 | 13.8 | 76.7 | 978 | 14 | US-10-219-076-51     | Sequence 51, Appl  |
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| 149 | 13.8 | 76.7 | 554     | 17 | US-10-425-114-869    | Sequence 869, App  | c 222 | 13.8 | 76.7 | 978 | 14 | US-10-219-003-51     | Sequence 51, Appl  |
| 150 | 13.8 | 76.7 | 560     | 17 | US-10-424-599-130833 | Sequence 130833,   | c 223 | 13.8 | 76.7 | 978 | 14 | US-10-219-075-51     | Sequence 51, Appl  |
| 151 | 13.8 | 76.7 | 560     | 18 | US-10-767-701-19354  | Sequence 19354, A  | c 224 | 13.8 | 76.7 | 978 | 14 | US-10-219-464-51     | Sequence 51, Appl  |
| 152 | 13.8 | 76.7 | 583     | 18 | US-10-425-115-66546  | Sequence 66546, A  | c 225 | 13.8 | 76.7 | 978 | 14 | US-10-219-466-51     | Sequence 51, Appl  |
| 153 | 13.8 | 76.7 | 590     | 18 | US-10-425-115-11524  | Sequence 11524, A  | c 226 | 13.8 | 76.7 | 978 | 14 | US-10-219-479-51     | Sequence 51, Appl  |
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| C 231 | 13.8 | 76.7 | 978 | 14 | US-10-232-233-51 | Sequence 51, Appl | C 304 | 13.8 | 76.7 | 978  | 16 | US-10-219-531-51     | Sequence 51, Appl  |
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| C 235 | 13.8 | 76.7 | 978 | 14 | US-10-219-478-51 | Sequence 51, Appl | C 308 | 13.8 | 76.7 | 978  | 16 | US-10-232-228-51     | Sequence 51, Appl  |
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| C 240 | 13.8 | 76.7 | 978 | 14 | US-10-219-474-51 | Sequence 51, Appl | C 313 | 13.8 | 76.7 | 978  | 17 | US-10-119-480-51     | Sequence 51, Appl  |
| C 241 | 13.8 | 76.7 | 978 | 14 | US-10-219-524-51 | Sequence 51, Appl | C 314 | 13.8 | 76.7 | 978  | 18 | US-10-219-477-51     | Sequence 51, Appl  |
| C 242 | 13.8 | 76.7 | 978 | 14 | US-10-219-528-51 | Sequence 51, Appl | C 315 | 13.8 | 76.7 | 1040 | 18 | US-10-767-701-7401   | Sequence 7401, Ap  |
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| C 246 | 13.8 | 76.7 | 978 | 14 | US-10-230-436-51 | Sequence 51, Appl | C 319 | 13.8 | 76.7 | 1108 | 17 | US-10-424-599-65473  | Sequence 65473, A  |
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| C 248 | 13.8 | 76.7 | 978 | 14 | US-10-232-225-51 | Sequence 51, Appl | C 321 | 13.8 | 76.7 | 1250 | 17 | US-10-425-114-26729  | Sequence 26729, A  |
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| C 250 | 13.8 | 76.7 | 978 | 14 | US-10-232-229-51 | Sequence 51, Appl | C 323 | 13.8 | 76.7 | 1281 | 17 | US-10-369-493-23719  | Sequence 23719, A  |
| C 251 | 13.8 | 76.7 | 978 | 14 | US-10-232-234-51 | Sequence 51, Appl | C 324 | 13.8 | 76.7 | 1326 | 17 | US-10-425-114-8828   | Sequence 8828, Ap  |
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| C 253 | 13.8 | 76.7 | 978 | 15 | US-10-216-160-51 | Sequence 51, Appl | C 326 | 13.8 | 76.7 | 1386 | 18 | US-10-437-963-62155  | Sequence 62155, A  |
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| C 255 | 13.8 | 76.7 | 978 | 15 | US-10-216-164-51 | Sequence 51, Appl | C 328 | 13.8 | 76.7 | 1391 | 17 | US-10-425-114-20914  | Sequence 20914, A  |
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| C 258 | 13.8 | 76.7 | 978 | 15 | US-10-219-071-51 | Sequence 51, Appl | C 331 | 13.8 | 76.7 | 1472 | 17 | US-10-424-599-10250  | Sequence 10250, A  |
| C 259 | 13.8 | 76.7 | 978 | 15 | US-10-219-074-51 | Sequence 51, Appl | C 332 | 13.8 | 76.7 | 1485 | 18 | US-10-425-115-184438 | Sequence 184438, A |
| C 260 | 13.8 | 76.7 | 978 | 15 | US-10-219-473-51 | Sequence 51, Appl | C 333 | 13.8 | 76.7 | 1500 | 17 | US-10-424-599-65086  | Sequence 65086, A  |
| C 261 | 13.8 | 76.7 | 978 | 15 | US-10-219-077-51 | Sequence 51, Appl | C 334 | 13.8 | 76.7 | 1500 | 17 | US-10-425-114-6300   | Sequence 6300, Ap  |
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| C 266 | 13.8 | 76.7 | 978 | 15 | US-10-219-473-51 | Sequence 51, Appl | C 339 | 13.8 | 76.7 | 1641 | 18 | US-10-437-963-88974  | Sequence 88974, A  |
| C 267 | 13.8 | 76.7 | 978 | 15 | US-10-219-476-51 | Sequence 51, Appl | C 340 | 13.8 | 76.7 | 1641 | 18 | US-10-437-963-88978  | Sequence 88978, A  |
| C 268 | 13.8 | 76.7 | 978 | 15 | US-10-219-482-51 | Sequence 51, Appl | C 341 | 13.8 | 76.7 | 1652 | 18 | US-10-425-115-26873  | Sequence 26873, A  |
| C 269 | 13.8 | 76.7 | 978 | 15 | US-10-227-874-51 | Sequence 51, Appl | C 342 | 13.8 | 76.7 | 1674 | 18 | US-10-425-115-78655  | Sequence 78655, A  |
| C 270 | 13.8 | 76.7 | 978 | 15 | US-10-227-876-51 | Sequence 51, Appl | C 343 | 13.8 | 76.7 | 1693 | 18 | US-10-739-930-4348   | Sequence 4348, Ap  |
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| C 281 | 13.8 | 76.7 | 978 | 15 | US-10-230-435-51 | Sequence 51, Appl | C 354 | 13.8 | 76.7 | 2205 | 18 | US-10-425-115-78651  | Sequence 78651, A  |
| C 282 | 13.8 | 76.7 | 978 | 15 | US-10-230-438-51 | Sequence 51, Appl | C 355 | 13.8 | 76.7 | 2291 | 17 | US-10-094-749-379    | Sequence 379, App  |
| C 283 | 13.8 | 76.7 | 978 | 15 | US-10-232-222-51 | Sequence 51, Appl | C 356 | 13.8 | 76.7 | 2298 | 17 | US-10-369-493-36489  | Sequence 36489, A  |
| C 284 | 13.8 | 76.7 | 978 | 15 | US-10-219-070-51 | Sequence 51, Appl | C 357 | 13.8 | 76.7 | 2304 | 17 | US-10-369-493-26433  | Sequence 26433, A  |
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| C 286 | 13.8 | 76.7 | 978 | 15 | US-10-219-527-51 | Sequence 51, Appl | C 359 | 13.8 | 76.7 | 2396 | 9  | US-09-776-874A-43    | Sequence 43, Appl  |
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| C 289 | 13.8 | 76.7 | 978 | 15 | US-10-218-612-51 | Sequence 51, Appl | C 362 | 13.8 | 76.7 | 2396 | 9  | US-09-988-113-45     | Sequence 45, Appl  |
| C 290 | 13.8 | 76.7 | 978 | 15 | US-10-216-163-51 | Sequence 51, Appl | C 363 | 13.8 | 76.7 | 2396 | 16 | US-10-341-582-43     | Sequence 43, Appl  |
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| C 292 | 13.8 | 76.7 | 978 | 16 | US-10-219-063-51 | Sequence 51, Appl | C 365 | 13.8 | 76.7 | 2396 | 16 | US-10-384-451-43     | Sequence 43, Appl  |
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| C 294 | 13.8 | 76.7 | 978 | 16 | US-10-219-067-51 | Sequence 51, Appl | C 367 | 13.8 | 76.7 | 2396 | 16 | US-10-384-450-43     | Sequence 43, Appl  |
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| C 298 | 13.8 | 76.7 | 978 | 16 | US-10-219-475-51 | Sequence 51, Appl | C 371 | 13.8 | 76.7 | 2396 | 17 | US-10-456-573-43     | Sequence 43, Appl  |
| C 299 | 13.8 | 76.7 | 978 | 16 | US-10-219-480-51 | Sequence 51, Appl | C 372 | 13.8 | 76.7 | 2396 | 17 | US-10-456-573-45     | Sequence 45, Appl  |
| C 300 | 13.8 | 76.7 | 978 | 16 | US-10-219-483-51 | Sequence 51, Appl | C 373 | 13.8 | 76.7 | 2396 | 18 | US-10-785-116-43     | Sequence 43, Appl  |
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| C 303 | 13.8 | 76.7 | 978 | 16 | US-10-219-530-51 | Sequence 51, Appl | C 376 | 13.8 | 76.7 | 2472 | 17 | US-10-425-114-24839  | Sequence 24839, A  |





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; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 64
; LENGTH: 18
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-64

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Db 1 CGCCACCGGAGTTGAGT 18

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RESULT 2
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; Sequence 66, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
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; SEQ ID NO 66
; LENGTH: 19
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-66

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QY 1 CGCCACCGGAGTTGAGT 18
Db 1 CGCCACCGGAGTTGAGT 18

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RESULT 3
US-10-688-489-62
; Sequence 62, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489

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; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
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; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-62

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Db 3 CGCCACCGGAGTTGAGT 20

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RESULT 4
US-10-688-489-63
; Sequence 63, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
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; SEQ ID NO 63
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-63

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Db 3 CGCCACCGGAGTTGAGT 20

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RESULT 5
US-10-688-489-59
; Sequence 59, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting

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; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
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; PRIOR FILING DATE: 2003-02-24
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; ORGANISM: West Nile Virus
US-10-688-489-59

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 CGCCACCGGAAGTTGAGT 20
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RESULT 6
US-10-361-002-5
; Sequence 5, Application US/10361002
; Publication No. US20040170954A1
; GENERAL INFORMATION:
; APPLICANT: Clearant, Inc.
; APPLICANT: McKenney, Keith
; APPLICANT: Gilmeister, Lidja
; APPLICANT: Marlowe, Kristina
; APPLICANT: Armistead, David
; TITLE OF INVENTION: Pathogen Inactivation Assay
; FILE REFERENCE: CI-0043
; CURRENT APPLICATION NUMBER: US/10/361,002
; CURRENT FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 10945
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-361-002-5

Query Match      100.0%; Score 18; DB 18; Length 10945;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
   |||||
Db 10482 CGCCACCGGAAGTTGAGT 10499
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RESULT 7
US-10-361-004-5
; Sequence 5, Application US/10361004
; Publication No. US20040170981A1
; GENERAL INFORMATION:
; APPLICANT: Clearant, Inc.
; APPLICANT: McKenney, Keith
; APPLICANT: Gilmeister, Lidja
; APPLICANT: Marlowe, Kristina
; APPLICANT: Armistead, David
; TITLE OF INVENTION: Real-time Polymerase Chain Reaction Using Large Target Amplicons
; FILE REFERENCE: CI-0042
; CURRENT APPLICATION NUMBER: US/10/361,004
; CURRENT FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 99
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 10945
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-361-004-5

Query Match      100.0%; Score 18; DB 18; Length 10945;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
   |||||
Db 10482 CGCCACCGGAAGTTGAGT 10499
   |||||

RESULT 8
US-10-699-550-1
; Sequence 1, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1
; LENGTH: 10975
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-699-550-1

Query Match      100.0%; Score 18; DB 18; Length 10975;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
   |||||
Db 10506 CGCCACCGGAAGTTGAGT 10523
   |||||

RESULT 9
US-10-699-550-2
; Sequence 2, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
```

; PRIOR APPLICATION NUMBER: 60/402,860  
; PRIOR FILING DATE: 2002-08-08  
; PRIOR APPLICATION NUMBER: 60/281,947  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/275,025  
; PRIOR FILING DATE: 2001-03-12  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 2  
; LENGTH: 11029  
; TYPE: DNA  
; ORGANISM: West Nile virus  
US-10-699-550-2

Query Match 100.0%; Score 18; DB 18; Length 11029;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18  
|||  
DB 10524 CGCCACCGGAAGTTGAGT 10541

RESULT 10  
US-10-679-520A-66  
; Sequence 66, Application US/10679520A  
; Publication No. US20050031641A1  
; GENERAL INFORMATION:  
; APPLICANT: LOOSMORE, SHEENA MAY  
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE FRANCIS  
; APPLICANT: MINKS, JULES MAARTEN  
; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS  
; FILE REFERENCE: 574313-3161.4  
; CURRENT APPLICATION NUMBER: US/10/679,520A  
; CURRENT FILING DATE: 2003-10-06  
; PRIOR APPLICATION NUMBER: 10/374,953  
; PRIOR FILING DATE: 2003-02-26  
; PRIOR APPLICATION NUMBER: 10/116,298  
; PRIOR FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: 60/281,923  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: PCT/FR02/01200  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: FR 01/04737  
; PRIOR FILING DATE: 2001-04-06  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 66  
; LENGTH: 11029  
; TYPE: DNA  
; ORGANISM: West Nile virus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (97)..(10395)  
US-10-679-520A-66

Query Match 100.0%; Score 18; DB 19; Length 11029;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18  
|||  
DB 10524 CGCCACCGGAAGTTGAGT 10541

RESULT 11  
US-10-706-892-1  
; Sequence 1, Application US/10706892  
; Publication No. US20050058987A1  
; GENERAL INFORMATION:  
; APPLICANT: SHI, PEI-YONG  
; TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY  
; FILE REFERENCE: 454311-2231.1

; CURRENT APPLICATION NUMBER: US/10/706,892  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/427,117  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 11029  
; TYPE: DNA  
; ORGANISM: West Nile virus  
US-10-706-892-1

Query Match 100.0%; Score 18; DB 19; Length 11029;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18  
|||  
DB 10524 CGCCACCGGAAGTTGAGT 10541

RESULT 12  
US-10-706-892-2  
; Sequence 2, Application US/10706892  
; Publication No. US20050058987A1  
; GENERAL INFORMATION:  
; APPLICANT: SHI, PEI-YONG  
; TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY  
; FILE REFERENCE: 454311-2231.1  
; CURRENT APPLICATION NUMBER: US/10/706,892  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/427,117  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 2  
; LENGTH: 11029  
; TYPE: DNA  
; ORGANISM: West Nile virus  
US-10-706-892-2

Query Match 100.0%; Score 18; DB 19; Length 11029;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18  
|||  
DB 10524 CGCCACCGGAAGTTGAGT 10541

RESULT 13  
US-10-688-489-65  
; Sequence 65, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linmen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GP140-04.UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0

```
; SEQ ID NO 65
; LENGTH: 18
; TYPE: DNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)...(1)
; OTHER INFORMATION: I
US-10-688-489-65
```

```
Query Match          94.4%; Score 17; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 GCCACCGGAAGTTGAGT 18
    |||||
Db 2 GCCACCGGAAGTTGAGT 18
```

```
RESULT 14
US-10-688-489-60
; Sequence 60, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 19
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-60
```

```
Query Match          94.4%; Score 17; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CGCCACCGGAAGTTGAGT 17
    |||||
Db 3 CGCCACCGGAAGTTGAGT 19
```

```
RESULT 15
US-10-688-489-61
; Sequence 61, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
```

```
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 19
; TYPE: DNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)...(1)
; OTHER INFORMATION: I
US-10-688-489-61
```

```
Query Match          94.4%; Score 17; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CGCCACCGGAAGTTGAGT 17
    |||||
Db 3 CGCCACCGGAAGTTGAGT 19
```

```
RESULT 16
US-10-719-900-668130/c
; Sequence 668130, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 668130
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-668130
```

```
Query Match          91.1%; Score 16.4; DB 19; Length 25;
Best Local Similarity 94.4%; Pred. No. 57;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 CGCCACCGGAAGTTGAGT 18
    |||||
Db 20 CGCCACCGGAAGTTGAGT 3
```

```
RESULT 17
US-10-481-265-136/c
; Sequence 136, Application US/10481265
; Publication No. US20040254349A1
; GENERAL INFORMATION:
; APPLICANT: James, Brian William
; APPLICANT: Bacon, Joanna
; APPLICANT: Marsh, Philip
; TITLE OF INVENTION: Mycobacterial Antigens Expressed Under Low Oxygen Tension
; FILE REFERENCE: 1581.1020000
; CURRENT APPLICATION NUMBER: US/10/481,265
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: GB 0115365.9
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: GB 0121780.1
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: PCT/GB02/02845
; PRIOR FILING DATE: 2002-06-21
```

; NUMBER OF SEQ ID NOS: 138  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 136  
; LENGTH: 1323  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
US-10-481-263-136

Query Match 88.9%; Score 16; DB 18; Length 1323;

Best Local Similarity 100.0%; Pred. No. 96;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17

DB 1037 GCCACCGGAAGTTGAG 1022

#### RESULT 18

US-09-712-363-49/c

; Sequence 49, Application US/09712363  
; Patent No. US20020164588A1

; GENERAL INFORMATION:

; APPLICANT: Eisenberg, David

; APPLICANT: Rotstein, Sergio H.

; APPLICANT: Marcotte, Edward M.

; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND

; INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS

; FILE REFERENCE: 07419-032001

; CURRENT APPLICATION NUMBER: US/09/712,363

; CURRENT FILING DATE: 2000-11-13

; PRIOR APPLICATION NUMBER: PCT/US00/02246

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: 60/179,531

; PRIOR FILING DATE: 2000-02-01

; PRIOR APPLICATION NUMBER: 60/117,844

; PRIOR FILING DATE: 1999-01-29

; PRIOR APPLICATION NUMBER: 60/118,206,

; PRIOR FILING DATE: 1999-02-01

; PRIOR APPLICATION NUMBER: 60/126,593

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 60/134,093

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: 60/134,092

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: 60/165,124

; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: 60/165,086

; PRIOR FILING DATE: 1999-11-12

; NUMBER OF SEQ ID NOS: 292

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 49

; LENGTH: 1326

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

US-09-712-363-49

Query Match 88.9%; Score 16; DB 9; Length 1326;

Best Local Similarity 100.0%; Pred. No. 96;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17

DB 1037 GCCACCGGAAGTTGAG 1022

#### RESULT 19

US-10-027-632-299210/c

; Sequence 299210, Application US/10027632

; Publication No. US20020198371A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; POLYMORPHISMS IN THE HUMAN GENOME

; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 299210  
; LENGTH: 631  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-299210

Query Match 85.6%; Score 15.4; DB 13; Length 631;

Best Local Similarity 94.1%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18

DB 520 GCCACCGGAAGTTGAGT 504

#### RESULT 20

US-10-027-632-299210/c

; Sequence 299210, Application US/10027632

; Publication No. US20030204075A9

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; POLYMORPHISMS IN THE HUMAN GENOME

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 299210

; LENGTH: 631

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-299210

Query Match 85.6%; Score 15.4; DB 17; Length 631;

Best Local Similarity 94.1%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18

DB 520 GCCACCGGAAGTTGAGT 504

Db 520 GCCAACGGAAGTTGAGT 504

## RESULT 21

US-10-027-632-44859/c  
; Sequence 44859, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 44859  
; LENGTH: 669  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-44859

Query Match 85.6%; Score 15.4; DB 13; Length 669;  
Best Local Similarity 94.1%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18  
|||||  
Db 504 GCCAACGGAAGTTGAGT 488

## RESULT 22

US-10-027-632-44859/c  
; Sequence 44859, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 44859

; LENGTH: 669  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-44859

Query Match 85.6%; Score 15.4; DB 17; Length 669;  
Best Local Similarity 94.1%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18  
|||||  
Db 504 GCCAACGGAAGTTGAGT 488

## RESULT 23

US-10-767-701-11247/c  
; Sequence 11247, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 11247  
; LENGTH: 793  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS19479\_1  
US-10-767-701-11247

Query Match 85.6%; Score 15.4; DB 18; Length 793;  
Best Local Similarity 94.1%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17  
|||||  
Db 326 CGCCCGCGGAAGTTGAG 310

## RESULT 24

US-10-425-115-119320/c  
; Sequence 119320, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 119320  
; LENGTH: 1989  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_40302C.1  
US-10-425-115-119320

Query Match 85.6%; Score 15.4; DB 18; Length 1989;  
Best Local Similarity 94.1%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17

```
||||| ||||||| |||||||
Db 1470 CGCCCCCGGAAGTTGAG 1454

RESULT 25
US-10-425-115-119315/c
; Sequence 119315, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 119315
; LENGTH: 2358
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_40299C.1
US-10-425-115-119315

Query Match 85.6%; Score 15.4; DB 18; Length 2358;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
||||| ||||||| |||||||
Db 1874 CGCCCCCGGAAGTTGAG 1858

RESULT 26
US-10-600-230-69
; Sequence 69, Application US/10600230
; Publication No. US20040092020A1
; GENERAL INFORMATION:
; APPLICANT: Wilkinson, Jack
; APPLICANT: McBride, Kevin
; APPLICANT: Bertain, Sean
; TITLE OF INVENTION: GENETIC CONSTRUCTS HAVING HETEROLOGOUS
; FILE REFERENCE: 0325.210
; CURRENT APPLICATION NUMBER: US/10/600,230
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: 60/390,529
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 2878
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-600-230-69

Query Match 85.6%; Score 15.4; DB 17; Length 2878;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
||||| ||||||| |||||||
Db 727 CGCCACCGGAAGTCGAG 743

RESULT 27
US-10-719-993-7004/c
; Sequence 7004, Application US/10719993
; Publication No. US20040265849A1

; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7004
; LENGTH: 14416
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-7004

Query Match 85.6%; Score 15.4; DB 18; Length 14416;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18
||||| ||||||| |||||||
Db 10352 GCCACCGGAAGTTGAGT 10336

RESULT 28
US-10-322-281-208
; Sequence 208, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 64721
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(64721)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-208

Query Match 85.6%; Score 15.4; DB 18; Length 64721;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18
||||| ||||||| |||||||
Db 68 GCCACCGGAAGTTGAGT 84

RESULT 29
US-10-812-232-6
; Sequence 6, Application US/10812232
; Publication No. US20040265961A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Wei
; APPLICANT: Wu, Leeying
; APPLICANT: Channavajhala, Padma L,
; APPLICANT: Lin, Lih-ling
; APPLICANT: Zhang, Yunhua
; TITLE OF INVENTION: Novel Proteins Homologous to Kinase Suppressor of Ras
; FILE REFERENCE: 01997.026700
; CURRENT APPLICATION NUMBER: US/10/812,232
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/457,928
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/491,283
```

```
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 263852
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3814)..(4319)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6552)..(6571)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17206)..(17225)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19680)..(19699)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (24320)..(24339)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (26572)..(26591)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (32986)..(33005)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (56103)..(56724)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (59672)..(59691)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (61525)..(61544)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (71035)..(71054)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (79771)..(79807)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (91343)..(91801)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (141749)..(141768)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (144739)..(144758)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (164171)..(164340)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature-
```

```
; LOCATION: (173689)..(173708)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (175051)..(175070)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (192924)..(192993)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (202010)..(202029)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (247837)..(247856)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (251852)..(252421)
; OTHER INFORMATION: n is a, c, g, or t
US-10-812-232-6
```

```
Query Match 85.6%; Score 15.4; DB 18; Length 263852;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Oy 2 GCCACCGGAAGTTGAGT 18

Db 208679 GCCACCTGAAGTTGAGT 208695

## RESULT 30

```
US-10-719-993-6822
; Sequence 6822, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; NUMBER OF SEQ ID NOS: 5342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6822
; LENGTH: 786452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(786452)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-719-993-6822
```

```
Query Match 85.6%; Score 15.4; DB 18; Length 786452;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Oy 2 GCCACCGGAAGTTGAGT 18

Db 503852 GCCACCTGAAGTTGAGT 503868

## RESULT 31

```
US-10-098-263B-27587
; Sequence 27587, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
```



; CURRENT APPLICATION NUMBER: US/10/098,263B  
 ; CURRENT FILING DATE: 2003-01-08  
 ; PRIOR APPLICATION NUMBER: 60/276,759  
 ; PRIOR FILING DATE: 2001-03-16  
 ; NUMBER OF SEQ ID NOS: 131066  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 27587  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-098-263B-27587

Query Match 83.3%; Score 15; DB 15; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACCGGAAGTTGAGT 18  
 |||||  
 Db 2 CACCGGAAGTTGAGT 16  
 |||||

RESULT 32  
 US-10-425-115-139988/c  
 ; Sequence 139988, Application US/10425115  
 ; Publication No. US20040214272A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; FILE REFERENCE: 38-21(53222)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,115  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 369326  
 ; SEQ ID NO 139988  
 ; LENGTH: 351  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: MRT4577\_59153C.1  
 US-10-425-115-139988

Query Match 83.3%; Score 15; DB 18; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CACCGGAAGTTGAG 17  
 |||||  
 Db 268 CACCGGAAGTTGAG 254  
 |||||

RESULT 33  
 US-10-767-701-25132/c  
 ; Sequence 25132, Application US/10767701  
 ; Publication No. US20040172684A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; FILE REFERENCE: 38-21(53535)B  
 ; CURRENT APPLICATION NUMBER: US/10/767,701  
 ; CURRENT FILING DATE: 2004-01-29  
 ; NUMBER OF SEQ ID NOS: 63128  
 ; SEQ ID NO 25132  
 ; LENGTH: 685  
 ; TYPE: DNA  
 ; ORGANISM: Sorghum bicolor  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: 30947447

US-10-767-701-25132

Query Match 83.3%; Score 15; DB 18; Length 685;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAG 17  
 |||||  
 Db 250 CCACCGGAAGTTGAG 236  
 |||||

RESULT 34  
 US-09-738-626-437/c  
 ; Sequence 437, Application US/09738626  
 ; Publication No. US20020197605A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NAKAGAWA, SATOSHI  
 ; APPLICANT: MIZOGUCHI, HIROSHI  
 ; APPLICANT: ANDO, SEIKO  
 ; APPLICANT: HAYASHI, MIKIRO  
 ; APPLICANT: OCHIAI, KEIKO  
 ; APPLICANT: YOKOI, HARUHIKO  
 ; APPLICANT: TATEISHI, NAKO  
 ; APPLICANT: SENOH, AKIHIRO  
 ; APPLICANT: IKEDA, MASATO  
 ; APPLICANT: OZAKI, AKIO  
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 ; FILE REFERENCE: 249-125  
 ; CURRENT APPLICATION NUMBER: US/09/738,626  
 ; CURRENT FILING DATE: 2000-12-18  
 ; PRIOR APPLICATION NUMBER: JP 99/377484  
 ; PRIOR FILING DATE: 1999-12-16  
 ; PRIOR APPLICATION NUMBER: JP 00/159162  
 ; PRIOR FILING DATE: 2000-04-07  
 ; PRIOR APPLICATION NUMBER: JP 00/280988  
 ; PRIOR FILING DATE: 2000-08-03  
 ; NUMBER OF SEQ ID NOS: 7059  
 ; SOFTWARE: PatentIn ver. 3.0  
 ; SEQ ID NO 437  
 ; LENGTH: 1863  
 ; TYPE: DNA  
 ; ORGANISM: Corynebacterium glutamicum  
 US-09-738-626-437

Query Match 83.3%; Score 15; DB 9; Length 1863;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAG 17  
 |||||  
 Db 734 CCACCGGAAGTTGAG 720  
 |||||

RESULT 35  
 US-10-494-672-341/c  
 ; Sequence 341, Application US/10494672  
 ; Publication No. US20050003494A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zelder, Oskar  
 ; APPLICANT: Pompejus, Markus  
 ; APPLICANT: Schroder, Hartwig  
 ; APPLICANT: Kroger, Burkhard  
 ; APPLICANT: Kloppe, Corinna  
 ; APPLICANT: Haberhauser, Gregor  
 ; TITLE OF INVENTION: Genes coding for novel proteins  
 ; FILE REFERENCE: BGI-169US  
 ; CURRENT APPLICATION NUMBER: US/10/494,672  
 ; CURRENT FILING DATE: 2004-05-04  
 ; PRIOR APPLICATION NUMBER: PCT/EP02/12134  
 ; PRIOR FILING DATE: 2002-10-31  
 ; PRIOR APPLICATION NUMBER: DE 10154177  
 ; PRIOR FILING DATE: 2001-11-05  
 ; NUMBER OF SEQ ID NOS: 434



```
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70594C.1
US-10-437-963-69977

Query Match      82.2%; Score 14.8; DB 18; Length 447;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
    |||||
Db 258 CGCCGCCCGAAGTTGAGT 241

RESULT 40
US-10-767-701-4048/c
; Sequence 4048, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 4048
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS7084_1
US-10-767-701-4048

Query Match      82.2%; Score 14.8; DB 18; Length 590;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
    |||||
Db 146 CGCCACCGGTAGTGAGT 129

RESULT 41
US-10-357-930-23087/c
; Sequence 23087, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28954
; LENGTH: 872
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 2, 3, 866, 867, 868, 869, 870, 871, 872
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-28954

Query Match      82.2%; Score 14.8; DB 18; Length 872;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
    |||||
Db 236 CGCCACCGGAAGTTGAGT 219

RESULT 42
US-10-357-930-28954/c
; Sequence 28954, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28954
; LENGTH: 872
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 2, 3, 866, 867, 868, 869, 870, 871, 872
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-28954

Query Match      82.2%; Score 14.8; DB 18; Length 872;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
    |||||
Db 236 CGCCACCGGAAGTTGAGT 219

RESULT 43
US-09-938-842A-1526/c
; Sequence 1526, Application US/09938842A
```

```
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1526
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1526
```

```
Query Match 82.2%; Score 14.8; DB 9; Length 945;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 CGCCACCGGAGTTGAGT 18
Db 770 CGCCACCGTGGTTGAGT 753
```

```
RESULT 44
US-09-938-842A-1526/c
; Sequence 1526, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1526
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1526
```

```
Query Match 82.2%; Score 14.8; DB 11; Length 945;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 CGCCACCGGAGTTGAGT 18
Db 770 CGCCACCGTGGTTGAGT 753
```

```
RESULT 45
US-09-956-004-27/c
; Sequence 27, Application US/09956004
; Patent No. US20020072595A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Patrick J. Dillon et al.
; TITLE OF INVENTION: Nucleotide Sequences of Escherichia coli Pathogenicity Islands
; FILE REFERENCE: PB324D1
; CURRENT APPLICATION NUMBER: US/09/956,004
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 08/976,259
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/061,953
; PRIOR FILING DATE: 1997-10-14
; PRIOR APPLICATION NUMBER: 60/031,626
; PRIOR FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 1118
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (142)..(142)
; OTHER INFORMATION: n equals a, t, g, or c
; NAME/KEY: misc feature
; LOCATION: (228)..(228)
; OTHER INFORMATION: n equals a, t, g, or c
; NAME/KEY: misc feature
; LOCATION: (261)..(261)
; OTHER INFORMATION: n equals a, t, g, or c
; NAME/KEY: misc feature
; LOCATION: (693)..(693)
; OTHER INFORMATION: n equals a, t, g, or c
US-09-956-004-27
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Query Match 82.2%; Score 14.8; DB 9; Length 1118;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CGCCACCGGAGTTGAGT 18
Db 1054 CGCCACGAGGTTGAGT 1037
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RESULT 46
US-10-808-570-27/c
; Sequence 27, Application US/10808570
; Publication No. US20040192903A1
; GENERAL INFORMATION:
; APPLICANT: Patrick J. Dillon et al.
; TITLE OF INVENTION: Nucleotide Sequences of Escherichia coli Pathogenicity Islands
; FILE REFERENCE: PB324D1
; CURRENT APPLICATION NUMBER: US/10/808,570
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/956,004
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 08/976,259
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/061,953
; PRIOR FILING DATE: 1997-10-14
; PRIOR APPLICATION NUMBER: 60/031,626
; PRIOR FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 1118
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (142)..(142)
; OTHER INFORMATION: n equals a, t, g, or c
; NAME/KEY: misc feature
; LOCATION: (228)..(228)
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OTHER INFORMATION: n equals a, t, g, or c  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (261)..(261)  
OTHER INFORMATION: n equals a, t, g, or c  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (693)..(693)  
OTHER INFORMATION: n equals a, t, g, or c  
US-10-808-570-27

Query Match 82.2%; Score 14.8; DB 18; Length 1118;  
Best Local Similarity 88.9%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTTGAGT 18

DB 1054 CGCCACGAGGTTTGAGT 1037

## RESULT 47

US-09-738-626-3346/c

Sequence 3346, Application US/09738626

Publication No. US20020197605A1

GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI

APPLICANT: MIZOGUCHI, HIROSHI

APPLICANT: ANDO, SEIKO

APPLICANT: HAYASHI, MIKIRO

APPLICANT: OCHIAI, KEIKO

APPLICANT: YOKOI, HARUHIKO

APPLICANT: TATEISHI, NAKO

APPLICANT: SENOH, AKIHIRO

APPLICANT: IKEDA, MASATO

APPLICANT: OZAKI, AKIO

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-125

CURRENT APPLICATION NUMBER: US/09/738,626

PRIOR FILING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: JP 99/377484

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: JP 00/159162

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: JP 00/280988

PRIOR FILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 7059

SOFTWARE: PatentIn ver. 3.0

SEQ ID NO 3346

LENGTH: 1125

TYPE: DNA

ORGANISM: Corynebacterium glutamicum

US-09-738-626-3346

Query Match 82.2%; Score 14.8; DB 9; Length 1125;  
Best Local Similarity 88.9%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTTGAGT 18

DB 838 CGCCACCGGAGTTGGGT 821

## RESULT 48

US-10-282-122A-6914/c

Sequence 6914, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6914

LENGTH: 1149

TYPE: DNA

ORGANISM: Escherichia coli

US-10-282-122A-6914

Query Match 82.2%; Score 14.8; DB 17; Length 1149;  
Best Local Similarity 88.9%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTTGAGT 18

DB 1107 CGGCACCGGAGATGAGT 1090

## RESULT 49

US-10-282-122A-7527

Sequence 7527, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/230,335  
 ; PRIOR FILING DATE: 2000-09-06  
 ; PRIOR APPLICATION NUMBER: 60/230,347  
 ; PRIOR FILING DATE: 2000-09-09  
 ; PRIOR APPLICATION NUMBER: 60/242,578  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: 60/253,625  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/257,931  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: 60/267,636  
 ; PRIOR FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: 60/269,308  
 ; PRIOR FILING DATE: 2001-02-16  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 78614  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 7527  
 ; LENGTH: 1479  
 ; TYPE: DNA  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-10-282-122A-7527

Query Match 82.2%; Score 14.8; DB 17; Length 1479;  
 Best Local Similarity 88.9%; Pred. No. 4.4e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18  
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 DB 1184 CGCCACCGGAGCGGAGT 1201

RESULT 50  
 US-09-738-626-2696/c  
 ; Sequence 2696, Application US/09738626  
 ; Publication No. US20020197605A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NAKAGAWA, SATOSHI  
 ; APPLICANT: MIZOGUCHI, HIROSHI  
 ; APPLICANT: ANDO, SEIKO  
 ; APPLICANT: HAYASHI, MIKIRO  
 ; APPLICANT: OCHIAI, KEIKO  
 ; APPLICANT: YOKOI, HARUHIKO  
 ; APPLICANT: TATEISHI, NAOKO  
 ; APPLICANT: SENOH, AKIHIRO  
 ; APPLICANT: IKEDA, MASATO  
 ; APPLICANT: OZAKI, AKIO  
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 ; FILE REFERENCE: 249-125  
 ; CURRENT APPLICATION NUMBER: US/09/738,626  
 ; CURRENT FILING DATE: 2000-12-18  
 ; PRIOR APPLICATION NUMBER: JP 99/377484  
 ; PRIOR FILING DATE: 1999-12-16  
 ; PRIOR APPLICATION NUMBER: JP 00/159162  
 ; PRIOR FILING DATE: 2000-04-07  
 ; PRIOR APPLICATION NUMBER: JP 00/280988  
 ; PRIOR FILING DATE: 2000-08-03  
 ; NUMBER OF SEQ ID NOS: 7059  
 ; SOFTWARE: PatentIn ver. 3.0  
 ; SEQ ID NO 2696  
 ; LENGTH: 2103  
 ; TYPE: DNA  
 ; ORGANISM: Corynebacterium glutamicum  
 US-09-738-626-2696

Query Match 82.2%; Score 14.8; DB 9; Length 2103;  
 Best Local Similarity 88.9%; Pred. No. 4.4e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18  
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Db 640 CGCCACCGGAGCTGAGT 623

Search completed: March 25, 2005, 14:02:52  
 Job time : 259.286 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 07:23:09 ; Search time 945.418 Seconds  
(without alignments)  
2460.130 Million cell updates/sec

Title: US-10-688-489-73

Perfect score: 48  
Sequence: 1 tcgcgagcgttcttgaggc.....atcacttcgagctttgttc 48

Scoring table: OLIGO NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : GenEmbl.\*

1: gb\_ba.\*

2: gb\_hhg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sta.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| C 1        | 48    | 100.0       | 463    | 14 | AF458344 West Nile |
| C 2        | 48    | 100.0       | 463    | 14 | AF458347 West Nile |
| C 3        | 48    | 100.0       | 463    | 14 | AF458355 West Nile |
| C 4        | 48    | 100.0       | 542    | 14 | AF297854 Kunjin vi |
| C 5        | 48    | 100.0       | 587    | 14 | KUNNS5GAA          |
| C 6        | 48    | 100.0       | 587    | 14 | KUNNS5GAB          |
| C 7        | 48    | 100.0       | 601    | 14 | AF297844 Kunjin vi |
| C 8        | 48    | 100.0       | 607    | 14 | AF297841 Kunjin vi |
| C 9        | 48    | 100.0       | 616    | 14 | AF297845 Kunjin vi |
| C 10       | 48    | 100.0       | 620    | 14 | AF297859 Kunjin vi |
| C 11       | 48    | 100.0       | 622    | 14 | AF297842 Kunjin vi |
| C 12       | 48    | 100.0       | 623    | 14 | AF297843 Kunjin vi |
| C 13       | 48    | 100.0       | 627    | 14 | KUNNONCODB         |
| C 14       | 48    | 100.0       | 633    | 14 | AF297858 Kunjin vi |
| C 15       | 48    | 100.0       | 644    | 14 | AF297848 Kunjin vi |
| C 16       | 48    | 100.0       | 652    | 14 | AF297855 Kunjin vi |
| C 17       | 48    | 100.0       | 657    | 14 | AF297849 Kunjin vi |
| C 18       | 48    | 100.0       | 1524   | 14 | AF017254 West Nile |
| C 19       | 48    | 100.0       | 10664  | 14 | D00246 Kunjin vi   |

|          |           |       |       |          |
|----------|-----------|-------|-------|----------|
| AY274504 | Kunjin vi | 11022 | 14    | AY274504 |
| AY274505 | Kunjin vi | 11022 | 14    | AY274505 |
| AY490240 | West Nile | 11028 | 14    | AY490240 |
| AF260968 | West Nile | 11029 | 14    | AF260968 |
| AF458351 | Kunjin vi | 456   | 14    | AF458351 |
| AF297856 | Kunjin vi | 609   | 14    | AF297856 |
| AF458356 | Kunjin vi | 458   | 14    | AF458356 |
| AF297851 | Kunjin vi | 524   | 14    | AF297851 |
| AF297850 | Kunjin vi | 545   | 14    | AF297850 |
| AF297840 | Kunjin vi | 585   | 14    | AF297840 |
| AF297847 | Kunjin vi | 593   | 14    | AF297847 |
| AF297852 | Kunjin vi | 593   | 14    | AF297852 |
| AF297853 | Kunjin vi | 594   | 14    | AF297853 |
| AF297846 | Kunjin vi | 600   | 14    | AF297846 |
| AF458350 | West Nile | 462   | 14    | AF458350 |
| AF458348 | West Nile | 463   | 14    | AF458348 |
| AF458360 | West Nile | 463   | 14    | AF458360 |
| AF458361 | West Nile | 463   | 14    | AF458361 |
| AY590190 | West Nile | 79.2  | 464   | AY590190 |
| AY590191 | West Nile | 79.2  | 464   | AY590191 |
| AY590192 | West Nile | 79.2  | 464   | AY590192 |
| AY590193 | West Nile | 79.2  | 464   | AY590193 |
| AY590194 | West Nile | 79.2  | 464   | AY590194 |
| AY590195 | West Nile | 79.2  | 464   | AY590195 |
| AY590196 | West Nile | 79.2  | 464   | AY590196 |
| AY590197 | West Nile | 79.2  | 464   | AY590197 |
| AY590198 | West Nile | 79.2  | 464   | AY590198 |
| AY590199 | West Nile | 79.2  | 464   | AY590199 |
| AY590200 | West Nile | 79.2  | 464   | AY590200 |
| AY590201 | West Nile | 79.2  | 464   | AY590201 |
| AY590202 | West Nile | 79.2  | 464   | AY590202 |
| AY590203 | West Nile | 79.2  | 464   | AY590203 |
| AY590204 | West Nile | 79.2  | 464   | AY590204 |
| AY590205 | West Nile | 79.2  | 464   | AY590205 |
| AY590206 | West Nile | 79.2  | 464   | AY590206 |
| AY590207 | West Nile | 79.2  | 464   | AY590207 |
| AY590208 | West Nile | 79.2  | 464   | AY590208 |
| AY590209 | West Nile | 79.2  | 464   | AY590209 |
| AY187012 | West Nile | 645   | 14    | AY187012 |
| AY187014 | West Nile | 645   | 14    | AY187014 |
| AY187015 | West Nile | 645   | 14    | AY187015 |
| AF196536 | West Nile | 659   | 14    | AF196536 |
| AF196541 | West Nile | 669   | 14    | AF196541 |
| AF196542 | West Nile | 670   | 14    | AF196542 |
| AY278441 | West Nile | 10842 | 14    | AY278441 |
| AY277252 | West Nile | 10845 | 14    | AY277252 |
| AF202541 | West Nile | 10945 | 14    | AF202541 |
| AF317203 | West Nile | 10972 | 14    | AF317203 |
| AF206518 | West Nile | 10975 | 14    | AF206518 |
| AY262283 | West Nile | 10984 | 14    | AY262283 |
| AY268133 | West Nile | 10989 | 14    | AY268133 |
| AY278441 | West Nile | 10998 | 14    | AY278441 |
| AX576542 | Sequence  | 11029 | 6     | AX576542 |
| AX577796 | Sequence  | 11029 | 6     | AX577796 |
| AB185914 | West Nile | 11029 | 14    | AB185914 |
| AB185915 | West Nile | 11029 | 14    | AB185915 |
| AB185916 | West Nile | 11029 | 14    | AB185916 |
| AB185917 | West Nile | 11029 | 14    | AB185917 |
| AF196835 | West Nile | 11029 | 14    | AF196835 |
| AF260967 | West Nile | 79.2  | 11029 | AF260967 |
| AF260969 | West Nile | 79.2  | 11029 | AF260969 |
| AF404753 | West Nile | 79.2  | 11029 | AF404753 |
| AF404754 | West Nile | 79.2  | 11029 | AF404754 |
| AF404755 | West Nile | 79.2  | 11029 | AF404755 |
| AF404756 | West Nile | 79.2  | 11029 | AF404756 |
| AF481864 | West Nile | 79.2  | 11029 | AF481864 |
| AF533540 | West Nile | 79.2  | 11029 | AF533540 |
| AY289214 | West Nile | 79.2  | 11029 | AY289214 |
| AF404757 | West Nile | 75.0  | 11029 | AF404757 |
| AY187013 | West Nile | 645   | 14    | AY187013 |
| AF458353 | West Nile | 451   | 14    | AF458353 |
| AF196538 | West Nile | 644   | 14    | AF196538 |
| AF196540 | West Nile | 648   | 14    | AF196540 |

|       |    |      |       |    |            |                       |       |    |      |        |    |           |                       |
|-------|----|------|-------|----|------------|-----------------------|-------|----|------|--------|----|-----------|-----------------------|
| C 93  | 31 | 64.6 | 664   | 14 | AF196537   | AF196537 West Nile    | C 166 | 22 | 45.8 | 10977  | 14 | AF069076  | AF069076 Japanese     |
| C 94  | 25 | 52.1 | 10989 | 14 | AY268132   | AY268132 West Nile    | C 167 | 22 | 45.8 | 10977  | 14 | AF486638  | AF486638 Japanese     |
| C 95  | 24 | 50.0 | 395   | 14 | AF458358   | AF458358 West Nile    | C 168 | 22 | 45.8 | 10978  | 14 | AY184212  | AY184212 Japanese     |
| C 96  | 24 | 50.0 | 451   | 14 | AF458352   | AF458352 West Nile    | C 169 | 21 | 43.8 | 583    | 14 | AF297857  | AF297857 Kunjin vi    |
| C 97  | 24 | 50.0 | 481   | 14 | AF458349   | AF458349 West Nile    | C 170 | 20 | 41.7 | 225005 | 2  | AC102985  | AC102985 Rattus no    |
| C 98  | 24 | 50.0 | 481   | 14 | AF458359   | AF458359 West Nile    | C 171 | 20 | 41.7 | 239694 | 2  | AC128965  | AC128965 Rattus no    |
| C 99  | 24 | 50.0 | 483   | 14 | AF458345   | AF458345 West Nile    | C 172 | 19 | 39.6 | 459    | 14 | JEVNS5GAB | JEVNS5GAB Japanese en |
| C 100 | 24 | 50.0 | 483   | 14 | AF458357   | AF458357 West Nile    | C 173 | 19 | 39.6 | 562    | 14 | FVNS5GAB  | FVNS5GAB Japanese en  |
| C 101 | 24 | 50.0 | 484   | 14 | AF458354   | AF458354 West Nile    | C 174 | 18 | 37.5 | 99592  | 9  | AF263284  | AF263284 Homo sapi    |
| C 102 | 24 | 50.0 | 591   | 14 | AF196543   | AF196543 West Nile    | C 175 | 18 | 37.5 | 129841 | 2  | AC140102  | AC140102 Fella cat    |
| C 103 | 24 | 50.0 | 593   | 14 | WVNS5GAA   | WVNS5GAA West Nile v  | C 176 | 18 | 37.5 | 173053 | 10 | AL844145  | AL844145 Mouse DNA    |
| C 104 | 24 | 50.0 | 604   | 14 | KUNNS5     | L49311 Kunjin viru    | C 177 | 18 | 37.5 | 187204 | 9  | AC084082  | AC084082 Homo sapi    |
| C 105 | 24 | 50.0 | 677   | 14 | AF196535   | AF196535 West Nile    | C 178 | 17 | 35.4 | 2774   | 5  | BC076107  | BC076107 Danio rer    |
| C 106 | 24 | 50.0 | 687   | 14 | AF196539   | AF196539 West Nile    | C 179 | 17 | 35.4 | 70203  | 2  | AC091058  | AC091058 Homo sapi    |
| C 107 | 24 | 50.0 | 917   | 14 | AF208017   | AF208017 West Nile    | C 180 | 17 | 35.4 | 91436  | 8  | NCB14A6   | NCB14A6 Neurospor     |
| C 108 | 24 | 50.0 | 10962 | 14 | WNEFCG     | WNEFCG West Nile      | C 181 | 17 | 35.4 | 131140 | 2  | AC027474  | AC027474 Homo sapi    |
| C 109 | 24 | 50.0 | 11057 | 14 | AY688948   | AY688948 West Nile    | C 182 | 17 | 35.4 | 151032 | 9  | AC105201  | AC105201 Homo sapi    |
| C 110 | 22 | 45.8 | 346   | 14 | AF148902   | AF148902 Japanese     | C 183 | 17 | 35.4 | 153072 | 9  | AL360015  | AL360015 Human DNA    |
| C 111 | 22 | 45.8 | 424   | 14 | AF092550   | AF092550 Japanese     | C 184 | 17 | 35.4 | 162508 | 2  | AC025870  | AC025870 Homo sapi    |
| C 112 | 22 | 45.8 | 424   | 14 | AF092552   | AF092552 Japanese     | C 185 | 17 | 35.4 | 171729 | 2  | BC232824  | BC232824 Danio rer    |
| C 113 | 22 | 45.8 | 424   | 14 | AF092553   | AF092553 Japanese     | C 186 | 17 | 35.4 | 174200 | 2  | AC022797  | AC022797 Homo sapi    |
| C 114 | 22 | 45.8 | 424   | 14 | JEVNS5GAC  | JEVNS5GAC Japanese en | C 187 | 17 | 35.4 | 177675 | 10 | AC123034  | AC123034 Mus muscu    |
| C 115 | 22 | 45.8 | 424   | 14 | JEVNS5GAD  | JEVNS5GAD Japanese en | C 188 | 17 | 35.4 | 180360 | 9  | AC011139  | AC011139 Homo sapi    |
| C 116 | 22 | 45.8 | 424   | 14 | JEVNS5GAE  | JEVNS5GAE Japanese en | C 189 | 17 | 35.4 | 182448 | 2  | AC090323  | AC090323 Homo sapi    |
| C 117 | 22 | 45.8 | 424   | 14 | JEVNS5GAF  | JEVNS5GAF Japanese en | C 190 | 17 | 35.4 | 184683 | 2  | AP001640  | AP001640 Homo sapi    |
| C 118 | 22 | 45.8 | 424   | 14 | JEVNS5GAG  | JEVNS5GAG Japanese en | C 191 | 17 | 35.4 | 186773 | 10 | AC135356  | AC135356 Mus muscu    |
| C 119 | 22 | 45.8 | 424   | 14 | JEVNS5GAH  | JEVNS5GAH Japanese en | C 192 | 17 | 35.4 | 188893 | 10 | AL147108  | AL147108 Mus muscu    |
| C 120 | 22 | 45.8 | 424   | 14 | JEVNS5GAI  | JEVNS5GAI Japanese en | C 193 | 17 | 35.4 | 189104 | 10 | AL806522  | AL806522 Mouse DNA    |
| C 121 | 22 | 45.8 | 424   | 14 | JEVNS5GAJ  | JEVNS5GAJ Japanese en | C 194 | 17 | 35.4 | 189115 | 2  | AC107680  | AC107680 Mus muscu    |
| C 122 | 22 | 45.8 | 463   | 14 | AF458343   | AF458343 West Nile    | C 195 | 17 | 35.4 | 220458 | 9  | AC010320  | AC010320 Homo sapi    |
| C 123 | 22 | 45.8 | 463   | 14 | AF278556   | AF278556 Japanese     | C 196 | 17 | 35.4 | 255755 | 2  | AC115792  | AC115792 Mus muscu    |
| C 124 | 22 | 45.8 | 533   | 14 | JEVNS5GAA  | JEVNS5GAA Japanese en | C 197 | 16 | 33.3 | 576    | 14 | AF306515  | AF306515 Japanese     |
| C 125 | 22 | 45.8 | 536   | 14 | AF148900   | AF148900 Japanese     | C 198 | 16 | 33.3 | 576    | 14 | AF306516  | AF306516 Japanese     |
| C 126 | 22 | 45.8 | 566   | 14 | VPNG6544P2 | VPNG6544P2 Japanese   | C 199 | 16 | 33.3 | 681    | 9  | HS330526  | HS330526 Homo sapi    |
| C 127 | 22 | 45.8 | 572   | 14 | AF306514   | AF306514 Japanese     | C 200 | 16 | 33.3 | 1336   | 8  | BT003419  | BT003419 Arabidops    |
| C 128 | 22 | 45.8 | 582   | 14 | AF218068   | AF218068 Japanese     | C 201 | 16 | 33.3 | 1389   | 8  | AK062201  | AK062201 Arabidops    |
| C 129 | 22 | 45.8 | 583   | 14 | AF251616   | AF251616 Japanese     | C 202 | 16 | 33.3 | 1516   | 8  | BT006103  | BT006103 Oryza sat    |
| C 130 | 22 | 45.8 | 598   | 14 | AF289816   | AF289816 Japanese     | C 203 | 16 | 33.3 | 1585   | 8  | ATU79159  | ATU79159 Arabidops    |
| C 131 | 22 | 45.8 | 625   | 14 | AF318291   | AF318291 Japanese     | C 204 | 16 | 33.3 | 1589   | 8  | AT099868  | AT099868 Arabidops    |
| C 132 | 22 | 45.8 | 972   | 14 | AF311748   | AF311748 Japanese     | C 205 | 16 | 33.3 | 1599   | 8  | AT099868  | AT099868 Arabidops    |
| C 133 | 22 | 45.8 | 10951 | 14 | JEVLINGCG  | JEVLINGCG Japanese en | C 206 | 16 | 33.3 | 1744   | 8  | AT099868  | AT099868 Arabidops    |
| C 134 | 22 | 45.8 | 10963 | 14 | AF045551   | AF045551 Japanese     | C 207 | 16 | 33.3 | 1860   | 8  | BT005786  | BT005786 Arabidops    |
| C 135 | 22 | 45.8 | 10964 | 14 | AF217620   | AF217620 Japanese     | C 208 | 16 | 33.3 | 2886   | 8  | AY491400  | AY491400 Setaria i    |
| C 136 | 22 | 45.8 | 10965 | 14 | AB051292   | AB051292 Japanese     | C 209 | 16 | 33.3 | 2886   | 8  | AY251482  | AY251482 Echinocyl    |
| C 137 | 22 | 45.8 | 10968 | 14 | AY585242   | AY585242 Japanese     | C 210 | 16 | 33.3 | 3307   | 8  | AF271995  | AF271995 Oryza sat    |
| C 138 | 22 | 45.8 | 10968 | 14 | AY585243   | AY585243 Japanese     | C 211 | 16 | 33.3 | 3310   | 8  | AK065029  | AK065029 Oryza sat    |
| C 139 | 22 | 45.8 | 10969 | 14 | JEU15763   | JEU15763 Japanese en  | C 212 | 16 | 33.3 | 3319   | 8  | AK065029  | AK065029 Oryza sat    |
| C 140 | 22 | 45.8 | 10969 | 14 | JEVCMNAA   | JEVCMNAA Japanese en  | C 213 | 16 | 33.3 | 3565   | 8  | AF004560  | AF004560 Arabidops    |
| C 141 | 22 | 45.8 | 10970 | 14 | AF254452   | AF254452 Japanese     | C 214 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 142 | 22 | 45.8 | 10970 | 14 | AF254453   | AF254453 Japanese     | C 215 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 143 | 22 | 45.8 | 10970 | 14 | AY303791   | AY303791 Japanese     | C 216 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 144 | 22 | 45.8 | 10970 | 14 | AY303792   | AY303792 Japanese     | C 217 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 145 | 22 | 45.8 | 10970 | 14 | AY303793   | AY303793 Japanese     | C 218 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 146 | 22 | 45.8 | 10970 | 14 | AY303794   | AY303794 Japanese     | C 219 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 147 | 22 | 45.8 | 10970 | 14 | AY303795   | AY303795 Japanese     | C 220 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 148 | 22 | 45.8 | 10970 | 14 | AY303796   | AY303796 Japanese     | C 221 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 149 | 22 | 45.8 | 10970 | 14 | AY303797   | AY303797 Japanese     | C 222 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 150 | 22 | 45.8 | 10970 | 14 | AY303798   | AY303798 Japanese     | C 223 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 151 | 22 | 45.8 | 10976 | 14 | AF014160   | AF014160 Japanese     | C 224 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 152 | 22 | 45.8 | 10976 | 14 | AF014161   | AF014161 Japanese     | C 225 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 153 | 22 | 45.8 | 10976 | 14 | AF075723   | AF075723 Japanese     | C 226 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 154 | 22 | 45.8 | 10976 | 14 | AF098735   | AF098735 Japanese     | C 227 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 155 | 22 | 45.8 | 10976 | 14 | AF098736   | AF098736 Japanese     | C 228 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 156 | 22 | 45.8 | 10976 | 14 | AF098737   | AF098737 Japanese     | C 229 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 157 | 22 | 45.8 | 10976 | 14 | AF221499   | AF221499 Japanese     | C 230 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 158 | 22 | 45.8 | 10976 | 14 | AF221500   | AF221500 Japanese     | C 231 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 159 | 22 | 45.8 | 10976 | 14 | AF221501   | AF221501 Japanese     | C 232 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 160 | 22 | 45.8 | 10976 | 14 | AF221502   | AF221502 Japanese     | C 233 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 161 | 22 | 45.8 | 10976 | 14 | AF221503   | AF221503 Japanese     | C 234 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 162 | 22 | 45.8 | 10976 | 14 | AF221504   | AF221504 Japanese     | C 235 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 163 | 22 | 45.8 | 10976 | 14 | AF221505   | AF221505 Japanese     | C 236 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 164 | 22 | 45.8 | 10976 | 14 | AF221506   | AF221506 Japanese     | C 237 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |
| C 165 | 22 | 45.8 | 10976 | 14 | AF221507   | AF221507 Japanese     | C 238 | 16 | 33.3 | 3809   | 8  | AK065425  | AK065425 Oryza sat    |



|       |    |      |        |    |           |           |           |       |    |      |        |    |           |                       |            |
|-------|----|------|--------|----|-----------|-----------|-----------|-------|----|------|--------|----|-----------|-----------------------|------------|
| C 239 | 16 | 33.3 | 130968 | 8  | AP004117  | AP004117  | Oryza sat | 312   | 16 | 33.3 | 228059 | 2  | AC109886  | AC109886              | Rattus no  |
| C 240 | 16 | 33.3 | 132353 | 9  | AC134393  | AC134393  | Homo sapi | 313   | 16 | 33.3 | 232657 | 2  | AC108234  | AC108234              | Rattus no  |
| C 241 | 16 | 33.3 | 144429 | 2  | AC032017  | AC032017  | Homo sapi | 314   | 16 | 33.3 | 234771 | 9  | AC133536  | AC133536              | Homo sapi  |
| C 242 | 16 | 33.3 | 145416 | 5  | AC147826  | AC147826  | Xenopus t | 315   | 16 | 33.3 | 237258 | 2  | AC124867  | AC124867              | Rattus no  |
| C 243 | 16 | 33.3 | 149143 | 2  | AC092974  | AC092974  | Homo sapi | 316   | 16 | 33.3 | 241179 | 10 | AC111141  | AC111141              | Mus muscu  |
| C 244 | 16 | 33.3 | 150887 | 2  | AC018580  | AC018580  | Homo sapi | 317   | 16 | 33.3 | 241792 | 2  | AC134640  | AC134640              | Rattus no  |
| C 245 | 16 | 33.3 | 153997 | 9  | AC073348  | AC073348  | Homo sapi | C 318 | 16 | 33.3 | 246941 | 2  | AC145215  | AC145215              | Homo sapi  |
| C 246 | 16 | 33.3 | 154485 | 2  | AC116894  | AC116894  | Mus muscu | C 319 | 16 | 33.3 | 249232 | 2  | AC102120  | AC102120              | Mus muscu  |
| C 247 | 16 | 33.3 | 154758 | 9  | AC112491  | AC112491  | Homo sapi | C 320 | 16 | 33.3 | 250666 | 2  | AC103019  | AC103019              | Rattus no  |
| C 248 | 16 | 33.3 | 162041 | 2  | AC137797  | AC137797  | Homo sapi | C 321 | 16 | 33.3 | 255066 | 2  | AC109139  | AC109139              | Mus muscu  |
| C 249 | 16 | 33.3 | 162902 | 8  | AC137609  | AC137609  | Oryza sat | C 322 | 16 | 33.3 | 258387 | 2  | AC125590  | AC125590              | Rattus no  |
| C 250 | 16 | 33.3 | 163357 | 2  | AC023276  | AC023276  | Homo sapi | C 323 | 16 | 33.3 | 259387 | 2  | AC125990  | AC125990              | Rattus no  |
| C 251 | 16 | 33.3 | 165653 | 2  | AC117818  | AC117818  | Mus muscu | C 324 | 16 | 33.3 | 259921 | 2  | AC114206  | AC114206              | Rattus no  |
| C 252 | 16 | 33.3 | 168421 | 10 | AC113328  | AC113328  | Mus muscu | C 325 | 16 | 33.3 | 260145 | 2  | AC099658  | AC099658              | Rattus no  |
| C 253 | 16 | 33.3 | 168991 | 2  | AC090411  | AC090411  | Homo sapi | C 326 | 16 | 33.3 | 276742 | 2  | AC096514  | AC096514              | Rattus no  |
| C 254 | 16 | 33.3 | 169866 | 9  | AC133561  | AC133561  | Homo sapi | C 327 | 15 | 31.2 | 422    | 6  | BD058596  | BD058596              | Secreted   |
| C 255 | 16 | 33.3 | 169866 | 9  | AC133561  | AC133561  | Homo sapi | C 328 | 15 | 31.2 | 459    | 8  | BT014827  | BT014827              | Arabidops  |
| C 256 | 16 | 33.3 | 171987 | 9  | AC100757  | AC100757  | Homo sapi | C 329 | 15 | 31.2 | 463    | 6  | CQ424549  | CQ424549              | Sequence   |
| C 257 | 16 | 33.3 | 171987 | 9  | AC079775  | AC079775  | Homo sapi | C 330 | 15 | 31.2 | 463    | 6  | CQ424549  | CQ424549              | Sequence   |
| C 258 | 16 | 33.3 | 172659 | 2  | AC024320  | AC024320  | Homo sapi | C 331 | 15 | 31.2 | 489    | 5  | AF202806  | AF202806              | Emplidomax |
| C 259 | 16 | 33.3 | 172755 | 9  | CNS01RGL  | AL158111  | Human chr | C 332 | 15 | 31.2 | 495    | 14 | NVEN5SGAD | L48975 Murray Vall    |            |
| C 260 | 16 | 33.3 | 173913 | 2  | AC139181  | AC139181  | Pan trogl | C 333 | 15 | 31.2 | 525    | 14 | NVEN5SGAA | L48972 Murray Vall    |            |
| C 261 | 16 | 33.3 | 174423 | 2  | AC141189  | AC141189  | Rattus no | C 334 | 15 | 31.2 | 525    | 14 | NVEN5SGAB | L48973 Murray Vall    |            |
| C 262 | 16 | 33.3 | 174477 | 9  | AC136616  | AC136616  | Homo sapi | C 335 | 15 | 31.2 | 558    | 14 | NVEN5SGAB | M35172 Murray Vall    |            |
| C 263 | 16 | 33.3 | 174844 | 8  | AC137003  | AC137003  | Oryza sat | C 336 | 15 | 31.2 | 571    | 11 | G87185    | G87185 S208P6541RH    |            |
| C 264 | 16 | 33.3 | 174930 | 9  | AC145889  | AC145889  | Pan trogl | C 337 | 15 | 31.2 | 645    | 6  | CQ717980  | CQ717980 Sequence     |            |
| C 265 | 16 | 33.3 | 175050 | 2  | AC136439  | AC136439  | Homo sapi | C 338 | 15 | 31.2 | 652    | 11 | PM4A4B    | AL685780 Penicilli    |            |
| C 266 | 16 | 33.3 | 175691 | 9  | AC136440  | AC136440  | Homo sapi | C 339 | 15 | 31.2 | 721    | 6  | AX508057  | AX508057 Sequence     |            |
| C 267 | 16 | 33.3 | 175993 | 9  | AL445310  | Human DNA | Human chr | C 340 | 15 | 31.2 | 721    | 6  | AX508057  | AX508057 Sequence     |            |
| C 268 | 16 | 33.3 | 176399 | 9  | CNS05TE1  | AL445310  | Human DNA | C 341 | 15 | 31.2 | 747    | 6  | AX58728   | AX58728 Sequence      |            |
| C 269 | 16 | 33.3 | 177355 | 9  | AC023310  | AC023310  | Homo sapi | C 342 | 15 | 31.2 | 860    | 5  | AY488254  | AY488254 Sericorni    |            |
| C 270 | 16 | 33.3 | 177574 | 9  | AC142086  | AC142086  | Homo sapi | C 343 | 15 | 31.2 | 873    | 8  | AF141967  | AF141967 Oryza sat    |            |
| C 271 | 16 | 33.3 | 180708 | 9  | AC136687  | AC136687  | Homo sapi | C 344 | 15 | 31.2 | 918    | 1  | UBZ93994  | UBZ93994 Unidentifie  |            |
| C 272 | 16 | 33.3 | 182559 | 9  | AC073476  | AC073476  | Homo sapi | C 345 | 15 | 31.2 | 918    | 10 | MURSLP19  | M29018 Mouse ribos    |            |
| C 273 | 16 | 33.3 | 183831 | 10 | AC134909  | AC134909  | Mus muscu | C 346 | 15 | 31.2 | 990    | 5  | GGU51737  | US1737 Gallus gall    |            |
| C 274 | 16 | 33.3 | 184202 | 2  | AC116475  | AC116475  | Mus muscu | C 347 | 15 | 31.2 | 1021   | 3  | TVCPI     | U77218 T.vaginalis    |            |
| C 275 | 16 | 33.3 | 184470 | 9  | AL589823  | AL589823  | Human DNA | C 348 | 15 | 31.2 | 1021   | 8  | BT012599  | BT012599 Arabidops    |            |
| C 276 | 16 | 33.3 | 185671 | 2  | AC084376  | AC084376  | Homo sapi | C 349 | 15 | 31.2 | 1022   | 8  | AK064184  | AK064184 Oryza sat    |            |
| C 277 | 16 | 33.3 | 187891 | 2  | AC140903  | AC140903  | Homo sapi | C 350 | 15 | 31.2 | 1027   | 6  | AR088959  | AR088959 Sequence     |            |
| C 278 | 16 | 33.3 | 190053 | 2  | AC132044  | AC132044  | Rattus no | C 351 | 15 | 31.2 | 1027   | 8  | OSU78890  | OSU78890 Oryza sativ  |            |
| C 279 | 16 | 33.3 | 190243 | 9  | AC146095  | AC146095  | Pan trogl | C 352 | 15 | 31.2 | 1180   | 4  | BT012599  | BT012599 Arabidops    |            |
| C 280 | 16 | 33.3 | 190925 | 2  | AL606665  | AL606665  | Homo sapi | C 353 | 15 | 31.2 | 1180   | 4  | BT012599  | BT012599 Arabidops    |            |
| C 281 | 16 | 33.3 | 191424 | 9  | BS000127  | BS000127  | Pan trogl | C 354 | 15 | 31.2 | 1370   | 1  | UBZ93991  | UBZ93991 Unidentifie  |            |
| C 282 | 16 | 33.3 | 193539 | 2  | AC022190  | AC022190  | Homo sapi | C 355 | 15 | 31.2 | 1405   | 3  | AF224339  | AF224339 Leishmani    |            |
| C 283 | 16 | 33.3 | 194490 | 9  | AC140899  | AC140899  | Homo sapi | C 356 | 15 | 31.2 | 1471   | 1  | HSP309519 | HSP309519 Halanaero   |            |
| C 284 | 16 | 33.3 | 194508 | 2  | AC145316  | AC145316  | Homo sapi | C 357 | 15 | 31.2 | 1486   | 1  | HSRNL16S2 | HSRNL16S2 Halanaero   |            |
| C 285 | 16 | 33.3 | 194754 | 9  | AC131280  | AC131280  | Homo sapi | C 358 | 15 | 31.2 | 1486   | 1  | HSRNL16S3 | HSRNL16S3 Halanaero   |            |
| C 286 | 16 | 33.3 | 195032 | 9  | AC006239  | AC006239  | Homo sapi | C 359 | 15 | 31.2 | 1488   | 1  | HS16SH150 | HS16SH150 Halanaero   |            |
| C 287 | 16 | 33.3 | 195921 | 8  | ATGHR1V81 | AL161585  | Arabidops | C 360 | 15 | 31.2 | 1500   | 1  | HKU086446 | HKU086446 Halanaero   |            |
| C 288 | 16 | 33.3 | 195950 | 9  | AC012003  | AC012003  | Homo sapi | C 361 | 15 | 31.2 | 1526   | 1  | HAU32594  | HAU32594 Halobaetero  |            |
| C 289 | 16 | 33.3 | 196021 | 9  | AC138807  | AC138807  | Homo sapi | C 362 | 15 | 31.2 | 1528   | 1  | HCU76832  | HCU76832 Halanaero    |            |
| C 290 | 16 | 33.3 | 198348 | 9  | AC141283  | AC141283  | Homo sapi | C 363 | 15 | 31.2 | 1539   | 9  | HOMMUC7G  | HOMMUC7G Halanaero    |            |
| C 291 | 16 | 33.3 | 198348 | 9  | AC148025  | AC148025  | Homo sapi | C 364 | 15 | 31.2 | 1549   | 3  | BC076075  | BC076075 Danio rer    |            |
| C 292 | 16 | 33.3 | 200538 | 10 | AC122476  | AC122476  | Mus muscu | C 365 | 15 | 31.2 | 1733   | 3  | SDO344162 | SDO344162 Suberites   |            |
| C 293 | 16 | 33.3 | 201929 | 2  | AC105863  | AC105863  | Rattus no | C 366 | 15 | 31.2 | 1839   | 6  | C0804202  | C0804202 Sequence     |            |
| C 294 | 16 | 33.3 | 204050 | 1  | AL646073  | AL646073  | Ralstonia | C 367 | 15 | 31.2 | 1870   | 8  | BT001966  | BT001966 Arabidops    |            |
| C 295 | 16 | 33.3 | 204655 | 2  | AC142537  | AC142537  | Homo sapi | C 368 | 15 | 31.2 | 1929   | 6  | AX412878  | AX412878 Sequence     |            |
| C 296 | 16 | 33.3 | 205191 | 2  | AC145314  | AC145314  | Homo sapi | C 369 | 15 | 31.2 | 1929   | 6  | AX506546  | AX506546 Sequence     |            |
| C 297 | 16 | 33.3 | 206056 | 2  | AC141453  | AC141453  | Homo sapi | C 370 | 15 | 31.2 | 1929   | 6  | AX506546  | AX506546 Sequence     |            |
| C 298 | 16 | 33.3 | 206476 | 2  | AC112776  | AC112776  | Homo sapi | C 371 | 15 | 31.2 | 1937   | 5  | AF360282  | AF360282 Danio rer    |            |
| C 299 | 16 | 33.3 | 206536 | 2  | AC145310  | AC145310  | Homo sapi | C 372 | 15 | 31.2 | 2099   | 8  | AP360282  | AP360282 Arabidops    |            |
| C 300 | 16 | 33.3 | 207477 | 2  | AC141262  | AC141262  | Homo sapi | C 373 | 15 | 31.2 | 2161   | 8  | AY062544  | AY062544 Arabidops    |            |
| C 301 | 16 | 33.3 | 211018 | 2  | AC140879  | AC140879  | Homo sapi | C 374 | 15 | 31.2 | 2193   | 8  | BT000695  | BT000695 Arabidops    |            |
| C 302 | 16 | 33.3 | 211998 | 10 | AL732530  | AL732530  | Mouse DNA | C 375 | 15 | 31.2 | 2260   | 5  | BC054716  | BC054716 Danio rer    |            |
| C 303 | 16 | 33.3 | 212399 | 10 | AC114591  | AC114591  | Mus muscu | C 376 | 15 | 31.2 | 2274   | 1  | AF321091  | AF321091 Pseudomon    |            |
| C 304 | 16 | 33.3 | 212693 | 2  | AC101843  | AC101843  | Mus muscu | C 377 | 15 | 31.2 | 2635   | 1  | PAHEMN    | PAHEMN Pseudomonas    |            |
| C 305 | 16 | 33.3 | 214025 | 9  | AC007882  | AC007882  | Homo sapi | C 378 | 15 | 31.2 | 2640   | 8  | AK176239  | AK176239 Arabidops    |            |
| C 306 | 16 | 33.3 | 214110 | 9  | AC007908  | AC007908  | Homo sapi | C 379 | 15 | 31.2 | 2851   | 5  | AF029260  | AF029260 Gallus ga    |            |
| C 307 | 16 | 33.3 | 214504 | 2  | AC141622  | AC141622  | Homo sapi | C 380 | 15 | 31.2 | 2872   | 8  | AK118741  | AK118741 Arabidops    |            |
| C 308 | 16 | 33.3 | 218807 | 2  | AX511249  | AX511249  | Mus muscu | C 381 | 15 | 31.2 | 3000   | 8  | AF430213  | AF430213 Cryptococ    |            |
| C 309 | 16 | 33.3 | 219720 | 2  | AC023364  | AC023364  | Mus muscu | C 382 | 15 | 31.2 | 3068   | 9  | AK056662  | AK056662 Homo sapi    |            |
| C 310 | 16 | 33.3 | 227182 | 5  | EX005355  | EX005355  | Zebrafish | C 383 | 15 | 31.2 | 3761   | 1  | PSEANRPRO | PSEANRPRO Pseudomonas |            |
| C 311 | 16 | 33.3 | 227395 | 10 | AC119248  | AC119248  | Mus muscu | C 384 | 15 | 31.2 | 3761   | 1  | PANR      | PANR Pseudomonas      |            |
| C 312 | 16 | 33.3 | 227524 | 2  | AC129956  | AC129956  | Bos tauru | C 385 | 15 | 31.2 | 4002   | 10 | BC048174  | BC048174 Mus muscu    |            |
| C 313 | 16 | 33.3 | 227524 | 2  | AC129956  | AC129956  | Bos tauru | C 386 | 15 | 31.2 | 4016   | 9  | BC013398  | BC013398 Homo sapi    |            |
| C 314 | 16 | 33.3 | 227524 | 2  | AC129956  | AC129956  | Bos tauru | C 387 | 15 | 31.2 | 4021   | 6  | BD190329  | BD190329 Elk1 phos    |            |

|     |    |      |        |    |             |                      |
|-----|----|------|--------|----|-------------|----------------------|
| 385 | 15 | 31.2 | 4037   | 10 | BC050747    | BC050747 Mus muscu   |
| 386 | 15 | 31.2 | 4190   | 9  | BS647437    | Homo sapi            |
| 387 | 15 | 31.2 | 4915   | 9  | HSU897582   |                      |
| 388 | 15 | 31.2 | 4942   | 9  | HSU89107    | U9107 Homo sapien    |
| 389 | 15 | 31.2 | 4951   | 9  | BS537782    | Homo sapi            |
| 390 | 15 | 31.2 | 5029   | 10 | AF321909    | AF321909 Mus muscu   |
| 391 | 15 | 31.2 | 5319   | 6  | AR146446    | Sequence             |
| 392 | 15 | 31.2 | 5319   | 6  | AX336321    | Sequence             |
| 393 | 15 | 31.2 | 5329   | 10 | AK122205    | AK122205 Mus muscu   |
| 394 | 15 | 31.2 | 5359   | 6  | BD190330    | BD190330 Elk1 phos   |
| 395 | 15 | 31.2 | 5390   | 9  | AF315592    | Homo sapi            |
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| 398 | 15 | 31.2 | 6166   | 9  | AF130844    | AF130844 Homo sapi   |
| 399 | 15 | 31.2 | 9086   | 5  | AB092649    | AB092649 Oryzias l   |
| 400 | 15 | 31.2 | 11014  | 14 | AF161266    | AF161266 Murray Va   |
| 401 | 15 | 31.2 | 11231  | 1  | AE012315    | AE012315 Xanthomon   |
| 402 | 15 | 31.2 | 11627  | 1  | AE004582    | AE004582 Pseudomon   |
| 403 | 15 | 31.2 | 12277  | 1  | AE010598    | AE010598 Fusedacte   |
| 404 | 15 | 31.2 | 15015  | 1  | AE000774    | AE000774 Aquifex a   |
| 405 | 15 | 31.2 | 22280  | 1  | AE008876    | AE008876 Salmonell   |
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| 416 | 15 | 31.2 | 58979  | 10 | BX511243    | BX511243 Mouse DNA   |
| 417 | 15 | 31.2 | 59030  | 5  | BX324184    | BX324184 Zebrafish   |
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| 424 | 15 | 31.2 | 72504  | 2  | AC123766    | AC123766 Homo sapi   |
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| 426 | 15 | 31.2 | 73994  | 2  | AC079000    | AC079000 Homo sapi   |
| 427 | 15 | 31.2 | 78810  | 5  | BX546481    | BX546481 Zebrafish   |
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| 461 | 15 | 31.2 | 113808 | 9  | AL139141    | AL139141 Human DNA   |
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| 466 | 15 | 31.2 | 118705 | 8  | AC126009    | AC126009 Medicago    |
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| 477 | 15 | 31.2 | 128091 | 2  | AC139626    | AC139626 Takifugu    |
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| 482 | 15 | 31.2 | 131813 | 2  | AC011067    | AC011067 Drosophil   |
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| 487 | 15 | 31.2 | 139255 | 2  | AC141580    | AC141580 Rattus no   |
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## ALIGNMENTS

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DEFINITION

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AF458344.1

GI:21636467

Accession

Version

Keywords

Source

Organism

West Nile virus (WNV)

West Nile virus

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Japanese encephalitis virus group.

(bases 1 to 463)

Beasley, D.W., Li, L., Suderman, M.T. and Barrett, A.D.

Mouse neuroinvasive phenotype of West Nile virus strains varies

depending upon virus genotype

Virology 296 (1), 17-23 (2002)

12036314

(bases 1 to 463)

Beasley, D.W.C., Li, L., Suderman, M.T. and Barrett, A.D.T.

Direct Submission

Submitted (14-DEC-2001) Department of Pathology and WHO

Collaborating Center for Tropical Diseases, The University of Texas

Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA

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ACCESSION
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VERSION
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ORGANISM
    West Nile virus
    Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
    Flavivirus; Japanese encephalitis virus group.
REFERENCE
    1 (bases 1 to 463)
AUTHORS
    Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE
    Mouse neuroinvasive phenotype of West Nile virus strains varies
    depending upon virus genotype
JOURNAL
    Virology 296 (1), 17-23 (2002)
MEDLINE
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PUBMED
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REFERENCE
    2 (bases 1 to 463)
AUTHORS
    Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE
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JOURNAL
    Submitted (14-DEC-2001) Department of Pathology and WHO
    Collaborating Center for Tropical Diseases, The University of Texas
    Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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DEFINITION
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ACCESSION
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VERSION
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KEYWORDS
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SOURCE
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ORGANISM
    Kunjin virus
    Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
    Flavivirus; Japanese encephalitis virus group.
REFERENCE
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AUTHORS
    Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
    Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.

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ACCESSION
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VERSION
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KEYWORDS
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SOURCE
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ORGANISM
    West Nile virus
    Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
    Flavivirus; Japanese encephalitis virus group.
REFERENCE
    1 (bases 1 to 463)
AUTHORS
    Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE
    Mouse neuroinvasive phenotype of West Nile virus strains varies
    depending upon virus genotype
JOURNAL
    Virology 296 (1), 17-23 (2002)
MEDLINE
    22033887
PUBMED
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REFERENCE
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AUTHORS
    Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE
    Direct Submission
JOURNAL
    Submitted (14-DEC-2001) Department of Pathology and WHO
    Collaborating Center for Tropical Diseases, The University of Texas
    Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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ACCESSION
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VERSION
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KEYWORDS
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SOURCE
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ORGANISM
    West Nile virus
    Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
    Flavivirus; Japanese encephalitis virus group.
REFERENCE
    1 (bases 1 to 463)
AUTHORS
    Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE
    Mouse neuroinvasive phenotype of West Nile virus strains varies
    depending upon virus genotype
JOURNAL
    Virology 296 (1), 17-23 (2002)
MEDLINE
    22033887
PUBMED
    12036314
REFERENCE
    2 (bases 1 to 463)
AUTHORS
    Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE
    Direct Submission
JOURNAL
    Submitted (14-DEC-2001) Department of Pathology and WHO
    Collaborating Center for Tropical Diseases, The University of Texas
    Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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ACCESSION
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VERSION
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KEYWORDS
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SOURCE
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ORGANISM
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    Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
    Flavivirus; Japanese encephalitis virus group.
REFERENCE
    1 (bases 1 to 542)
AUTHORS
    Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
    Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.

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TITLE The relationships between West Nile and Kunjin viruses  
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)  
MEDLINE 21469816  
PUBMED 11585535  
REFERENCE 2 (bases 1 to 542)  
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.  
TITLE Definitive studies of the relationships between West Nile and Kunjin viruses  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 542)  
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.  
TITLE Direct Submission  
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia  
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REFERENCE 1 (bases 1 to 587)  
AUTHORS Poidinger,M., Hall,R.A. and Mackenzie,J.S.  
TITLE Molecular characterization of the Japanese encephalitis serocomplex of the flavivirus genus  
JOURNAL Virology 218 (2), 417-421 (1996)  
MEDLINE 96193756  
PUBMED 8610471  
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LOCUS Kunjin virus nonstructural protein (NS5) gene, 3' end of cds. linear VRL 07-JUN-1996  
DEFINITION Kunjin virus nonstructural protein (NS5) gene, 3' end of cds.  
ACCESSION L48979  
VERSION L48979.1 GI:1066804  
KEYWORDS NS5 gene; nonstructural protein.  
SOURCE Kunjin virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.  
REFERENCE 1 (bases 1 to 587)  
AUTHORS Poidinger,M., Hall,R.A. and Mackenzie,J.S.  
TITLE Molecular characterization of the Japanese encephalitis serocomplex of the flavivirus genus  
JOURNAL Virology 218 (2), 417-421 (1996)  
MEDLINE 96193756  
PUBMED 8610471  
COMMENT Original source text: Kunjin virus (strain MRM16) cDNA to genomic RNA.  
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LOCUS Kunjin virus isolate CH16549E nonstructural protein 5 gene, partial cds. linear VRL 05-MAR-2002  
DEFINITION Kunjin virus isolate CH16549E nonstructural protein 5 gene, partial cds.  
ACCESSION AF297844  
VERSION AF297844.1 GI:11991978  
KEYWORDS  
SOURCE Kunjin virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

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Best Local Similarity 100.0%; Pred. No. 2.8e-19;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 461 TCCGAGACGGTCTCAGGGCTTACATGGATCACTTCGACGCTTTGTTTC 414  
RESULT 6  
KUNNS5GAB/c  
LOCUS Kunjin virus nonstructural protein (NS5) gene, 3' end of cds. linear VRL 07-JUN-1996  
DEFINITION Kunjin virus nonstructural protein (NS5) gene, 3' end of cds.  
ACCESSION L48979  
VERSION L48979.1 GI:1066804  
KEYWORDS NS5 gene; nonstructural protein.  
SOURCE Kunjin virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.  
REFERENCE 1 (bases 1 to 587)  
AUTHORS Poidinger,M., Hall,R.A. and Mackenzie,J.S.  
TITLE Molecular characterization of the Japanese encephalitis serocomplex of the flavivirus genus  
JOURNAL Virology 218 (2), 417-421 (1996)  
MEDLINE 96193756  
PUBMED 8610471  
COMMENT Original source text: Kunjin virus (strain MRM16) cDNA to genomic RNA.  
FEATURES  
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Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 461 TCCGAGACGGTCTCAGGGCTTACATGGATCACTTCGACGCTTTGTTTC 414  
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LOCUS Kunjin virus isolate CH16549E nonstructural protein 5 gene, partial cds. linear VRL 05-MAR-2002  
DEFINITION Kunjin virus isolate CH16549E nonstructural protein 5 gene, partial cds.  
ACCESSION AF297844  
VERSION AF297844.1 GI:11991978  
KEYWORDS  
SOURCE Kunjin virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;



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ORIGIN
Query Match      100.0%; Score 48; DB 14; Length 616;
Best Local Similarity 100.0%; Pred. No. 2.8e-19;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 452 TCCGAGACGGTCTGAGGGCTTACATGATCCTTCGACGCTTTGTC 405

RESULT 10
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LOCUS
Kunjin virus isolate MRM5373 nonstructural protein 5 gene, partial cds.
AF297859
AF297859.1 GI:11992008
Kunjin virus
Kunjin virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 620)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
The relationships between West Nile and Kunjin viruses
Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE
21469816
PUBMED
11585535
REFERENCE
2 (bases 1 to 620)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
and Hall,R.A.
Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
REFERENCE
3 (bases 1 to 622)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
and Hall,R.A.
Direct Submission
Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
FEATURES
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Best Local Similarity 100.0%; Pred. No. 2.8e-19;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 471 TCCGAGACGGTCTGAGGGCTTACATGATCCTTCGACGCTTTGTC 424

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Kunjin virus isolate CH16532C nonstructural protein 5 gene, partial cds.
AF297843
AF297843.1 GI:11991976
Kunjin virus
Kunjin virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 623)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
The relationships between West Nile and Kunjin viruses
Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE
21469816
PUBMED
11585535
REFERENCE
2 (bases 1 to 623)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
and Hall,R.A.
Definitive studies of the relationships between West Nile and
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Unpublished
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RESULT 11
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AF297842
AF297842.1 GI:11991974
Kunjin virus
Kunjin virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 622)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
The relationships between West Nile and Kunjin viruses
Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE
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REFERENCE
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Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
and Hall,R.A.
Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
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Best Local Similarity 100.0%; Pred. No. 2.8e-19;
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RESULT 11
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Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
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Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
The relationships between West Nile and Kunjin viruses
Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE
21469816
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REFERENCE
2 (bases 1 to 623)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
and Hall,R.A.
Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
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Kunjin viruses  
Unpublished  
REFERENCE 3 (bases 1 to 623)  
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.  
TITLE Direct Submission  
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia  
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Best Local Similarity 100.0%; Pred. No. 2.8e-19;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCCGAGACGGTTCTGAGGGCTTACATGGATCACTTCGACGTTTGTTC 48  
Db 472 TCCGAGACGGTTCTGAGGGCTTACATGGATCACTTCGACGTTTGTTC 425  
RESULT 13  
KUNNONCODE/c  
LOCUS KUNNONCODE 627 bp ss-RNA linear VRL 09-AUG-1994  
DEFINITION Kunjin virus 3' UTR.  
ACCESSION L24512  
VERSION L24512.1 GI:403464  
KEYWORDS  
SOURCE Kunjin virus  
ORGANISM Kunjin virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.  
REFERENCE 1 (bases 1 to 627)  
AUTHORS Coia,G., Parker,M.D., Speight,G., Byrne,M.E. and Westaway,E.G.  
TITLE Nucleotide and complete amino acid sequences of Kunjin virus: definitive gene order and characteristics of the virus-specified proteins  
J. Gen. Virol. 69 (Pt 1), 1-21 (1988)  
JOURNAL J. Gen. Virol. 69 (Pt 1), 1-21 (1988)  
MEDLINE 88089524  
PUBMED 2826659  
REFERENCE 2 (bases 1 to 627)  
AUTHORS Khromykh,A.A. and Westaway,E.G.  
TITLE Completion of Kunjin virus RNA sequence and recovery of an infectious RNA transcribed from stably cloned full-length cDNA  
J. Virol. 68 (7), 4580-4588 (1994)  
JOURNAL J. Virol. 68 (7), 4580-4588 (1994)  
MEDLINE 94267921  
PUBMED 8207832  
COMMENT Original source text: Kunjin virus (strain MRM 61C) mature RNA.  
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Best Local Similarity 100.0%; Pred. No. 2.8e-19;  
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Db 227 TCCGAGACGGTTCTGAGGGCTTACATGGATCACTTCGACGTTTGTTC 180  
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LOCUS AF297858 633 bp RNA linear VRL 05-MAR-2002  
DEFINITION Kunjin virus isolate OR205 nonstructural protein 5 gene, partial cds.  
ACCESSION AF297858  
VERSION AF297858.1 GI:11992006  
KEYWORDS  
SOURCE Kunjin virus  
ORGANISM Kunjin virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.  
REFERENCE 1 (bases 1 to 633)  
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.  
TITLE The relationships between West Nile and Kunjin viruses  
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)  
MEDLINE 21459816  
PUBMED 11585535  
REFERENCE 2 (bases 1 to 633)  
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.  
TITLE Definitive studies of the relationships between West Nile and Kunjin viruses  
Unpublished  
JOURNAL  
REFERENCE 3 (bases 1 to 633)  
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.  
TITLE Direct Submission  
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia  
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Db 487 TCCGAGACGGTTCTGAGGGCTTACATGGATCACTTCGACGTTTGTTC 440  
RESULT 15  
AF297848/c  
LOCUS AF297848 644 bp RNA linear VRL 05-MAR-2002  
DEFINITION Kunjin virus isolate K1738 nonstructural protein 5 gene, partial cds.  
ACCESSION AF297848  
VERSION AF297848.1 GI:11991986  
KEYWORDS  
SOURCE Kunjin virus



ORGANISM Kunjin virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Flavivirus; Japanese encephalitis virus group.  
 REFERENCE 1 (bases 1 to 644)  
 AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,  
 Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.  
 TITLE The relationships between West Nile and Kunjin viruses  
 JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)  
 MEDLINE 21469816  
 PUBMED 11585535  
 REFERENCE 2 (bases 1 to 644)  
 AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.  
 and Hall,R.A.  
 TITLE Definitive studies of the relationships between West Nile and  
 Kunjin viruses  
 JOURNAL Unpublished  
 REFERENCE 3 (bases 1 to 644)  
 AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.  
 and Hall,R.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University  
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 QY 1 TCCGAGACGGTCTGAGGCTTACATGATCATCTTCGACGCTTTGTC 48  
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 Db 485 TCCGAGACGGTCTGAGGCTTACATGATCATCTTCGACGCTTTGTC 438  
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 DEFINITION cds.  
 ACCESSION AF297855.1 GI:11992000  
 VERSION  
 KEYWORDS  
 SOURCE Kunjin virus  
 ORGANISM Kunjin virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Flavivirus; Japanese encephalitis virus group.  
 REFERENCE 1 (bases 1 to 652)  
 AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,  
 Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.  
 TITLE The relationships between West Nile and Kunjin viruses  
 JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)  
 MEDLINE 21469816  
 PUBMED 11585535  
 REFERENCE 2 (bases 1 to 652)  
 AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.  
 and Hall,R.A.  
 TITLE Definitive studies of the relationships between West Nile and  
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 JOURNAL Unpublished  
 REFERENCE 3 (bases 1 to 652)

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.  
 and Hall,R.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University  
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 Db 491 TCCGAGACGGTCTGAGGCTTACATGATCATCTTCGACGCTTTGTC 444  
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 ACCESSION AF297849.1 GI:11991988  
 VERSION  
 KEYWORDS  
 SOURCE Kunjin virus  
 ORGANISM Kunjin virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Flavivirus; Japanese encephalitis virus group.  
 REFERENCE 1 (bases 1 to 657)  
 AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,  
 Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.  
 TITLE The relationships between West Nile and Kunjin viruses  
 JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)  
 MEDLINE 21469816  
 PUBMED 11585535  
 REFERENCE 2 (bases 1 to 657)  
 AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.  
 and Hall,R.A.  
 TITLE Definitive studies of the relationships between West Nile and  
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 JOURNAL Unpublished  
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 and Hall,R.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University  
 of Queensland, St Lucia, QLD 4072, Australia  
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 /protein\_id="AAG42387.1"  
 /db\_xref="GI:11991989"



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ORIGIN  
Query Match 100.0%; Score 48; DB 14; Length 657;  
Best Local Similarity 100.0%; Pred. No. 2.8e-19;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGAGACGGTCTGAGGGCTTACATGGATCACTTCGACGCTTTGTTTC 48  
|||||  
DB 493 TCCGAGACGGTCTGAGGGCTTACATGGATCACTTCGACGCTTTGTTTC 446

RESULT 18  
AF017254/c  
LOCUS  
DEFINITION  
West Nile virus nonstructural protein NS5 (NS5) gene, partial cds.  
AF017254  
ACCESSION  
VERSION  
AF017254.2 GI:11497617  
KEYWORDS  
SOURCE  
West Nile virus  
ORGANISM  
West Nile virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Flavivirus; Japanese encephalitis virus group.  
REFERENCE  
Yamchikhov, V.F., Wengler, G., Brinton, M.A. and Compans, R.W.  
TITLE  
A stable infectious clone of West Nile flavivirus  
JOURNAL  
Unpublished  
REFERENCE  
2 (bases 1 to 1524)  
Yamchikhov, V.F. and Brinton, M.A.  
AUTHORS  
Direct Submission  
TITLE  
Submitted (04-AUG-1997) OVRP/DVP, FDA, 29 Lincoln Drive, Bethesda,  
JOURNAL  
MD 20892, USA  
REFERENCE  
3 (bases 1 to 1524)  
Yamchikhov, V.F. and Brinton, M.A.  
AUTHORS  
Direct Submission  
TITLE  
Submitted (01-DEC-2000) OVRP/DVP, FDA, 29 Lincoln Drive, Bethesda,  
JOURNAL  
MD 20892, USA  
REMARK  
Sequence update by submitter  
COMMENT  
On Dec 1, 2000 this sequence version replaced gi:2394279.  
FEATURES  
Location/Qualifiers  
1..1524  
/organism="West Nile virus"  
/mol\_type="genomic RNA"  
/strain="Eg101"  
/db\_xref="taxon:11082"  
<1..864  
/gene="NS5"  
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/notes="viral replicase; polypeptide; putative"  
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/db\_xref="GI:11497618"  
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MAVSGDDCVVQPLDDRFATSLFLNMSKVRDIOEWKPSGTGWQVPPFCNSHFT  
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LMAAICSAVPVNVPTGRTTWSIHAGSEWNTDMLVWNRVWIEENWEMDKTPVE  
KNSDVPYSGKREDIWCGSLIGTRATWAENIQAINQVRSIIIGDEKYVDYMSSLKRY  
EDTTLVEDTVL"

ORIGIN  
Query Match 100.0%; Score 48; DB 14; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 2.6e-19;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGAGACGGTCTGAGGGCTTACATGGATCACTTCGACGCTTTGTTTC 48  
|||||  
DB 1095 TCCGAGACGGTCTGAGGGCTTACATGGATCACTTCGACGCTTTGTTTC 1048

RESULT 19

KUNCG/c  
LOCUS  
DEFINITION  
Kunjin virus gene for polyprotein (C, prM, E, NS1, NS2A, NS2B, NS3,  
NS4A, NS4B, NS5), complete cds.  
D00246  
ACCESSION  
VERSION  
D00246.1 GI:221966  
KEYWORDS  
M (membrane protein); prM (precursor of M); NS5; NS4B; NS4A; NS3;  
NS2B; NS2A; NS1; E (envelope protein); C (core protein);  
polyprotein.  
SOURCE  
Kunjin virus  
ORGANISM  
Kunjin virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Flavivirus; Japanese encephalitis virus group.  
REFERENCE  
1 (bases 1 to 10664)  
Coia, G., Parker, M.D., Speight, G., Byrne, M.E. and Westaway, E.G.  
AUTHORS  
Nucleotide and complete amino acid sequences of Kunjin virus:  
TITLE  
definitive gene order and characteristics of the virus-specified  
proteins  
J. Gen. Virol. 69 (Pt 1), 1-21 (1988)  
JOURNAL  
MEDLINE  
88089524  
PUBMED  
2826659  
COMMENT  
A kunjin (KUN) virus cDNA sequence of 10664 nucleotides which  
encoded a single open reading frame for 3433 amino acids was  
obtained and compared with the complete amino acid sequences of  
yellow fever and West Nile viruses. Partial N-terminal amino acid  
analyses of KUN virus-specified proteins identified the polyprotein  
cleavage sites and the definitive gene order. Three stop codons in  
the correct reading frame occur within the first 25 nucleotides  
beyond the 3' end of the coding sequence.  
Location/Qualifiers  
1..10664  
/organism="Kunjin virus"  
/mol\_type="genomic RNA"  
/strain="MRM61C"  
/db\_xref="taxon:11077"  
/clone="pKV479, pKV681, pKV87, pKV761, pKV62, pKV71,  
pKV621, pKV75, pKV90, pKV66"  
76..10377  
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/protein\_id="BAA00176.1"  
/db\_xref="GI:221967"

CDS

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VQTGSESLSNKKGAWDSTKATRYLVKTESWILNPGVALVAIVGMWGSNTMORV  
VFAVLLLPAYSPNCLGMSNRDFLEGSGATWVDLVLESDSCVTIMSKOPIIDVK  
MMNMEANLAEVRSYCYLATVSELSKTAACPTMGHNDKADPSPFCVQGVDRGW  
NGGLFGKGSIDTCAKFCSTKATRTILKENIKYEVAIFVHGPTTVSHSGNVFTQT  
AAQGRFSITPAAPSYTLKGEYGVTVDCPRSGIDTSAYVYMTVTGTYFLVHREMF  
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PKTIPISVSLNDLTPVRLVTVNPFVSSTANAKVILIEPPFGDSYIVVGRGBQQ  
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RSLFCGMSWITQGLICALLWGINARDISIALTFGLVGVLLFLSVNVHADTGCAID  
ISROELRCGSGVFIHNDVEAMTDVYKYPETPGQAKIIQAKHSGVCLRSVSRLEH  
QMWAEVKDELNTLLKENGVDLSIVVEKQEGMYKSAPRLTATTEKLEIGCKWAGKSL  
FAPELANNTVIDGPTKECTPNRANWNEVEDFGLTSTRMELRVRESNTECDSS  
KIIGTAVKXNLAHSDLSWIESRFDNFNDKLERAVLGEVKSCTPTTETHLWDGCVLES  
DLIIPITLAGPRSNHNRPGYKTSQGGWDEGRVIDFCPTGTTVLSGCHRGPA  
TRTTTSGKLTDMCCRSCTPLPYQTDNGCWGWEIRPORHDEKTLVQSOVNAVNA  
DMIDPFOLGLLVFLATQSVLRKWTAKIOPVPMVASFLKARTNQENILMLAAAFQNAVY  
GNAFASNSGGDVHVALMATAFKIOPVPMVASFLKARTNQENILMLAAAFQNAVY  
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TEWTAAGMFIAVGLAEIDDSNAIPMTIAGLMFAAFVISKSTDMWIERADISV  
EGDAITGSSERVDRLDDGDFOLMNDPGAPKTIWMLRMACLAISATYTPWAILPSV  
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TLWHTTKAALMSGEGRLDPYMGSKEDRLCYGPGPKLQHKWNGDQVQMVVEGKN  
VANQTKPGVFKTPEGEIGAVTLDFPTGSGPVDKNGDVI GLTNGVIMNGSTYS  
AIVQGERMDEPVPAGFPEMLRKQITVLDLHPGAGKTRILPQI11KEAINRRLTAV  
LAPTRVAAEMAEALRGLPIRYQTSVAVAREHNGNEIVDMVCHATLTHRLRVPVNY



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CMEKTKGQPEYEDVNLGSTRVAGKPLNSDTSIKNRIERLREYSSTWHHDENH  
PYRTWNYHGSYEVKPTGSASSLVNGVRLLSKPDWDTITNVTMTAMDTTTPCQORVFK  
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EQNQRSAREAVEDPKFEMWDEEREHLRGEGCHICINNMGKREKKGFEKAGKSR  
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YADDTAGWRTITRADLENAKVELLEDEHRLARATIELTYRHKVVKVMPKPADGR  
TYMDVISREDQSGQVYALNTNLAVQLVRWMEGEGVCPDDVEKLTGKGGPKV  
RTWLSEGERLSRMAVSGDCCVKPPLDRFATSLHFLNAMSCKVKDIOEKPSGTWY  
DMQVPPFCSNHTELIMKDGRTLVTPCRQDELVGRARISPGAGWNVDRDTACLAKSYA  
OMKLLYFHERDLRLMANALCSAVPNWVPTGRTTWSIHAGGEMTTEDMLVNRWRV  
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DEKYDYSLSKRYEDTTLVEDTLV

mat\_peptide

97..411

/product="core protein"

/note="C"

mat\_peptide

412..966

/product="premembrane protein"

/note="prM"

mat\_peptide

967..2469

/product="envelope protein"

/note="E"

mat\_peptide

2470..3525

/product="nonstructural protein 1"

/note="NS1"

mat\_peptide

3526..4218

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/note="NS2A"

mat\_peptide

4219..4611

/product="nonstructural protein 2B"

/note="NS2B"

mat\_peptide

4612..6468

/product="nonstructural protein 3"

/note="serine protease and helicase; NS3"

mat\_peptide

6469..6915

/product="nonstructural protein 4A"

/note="NS4A"

mat\_peptide

6916..7680

/product="nonstructural protein 4B"

/note="NS4B"

mat\_peptide

7681..10395

/product="nonstructural protein 5"

/note="methyl transferase and RNA-dependent RNA

polymerase; NS5"

10399..11022

3'UTR

ORIGIN

Query Match 100.0%; Score 48; DB 14; Length 11022;

Best Local Similarity 100.0%; Pred. No. 2.2e-19;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGCTTACATGATCCTTCGAGCTTGTTC 48

Db 10622 TCCGAGACGGTCTGAGGCTTACATGATCCTTCGAGCTTGTTC 10575

RESULT 21

LOCUS

AY274505/c

DEFINITION

Kunjin virus clone pAKUN polyprotein mRNA, complete cds.

ACCESSION

AY274505

VERSION

AY274505.1

KEYWORDS

Kunjin virus

ORGANISM

Kunjin virus

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Japanese encephalitis virus group.

Liu W.J., Chen H.B. and Khromykh, A.A.

Molecular and Functional Analyses of Kunjin Virus Infectious cDNA

Clones Demonstrate the Essential Roles for NS2A in Virus Assembly

and for a Nonconservative Residue in NS3 in RNA Replication

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

J. Virol. 77 (14), 7804-7813 (2003)

22713678

12829820

2 (bases 1 to 11022)

Khromykh, A.A., Liu, W.J. and Chen, H.B.

Direct Submission

Submitted (11-APR-2003) Clinical Medical Virology Centre,

University of Queensland/Sir Albert Sakzewski Virus Research

Centre, Royal Children's Hospital, Herston Rd., Herston, Brisbane,

QLD 4029, Australia

location/Qualifiers

1..11022

/organism="Kunjin virus"

/mol\_type="mRNA"

/db\_xref="taxon:11077"

/clone="pAKUN"

1..96

97..10398

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TRTTESGKLTJDCCRSCTLPPIRYQTDNGCWMEIRPQRHDKTLVQSOVNAYNA

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GAFAESNSGGVWHLAMATFKIQPFVMAVSFLKARWNTQENILMLAAAPFQWAVY

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SAAORGRIGRNPQOVGECYFGHTNEDDSCNAHWTEARIMLDNMPNGLIAOFYO

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KSGVDVFPSPSECCDILLCDIGESSSAEVBEHRTLRLVLEMDVLMHGPKEFCVKVL

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RMEKTKGQPEYEDVNLGSTRVAGKPLNSDTSIKNRIERLREYSSTWHHDENH

PYRTWNYHGSYEVKPTGSASSLVNGVRLLSKPDWDTITNVTMTAMDTTTPCQORVFK

EKVDTKAPPEPBGKVLNETTNLWAFLEAREKRPMSREEFIRKVNNAALGAMFE

EQNWRSAEAVEDPKFEMWDEBEAHLRGCHTCTIYNMGKREKPKCFKAGKRS  
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RWLSENGERLSRAVSGDDCVKPLDDRFATSLHFLNAMSKVARDIQEWKPSGTWY  
DQQVFPFCNHFTLIMKDRITLVPICRQDBLGVGRARISPGAGWNRDITACLSA  
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mat\_peptide

97...411

/product="core protein"

/note="C"

mat\_peptide

412...966

/product="premembrane protein"

/note="prM"

mat\_peptide

967...2469

/product="envelope protein"

/note="E"

mat\_peptide

2470...3525

/product="nonstructural protein 1"

/note="NS1"

mat\_peptide

3526...4218

/product="nonstructural protein 2A"

/note="NS2A"

mat\_peptide

4219...4611

/product="nonstructural protein 2B"

/note="NS2B"

mat\_peptide

4612...6468

/product="nonstructural protein 3"

/note="serine protease and helicase, NS3"

mat\_peptide

6469...6915

/product="nonstructural protein 4A"

/note="NS4A"

mat\_peptide

6916...7680

/product="nonstructural protein 4B"

/note="NS4B"

mat\_peptide

7681...10395

/product="nonstructural protein 5"

/note="methyl transferase and RNA-dependent RNA

polymerase; NS5"

10399...11022

3' UTR

ORIGIN

Query Match 100.0%; Score 48; DB 14; Length 11022;

Best Local Similarity 100.0%; Pred. No. 2.2e-19;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCTGAGGCGCTTACATGATCCTTCGACGCTTTGTC 48

Db 10622 TCCGAGACGGTTCTGAGGCGCTTACATGATCCTTCGACGCTTTGTC 10575

RESULT 22

AY490240/c

LOCUS

DEFINITION

West Nile virus strain Chin-01, complete genome.

ACCESSION

AY490240

VERSION

AY490240.2

KEYWORDS

West Nile virus (WNV)

SOURCE

West Nile virus

ORGANISM

Flavivirus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

1 (bases 1 to 11028)

REFERENCE

Jiang, T., Qin, E. and Deng, Y.

TITLE

Sequence determination and analysis of West Nile Virus strain

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 11028)

Jiang, T., Qin, E. and Deng, Y.

AUTHORS

Direct Submission

TITLE

Submitted (28-NOV-2003) Virology, Institute of Microbiology and

JOURNAL

Epidemiology, Fengtai Dongda Street, Beijing 100071, China

REFERENCE

3 (bases 1 to 11028)

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

FEATURES

source

Jiang, T., Qin, E. and Deng, Y.

Direct Submission

Submitted (08-APR-2004) Virology, Institute of Microbiology and

Epidemiology, Fengtai Dongda Street, Beijing 100071, China

Sequence update by submitter

On Apr 8, 2004 this sequence version replaced gi:40362614.

Location/Qualifiers

1..11028

/organism="West Nile virus"

/mol\_type="genomic RNA"

/strain="Chin-01"

/db\_xref="taxon:11082"

/country="China"

97..10398

/codon\_start=1

/product="polyprotein precursor"

/protein\_id="AAR84614.1"

/db\_xref="GI:40362614"

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VQTHGESTLANKGAMDSATRYLVKTESWILRNPGLYVAIVGMLGNSMTQVR

VFVVLILVAPAYSFNCIGMSNRPDLGVSATWDLVLEGSCTVMSKDKPTIDVK

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NGCGLFGKGSIDTCAKACSTKAGRTILKENIKYVAIVFVHPTTVESHGNYPTQIG

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MDLNLPMSSAGSTVNRNRETLMEFEHPHATQSVIALGQEGALQAALAPVFPSS

NKTVLTSGLHCRVMEKLOLQGTGYGVCSKAFKPLGTPADTGHVTVLEIQTGDD

PCKVPISSASINDLTVPVRLTVNPFVSATANAKVILEPFPFGSYIVVGRGEQ

INHHWKSIGSIIKFAFTTLKGAQRALAGDTAWDFGSGVFTSVGKAVHQTGCAF

RSLGKMSWITQGLLGLALLWGINARDSIALTFLAIGGVLLPLSVNHDATGCAID

ISRLQRCGSGVFIHNDVEAWMDRYKYPETPQGLAKIIQAKHEGVCGLSVSRLEH

QWAEAVDELTLKENGDLVSVVVEQSGMKAPKRLTATTEKLEIGKNAWGSIL

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KIIGTAVKNLAIHSLSYIESINDTDLKLERAVLGEVSKCTWPTLTLWGEGLES

DLIIPTVLAGRNSHNRPPGYKTONQGWDEVRVIDPDCPTVTTLSESGHRGPA

TRTTTESGLITDMCRSCTLPPLRYOTDSCWYGMELRPORHDKTLVQSOVNAVNA

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TEIPDRANNSGEMITEVIGKTVAFPSVKMGNEIALCLORAGKVKVQLNKSIVETEY

PKCDNDWDVITTDISEMGANFKASVIDSRKSVKPTIITEGEGRVILGSPSATAA

SAAQRGRIGRNPQSGDEYCYGGHTNEDDSENFHWTAEARIMLONINPNNGIAQFYQ

PERKVTYMDGEYLRGEERKNFLELLTADLPVNLAYKAAAGVSHDRWCFDGP

TILLEDNNEVGTWILKGERKILRPWIDARVYSDHQALKAQKDPAGKRSIGLIEV

LGKPEHPMGKTEALDTMYVATAEKGRAHMAELBELPALOTIALIALLSVMTMG

VFLLMQKGIKIGLGVILGVAIFCQWAEVPTKIAGMLLSLMLVILIPREK

QRSQTDNQLAVFLICVLILNSAVANEMGLDKNDISSLISFGQRIDVKNPMSGEFL

LDLRPATASLYAVITAVITPLLLKHLITSDYINTSLTSINVOASQRTFLAGFPFVDV

VVDGIVATDVPLELRTTPIQKVGQIMLILVSLAAVNVNPSVTKTRAGLITAAAV

TLWNGASSVNNATTIAGLCHIMRGWLSLSITWTLLKNKPKLKGAGKAGRTIGE

VKERLNQMTKEETRYRKEAIIEVDRSAKHARKEGNTGTHGVSRCATKLMLVER

RPLEPVKVIDLGGCGWCYCYMATQKRVQEVGYTKGPGHEEPQLVQSQWNIIVTM

KSGVDVFRPSPCCDITLDCIGESSASABVEHRTIRVLEWNEWDLHHRGKEFCVKVL

CPYMPKIERMELLQRRYGGGLVNRPLSRNTHMYWVSAGNVNTHSVNMTSVLLG

RMEKTRWKGPQYEEEDVNLGSGTRAVGKPLNSDKTKNRIERREYSSVTHHNDEN

PYRTWNYHGSYDVKPTSGASSLVNGLLSKPDWTITNTVTMTDITTPFQQRVFK

EKVDTKAPPEPPEKPVNLTNNLWAFAREKPRMCSREEFIKVNNSNALGAMFE

EQNQWRSAREAVEDPKFEMWDEBEAHLRGCHTCTIYNMGKREKPKCFKAGKRS

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YADTAGWTRITRADLENEAKVLELLDGEHRLARALIELTYRHKVVMKPADGR

TMDVLSREDQSGGVVYALNTFTNLAVQLVRMVEGVI GPDDVEKLTGKGGPKV

RTWLPEGEERLSRMVSGDDCVVLPDDRFPATSLHFLNMSKVRKDIQEWKPESTGWY  
DQWQVFCNSHFTLMDGRTLVPCQDELGRARISPGAMNVTRETTACLAWSYA  
QMWLLYFRRDLRLMANAICSAVPVNVPTGRTTWSIHAGGEMTTEGLEVNRVW  
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## ORIGIN

Query Match 100.0%; Score 48; DB 14; Length 11028;  
Best Local Similarity 100.0%; Pred. No. 2.2e-19;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTGAGCGCTTACATGATCACTTCGACGCTTGTTC 48  
|||||  
Db 10629 TCCGAGACGGTCTGAGCGCTTACATGATCACTTCGACGCTTGTTC 10582

## RESULT 23

AF260968/c  
LOCUS West Nile virus strain Egi01, complete genome. VRL 27-AUG-2000  
DEFINITION  
ACCESSION AF260968  
VERSION AF260968.1 GI:9930135

## KEYWORDS

SOURCE

## ORGANISM

West Nile virus  
West Nile virus  
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Flavivirus; Japanese encephalitis virus group.

1 (bases 1 to 11029)

Bowen, M., Meyer, R.F., McKinney, N., Morrill, W. and Lanciotti, R.

Complete genomic sequence of West Nile virus strain Egi01

Unpublished

2 (bases 1 to 11029)

Bowen, M., Meyer, R.F., McKinney, N., Morrill, W. and Lanciotti, R.

Direct Submission

Submitted (27-APR-2000) Arbovirus Diseases Branch, Centers for

Disease Control & Prevention, Rampart Road, Fort Collins, CO 80521,

USA

## FEATURES

## Source

1. .11029

/organism="West Nile virus"

/mol\_type="genomic RNA"

/strain="Egi01"

/db\_xref="taxon:11082"

97. .10398

/codon\_start=1

/product="polyprotein precursor"

/protein\_id="AG02039.1"

/db\_xref="GI:9930135"

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AMDVGTCMDTITTECPVLASAGNDPEDICWCTKSADVVRGCTKTRHSRBSRLIT  
VQTHGESLTLANKGAMDSKATRYLVKTESNILRNPGLVAVAVIGWMLSGNTQWRV  
VFVLLLVAPAYSFNCLMSNRDPLEGSGATVDVLVEGSGATVIMSKRPTIDVK  
MNMNEANLAVRSYCYLATVSDLSKACPTMGAEHNDKADPAFCVCKGVYDRGWG  
NGCGLFGKSIDTCACFACSTRATGRTILKENIKYEVAIFVHGPTTVESHGNYPIQIG  
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PCKPVLSSVASLNDLTPVGLVTVNPFVSATANAKVLIIELEPPFGDSYIVVGRGEQQ  
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RSLFGMSQITQGLGALLMWINARDSIALTLFVAGVLLFLSVNVAHDTCAGID  
ILIIIPVTLGAPSRNHRREYKQNPQWDEGRVIDEDFCFTTTLVSSCGHGP  
TRTTTESGLITDWCRCSTPLPYQTDSGCWYMEIRPORHDEKTLVQSOVNAYNA  
DMIDPDLGLVLAQTOELRWKRTAKISMPAILIALILVLFVGGITVTVDLRVYLV  
GAFAESNSGGDVHLAATFKIQPVFNVASFLKRWNTQENILLMLAAVFFQAYH  
DARQILLWEIPDLNSLAVAMILRAITFTTNSVVPVLLALTPLGLRCLNDVYRIL  
LTMVGTGSLIRKRSAAAKKGSLLCLALSTGLFPNMLAAGLIACDPNRKWMPA  
LTVMTAVGLMFAIVAGLAEIDISMAIPMTIAGLMPAFAFVISGKSTDMWIERADISW

## CDS

mat\_peptide

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466. .741

/product="pre-membrane protein prM"

742. .966

/product="membrane protein M"

967. .2469

/product="envelope glycoprotein E"

2470. .3525

/product="non-structural protein 1 NS1"

3526. .4218

/product="non-structural protein 2A NS2A"

4219. .4611

/product="non-structural protein 2B NS2B"

4612. .6468

/product="non-structural protein 3 NS3"

6469. .6915

/product="non-structural protein 4A NS4A"

6916. .7680

/product="non-structural protein NS4B"

7681. .10395

/product="non-structural protein NS5"

## ORIGIN

Query Match 100.0%; Score 48; DB 14; Length 11029;  
Best Local Similarity 100.0%; Pred. No. 2.2e-19;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTGAGCGCTTACATGATCACTTCGACGCTTGTTC 48  
|||||  
Db 10629 TCCGAGACGGTCTGAGCGCTTACATGATCACTTCGACGCTTGTTC 10582

## RESULT 24

AF458351/c

LOCUS

DEFINITION

Kunjin virus strain MRM16 nonstructural protein 5 gene, partial

cds.

VRL 18-JUN-2003

linear

RNA

456 bp

nonstructural

protein 5 gene, partial

AF458351  
 AF458351.1 GI:21636481  
 Kunjin virus  
 Kunjin virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Flavivirus; Japanese encephalitis virus group.  
 1 (bases 1 to 456)  
 Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.  
 Mouse neuroinvasive phenotype of West Nile virus strains varies  
 depending upon virus genotype  
 Virology 296 (1), 17-23 (2002)  
 22033887  
 PUBMED  
 12036314  
 2 (bases 1 to 456)  
 Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.  
 Direct Submission  
 Submitted (14-DEC-2001) Department of Pathology and WHO  
 Collaborating Center for Tropical Diseases, The University of Texas  
 Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA  
 Location/Qualifiers  
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 RYEDTLVEDTVL"  
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 3'UTR  
 ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 1.2e-18;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 CCGAGACGGTCTGAGGGCTTACATGGATCCTTCGACGCTTGTTC 48  
 |||||  
 Db 397 CCGAGACGGTCTGAGGGCTTACATGGATCCTTCGACGCTTGTTC 351  
 |||||  
 RESULT 25  
 AF297856/c  
 LOCUS  
 Kunjin virus isolate P1553 nonstructural protein 5 gene, partial  
 DEFINITION  
 AF297856  
 VERSION  
 AF297856.1 GI:11992002  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Kunjin virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Flavivirus; Japanese encephalitis virus group.  
 1 (bases 1 to 609)  
 Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,  
 Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.  
 The relationships between West Nile and Kunjin viruses  
 Emerging Infect. Dis. 7 (4), 697-705 (2001)  
 21469816  
 PUBMED  
 11585535  
 2 (bases 1 to 609)  
 Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.  
 and Hall,R.A.  
 Definitive studies of the relationships between West Nile and  
 Kunjin viruses  
 Unpublished  
 3 (bases 1 to 609)  
 REFERENCE

Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.  
 and Hall,R.A.  
 Direct Submission  
 Submitted (22-AUG-2000) Microbiology and Parasitology, University  
 of Queensland, St Lucia, QLD 4072, Australia  
 Location/Qualifiers  
 source  
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 ORIGIN  
 Query Match 93.8%; Score 45; DB 14; Length 609;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-17;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGAGACGGTCTGAGGGCTTACATGGATCCTTCGACGCTTTC 45  
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 Db 490 TCCGAGACGGTCTGAGGGCTTACATGGATCCTTCGACGCTTTC 446  
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 RESULT 26  
 AF458356/c  
 LOCUS  
 Kunjin virus strain K6453 nonstructural protein 5 gene, partial  
 DEFINITION  
 AF458356  
 VERSION  
 AF458356.1 GI:21636491  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Kunjin virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Flavivirus; Japanese encephalitis virus group.  
 1 (bases 1 to 458)  
 Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.  
 Mouse neuroinvasive phenotype of West Nile virus strains varies  
 depending upon virus genotype  
 Virology 296 (1), 17-23 (2002)  
 22033887  
 PUBMED  
 12036314  
 2 (bases 1 to 458)  
 Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.  
 Direct Submission  
 Submitted (14-DEC-2001) Department of Pathology and WHO  
 Collaborating Center for Tropical Diseases, The University of Texas  
 Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA  
 Location/Qualifiers  
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Query Match      85.4%; Score 41; DB 14; Length 458;
Best Local Similarity 100.0%; Pred. No. 8.5e-15;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   8 CGGTTCTGAGGGCTTACATGGATCACTTCGCAGCTTTGTTC 48
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Db    393 CGGTTCTGAGGGCTTACATGGATCACTTCGCAGCTTTGTTC 353
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RESULT 27
AF297851/c      524 bp RNA linear VRL 05-MAR-2002
LOCUS           Kunjin virus isolate M1465 nonstructural protein 5 gene, partial
DEFINITION      cds.
ACCESSION       AF297851
VERSION         AF297851.1 GI:11991992
KEYWORDS        Kunjin virus
SOURCE          Kunjin virus
ORGANISM        Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                Flavivirus; Japanese encephalitis virus group.
REFERENCE
AUTHORS        Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
                Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE          The relationships between West Nile and Kunjin viruses
JOURNAL         Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE        21469816
PUBMED         11585535
AUTHORS        2 (bases 1 to 524)
Scherrret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
JOURNAL         3 (bases 1 to 524)
Scherrret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Direct Submission
Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
FEATURES
source         1..524
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Query Match      85.4%; Score 41; DB 14; Length 524;
Best Local Similarity 100.0%; Pred. No. 8.4e-15;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   8 CGGTTCTGAGGGCTTACATGGATCACTTCGCAGCTTTGTTC 48
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Db    425 CGGTTCTGAGGGCTTACATGGATCACTTCGCAGCTTTGTTC 385
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RESULT 28
AF297850/c      545 bp RNA linear VRL 05-MAR-2002
LOCUS           Kunjin virus isolate K6590 nonstructural protein 5 gene, partial
DEFINITION      cds.
ACCESSION       AF297850
VERSION         AF297850.1 GI:11991990
KEYWORDS        Kunjin virus
SOURCE          Kunjin virus
ORGANISM        Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                Flavivirus; Japanese encephalitis virus group.
REFERENCE
AUTHORS        Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
                Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE          The relationships between West Nile and Kunjin viruses
JOURNAL         Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE        21469816
PUBMED         11585535
AUTHORS        2 (bases 1 to 545)
Scherrret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
JOURNAL         3 (bases 1 to 545)
Scherrret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Direct Submission
Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
FEATURES
source         1..524
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CDS

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DEFINITION Kunjin virus isolate SH183 nonstructural protein 5 gene, partial cds.

ACCESSION AF297853

VERSION AF297853.1 GI:11991996

KEYWORDS Kunjin virus

SOURCE Kunjin virus

ORGANISM Kunjin virus

REFERENCE Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.

AUTHORS 1 (bases 1 to 594)

Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.

TITLE The relationships between West Nile and Kunjin viruses

JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)

MEDLINE 21469816

PUBMED 11585535

REFERENCE 2 (bases 1 to 594)

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.

TITLE Definitive studies of the relationships between West Nile and Kunjin viruses

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 594)

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.

TITLE Direct Submission

JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia

FEATURES

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/protein\_id="AAG42391.1"

/db\_xref="GI:11991997"

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ORIGIN

Query Match 85.4%; Score 41; DB 14; Length 594;

Best Local Similarity 100.0%; Pred. No. 8.3e-15;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGTTCTGAGGCTTACATGGATCACTTCGCAGCTTTGTC 48

|||||

Db 462 CGGTTCTGAGGCTTACATGGATCACTTCGCAGCTTTGTC 422

|||||

RESULT 33

AF297846/c

LOCUS Kunjin virus isolate FC15 nonstructural protein 5 gene, partial cds

DEFINITION

ACCESSION AF297846

VERSION AF297846.1 GI:11991982

KEYWORDS Kunjin virus

SOURCE Kunjin virus

ORGANISM Kunjin virus

REFERENCE Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.

AUTHORS 1 (bases 1 to 600)

Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.

TITLE The relationships between West Nile and Kunjin viruses

JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)

MEDLINE 21469816

PUBMED 11585535

REFERENCE 2 (bases 1 to 600)

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.

TITLE Definitive studies of the relationships between West Nile and Kunjin viruses

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 600)

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.

TITLE Direct Submission

JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia

FEATURES

source

1..600

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ORIGIN

Query Match 85.4%; Score 41; DB 14; Length 600;

Best Local Similarity 100.0%; Pred. No. 8.3e-15;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGTTCTGAGGCTTACATGGATCACTTCGCAGCTTTGTC 48

|||||

Db 455 CGGTTCTGAGGCTTACATGGATCACTTCGCAGCTTTGTC 415

|||||

RESULT 34

AF458350/c

LOCUS West Nile virus strain And-27875 nonstructural protein 5 gene, partial cds.

DEFINITION

ACCESSION AF458350

VERSION AF458350.1 GI:21636479

KEYWORDS West Nile virus (WNV)

SOURCE West Nile virus

ORGANISM West Nile virus

REFERENCE Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.

AUTHORS 1 (bases 1 to 462)

Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.

TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies depending upon virus genotype

JOURNAL Virology 296 (1), 17-23 (2002)

MEDLINE 22033887

PUBMED 12036314

REFERENCE 2 (bases 1 to 462)

AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.

TITLE Direct Submission

JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO Collaborating Center for Tropical Diseases, The University of Texas Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA

FEATURES

source

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/vifion

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/db\_xref="taxon:11082"

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/codon\_start=1

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/protein\_id="AAM70016.1"

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Best Local Similarity 100.0%; Pred. No. 7e-13;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGCTTACATGGATCATTGCG 38
|||||
Db 404 TCCGAGACGGTTCGAGGCTTACATGGATCATTGCG 367

RESULT 35
AF458348/c
LOCUS
DEFINITION West Nile virus strain IBn7019 nonstructural protein 5 gene,
partial cds. linear VRL 18-JUN-2003
ACCESSION AF458348
VERSION AF458348.1 GI:21636475
KEYWORDS
SOURCE
ORGANISM West Nile virus (WNV)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 463)
AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
Location/Qualifiers
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cds. linear VRL 18-JUN-2003
ACCESSION AF458361
VERSION AF458361.1 GI:21636501
KEYWORDS
SOURCE
ORGANISM West Nile virus (WNV)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 463)
AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
Location/Qualifiers
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|||||
Db 405 TCCGAGACGGTTCGAGGCTTACATGGATCATTGCG 368

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LOCUS
DEFINITION West Nile virus strain 385-99 nonstructural protein 5 gene, partial
cds. linear VRL 18-JUN-2003
ACCESSION AF458360

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AF458360.1 GI:21636499
West Nile virus (WNV)
West Nile virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 463)
AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
Location/Qualifiers
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|||||
Db 405 TCCGAGACGGTTCGAGGCTTACATGGATCATTGCG 368

RESULT 37
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DEFINITION West Nile virus strain 31A nonstructural protein 5 gene, partial
cds. linear VRL 18-JUN-2003
ACCESSION AF458361
VERSION AF458361.1 GI:21636501
KEYWORDS
SOURCE
ORGANISM West Nile virus (WNV)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 463)
AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
Location/Qualifiers
FEATURES
source
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| SOURCE     | West Nile virus (WNV)  |            |             |  |
| ORGANISM   | West Nile virus (WNV)  |            |             |  |
| REFERENCE  | Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.     |            |             |  |
| AUTHORS    | 1 (bases 1 to 464)<br>Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.                            |            |             |  |
| TITLE      | Genetic and phenotypic variation of West Nile virus in New York, 2000-2003   |            |             |  |
| JOURNAL    | Am. J. Trop. Med. Hyg. (2004) In press   |            |             |  |
| REFERENCE  | 2 (bases 1 to 464)<br>Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.                            |            |             |  |
| AUTHORS    | Direct Submission  |            |             |  |
| TITLE      | Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA |            |             |  |
| JOURNAL    |  |            |             |  |
| FEATURES   | Location/Qualifiers  |            |             |  |
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|            |  |            |             |  |
|            | 106 TCCGACGCGTTCTGAGGCGTTACATGGATCACTTCGC 69   |            |             |  |
| Db         |  |            |             |  |
| RESULT 40  |  |            |             |  |
| AY590192/c |  |            |             |  |
| LOCUS      | West Nile virus 464 bp RNA linear VRL 30-MAY-2004  |            |             |  |
| DEFINITION | West Nile virus strain 03001087 3' UTR, partial sequence.  |            |             |  |
| ACCESSION  | AY590192   |            |             |  |
| VERSION    | AY590192.1   |            |             |  |
| KEYWORDS   | GI:47121679  |            |             |  |
| SOURCE     | West Nile virus (WNV)  |            |             |  |
| ORGANISM   | West Nile virus (WNV)  |            |             |  |
| REFERENCE  | Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.     |            |             |  |
| AUTHORS    | 1 (bases 1 to 464)<br>Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.                            |            |             |  |
| TITLE      | Genetic and phenotypic variation of West Nile virus in New York, 2000-2003   |            |             |  |
| JOURNAL    | Am. J. Trop. Med. Hyg. (2004) In press   |            |             |  |
| REFERENCE  | 2 (bases 1 to 464)<br>Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.                            |            |             |  |
| AUTHORS    | Direct Submission  |            |             |  |
| TITLE      | Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA |            |             |  |
| JOURNAL    |  |            |             |  |
| FEATURES   | Location/Qualifiers  |            |             |  |
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## ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 7e-13;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 106 TCCGAGACGGTTCTGAGGGCTTACATGGATCACTTCGC 69

## RESULT 41

AY590193/c  
 LOCUS West Nile virus (WNV) 464 bp RNA linear VRL 30-MAY-2004  
 DEFINITION West Nile virus strain 03001426 3' UTR, partial sequence.  
 ACCESSION AY590193  
 VERSION AY590193.1 GI:47121680

## KEYWORDS

## SOURCE

## ORGANISM

West Nile virus (WNV)  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Flavivirus; Japanese encephalitis virus group.

## REFERENCE

## AUTHORS

## TITLE

Genetic and phenotypic variation of West Nile virus in New York,  
 2000-2003

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth  
 Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA

## FEATURES

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## ORIGIN

Query Match 79.2%; Score 38; DB 14; Length 464;  
 Best Local Similarity 100.0%; Pred. No. 7e-13;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 106 TCCGAGACGGTTCTGAGGGCTTACATGGATCACTTCGC 69

## RESULT 42

AY590194/c  
 LOCUS West Nile virus (WNV) 464 bp RNA linear VRL 30-MAY-2004  
 DEFINITION West Nile virus strain 03001516 3' UTR, partial sequence.  
 ACCESSION AY590194  
 VERSION AY590194.1 GI:47121681

## KEYWORDS

## SOURCE

## ORGANISM

West Nile virus (WNV)  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Flavivirus; Japanese encephalitis virus group.

## REFERENCE

## AUTHORS

## TITLE

Genetic and phenotypic variation of West Nile virus in New York,  
 2000-2003

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

## 3'UTR

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## Conservative

## Mismatches

## Indels

## Gaps

## Qy

## Db

## RESULT 43

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

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## TITLE

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## TITLE

## JOURNAL

## REFERENCE

Ebel, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and  
 Kramer, L.D.

Direct Submission  
 Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth  
 Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA

Location/Qualifiers

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Db 106 TCCGAGACGGTTCTGAGGGCTTACATGGATCACTTCGC 69

RESULT 43

AY590195/c

LOCUS West Nile virus (WNV) 464 bp RNA linear VRL 30-MAY-2004

DEFINITION West Nile virus strain 03001543 3' UTR, partial sequence.

ACCESSION AY590195

VERSION AY590195.1 GI:47121682

KEYWORDS

SOURCE

West Nile virus (WNV)

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Japanese encephalitis virus group.

1 (bases 1 to 464)

Ebel, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and

Kramer, L.D.

Genetic and phenotypic variation of West Nile virus in New York,

2000-2003

Am. J. Trop. Med. Hyg. (2004) In press

Ebel, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and

Kramer, L.D.

Direct Submission

Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth

Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA

Location/Qualifiers

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Db 106 TCCGAGACGGTTCTGAGGGCTTACATGGATCACTTCGC 69

RESULT 44

AY590196/c

LOCUS West Nile virus (WNV) 464 bp RNA linear VRL 30-MAY-2004

DEFINITION West Nile virus strain 03001543 3' UTR, partial sequence.

ACCESSION AY590196

VERSION AY590196.1 GI:47121683

KEYWORDS

SOURCE

West Nile virus (WNV)

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Japanese encephalitis virus group.

1 (bases 1 to 464)

Ebel, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and

Kramer, L.D.

Genetic and phenotypic variation of West Nile virus in New York,

2000-2003

Am. J. Trop. Med. Hyg. (2004) In press

Ebel, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and

Kramer, L.D.

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DEFINITION West Nile virus strain 03001619 3' UTR, partial sequence.
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KEYWORDS West Nile virus (WNV)
SOURCE West Nile virus
ORGANISM West Nile virus
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 106 TCCGAGACGGTCTCGAGGCTTACATGGATCACTTCGC 69

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LOCUS West Nile virus strain 03001700 3' UTR, partial sequence.
DEFINITION West Nile virus strain 03001700 3' UTR, partial sequence.
ACCESSION AY590197
VERSION AY590197.1 GI:47121684
KEYWORDS West Nile virus (WNV)
SOURCE West Nile virus
ORGANISM West Nile virus
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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Db 106 TCCGAGACGGTCTCGAGGCTTACATGGATCACTTCGC 69

RESULT 46
AY590198/c
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DEFINITION West Nile virus strain 03001721 3' UTR, partial sequence.
ACCESSION AY590198
VERSION AY590198.1 GI:47121685
KEYWORDS West Nile virus (WNV)
SOURCE West Nile virus
ORGANISM West Nile virus
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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Db 106 TCCGAGACGGTCTCGAGGCTTACATGGATCACTTCGC 69

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LOCUS West Nile virus strain 03001734 3' UTR, partial sequence.
DEFINITION West Nile virus strain 03001734 3' UTR, partial sequence.
ACCESSION AY590199
VERSION AY590199.1 GI:47121686
KEYWORDS West Nile virus (WNV)
SOURCE West Nile virus
ORGANISM West Nile virus
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
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REFERENCE      2 (bases 1 to 464)
AUTHORS        Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
                Kramer,L.D.
TITLE          Direct Submission
JOURNAL        Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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FEATURES       Location/Qualifiers
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Db      106 TCCGAGACGGTCTCAGGGCTTACATGATCATTCCG 69

RESULT 48
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DEFINITION      West Nile virus strain 03001816 3' UTR, partial sequence.
ACCESSION       AY590200
VERSION         AY590200.1 GI:47121687
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SOURCE          West Nile virus (WNV)
ORGANISM        Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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REFERENCE       1 (bases 1 to 464)
AUTHORS        Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
                Kramer,L.D.
TITLE          Genetic and phenotypic variation of West Nile virus in New York,
                2000-2003
JOURNAL        Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE       2 (bases 1 to 464)
AUTHORS        Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
                Kramer,L.D.
TITLE          Direct Submission
JOURNAL        Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
                Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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DEFINITION      West Nile virus strain 03001869 3' UTR, partial sequence.
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KEYWORDS
SOURCE          West Nile virus (WNV)
ORGANISM        Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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REFERENCE       1 (bases 1 to 464)
AUTHORS        Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
                Kramer,L.D.
TITLE          Genetic and phenotypic variation of West Nile virus in New York,
                2000-2003
JOURNAL        Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE       2 (bases 1 to 464)
AUTHORS        Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
                Kramer,L.D.
TITLE          Direct Submission
JOURNAL        Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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KEYWORDS
SOURCE          West Nile virus (WNV)
ORGANISM        Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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REFERENCE       1 (bases 1 to 464)
AUTHORS        Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
                Kramer,L.D.
TITLE          Genetic and phenotypic variation of West Nile virus in New York,
                2000-2003
JOURNAL        Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE       2 (bases 1 to 464)
AUTHORS        Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
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TITLE          Direct Submission
JOURNAL        Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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ORGANISM        Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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REFERENCE       1 (bases 1 to 464)
AUTHORS        Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
                Kramer,L.D.
TITLE          Genetic and phenotypic variation of West Nile virus in New York,
                2000-2003
JOURNAL        Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE       2 (bases 1 to 464)
AUTHORS        Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
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ACCESSION       AY590202
VERSION         AY590202.1 GI:47121689
KEYWORDS
SOURCE          West Nile virus (WNV)
ORGANISM        Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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REFERENCE       1 (bases 1 to 464)
AUTHORS        Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
                Kramer,L.D.
TITLE          Genetic and phenotypic variation of West Nile virus in New York,
                2000-2003
JOURNAL        Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE       2 (bases 1 to 464)
AUTHORS        Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
                Kramer,L.D.
TITLE          Direct Submission
JOURNAL        Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| C 95  | 15 | 31.2 | 726  | 11 | ABD07934 | Abd07934 Pseudomon | 168 | 15 | 31.2 | 5382  | 10 | ADE98378  | Ade98378 Cancer-li  |
| C 96  | 15 | 31.2 | 747  | 10 | ADC03361 | Adc03361 Rice flow | 169 | 15 | 31.2 | 5390  | 10 | ADF09690  | Adf09690 Human pum  |
| C 97  | 15 | 31.2 | 747  | 12 | ADJ39652 | Adj39652 Plant CDN | 170 | 15 | 31.2 | 5390  | 12 | ADI24469  | Adi24469 Human mod  |
| C 98  | 15 | 31.2 | 1028 | 3  | AAL44852 | Aal44852 Plant flo | 171 | 15 | 31.2 | 5390  | 13 | ADH86604  | Adh86604 Human hou  |
| C 99  | 15 | 31.2 | 1080 | 4  | AAK69934 | Aak69934 Human imm | 172 | 15 | 31.2 | 5407  | 10 | ADF81470  | Adf81470 Leukaemia  |
| C 100 | 15 | 31.2 | 1117 | 4  | AAK69935 | Aak69935 Human imm | 173 | 15 | 31.2 | 5434  | 10 | ADE98336  | Ade98336 Cancer-li  |
| C 101 | 15 | 31.2 | 1521 | 11 | ABD07891 | Abd07891 Pseudomon | 174 | 15 | 31.2 | 5436  | 10 | ADE98331  | Ade98331 Cancer-li  |
| C 102 | 15 | 31.2 | 1587 | 13 | ADS55261 | Ads55261 Bacterial | 175 | 15 | 31.2 | 5463  | 10 | ADE98353  | Ade98353 Cancer-li  |
| C 103 | 15 | 31.2 | 1611 | 13 | ADN72718 | Adn72718 Bacterial | 176 | 15 | 31.2 | 5531  | 10 | ADE98325  | Ade98325 Cancer-li  |
| C 104 | 15 | 31.2 | 1839 | 12 | ADN72718 | Adn72718 Thale cre | 177 | 15 | 31.2 | 5531  | 10 | ADE98350  | Ade98350 Cancer-li  |
| C 105 | 15 | 31.2 | 1929 | 6  | ABZ13436 | Abz13436 Arabidops | 178 | 15 | 31.2 | 5584  | 10 | ADE98350  | Ade98350 Cancer-li  |
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| C 107 | 15 | 31.2 | 1929 | 8  | ADA68221 | Ada68221 Arabidops | 180 | 14 | 29.2 | 17    | 6  | ACN04658  | Acn04658 Human zinz |
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| C 110 | 15 | 31.2 | 4021 | 8  | ACC42350 | Acc42350 Human MAP | 183 | 14 | 29.2 | 110   | 3  | AAc14443  | Aac14443 Human sec  |
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| C 113 | 15 | 31.2 | 4628 | 10 | ADE98365 | Ade98365 Cancer-li | 186 | 14 | 29.2 | 193   | 12 | ADP93096  | Adp93096 Cotton ex  |
| C 114 | 15 | 31.2 | 4693 | 10 | ADE98314 | Ade98314 Cancer-li | 187 | 14 | 29.2 | 238   | 2  | AAT91880  | Aat91880 Partial h  |
| C 115 | 15 | 31.2 | 4709 | 10 | ADE98340 | Ade98340 Cancer-li | 188 | 14 | 29.2 | 253   | 12 | ADP95556  | Adp95556 Cotton ex  |
| C 116 | 15 | 31.2 | 4728 | 10 | ADE98367 | Ade98367 Cancer-li | 189 | 14 | 29.2 | 255   | 10 | ACA55863  | Acas5863 Mouse eig  |
| C 117 | 15 | 31.2 | 4774 | 10 | ADE98327 | Ade98327 Cancer-li | 190 | 14 | 29.2 | 255   | 12 | ADI55659  | Adi55659 Human pol  |
| C 118 | 15 | 31.2 | 4777 | 10 | ADE98343 | Ade98343 Cancer-li | 191 | 14 | 29.2 | 265   | 12 | ADP62259  | Adp62259 Soybean c  |
| C 119 | 15 | 31.2 | 4795 | 10 | ADE98311 | Ade98311 Cancer-li | 192 | 14 | 29.2 | 272   | 12 | ADP62260  | Adp62260 Soybean c  |
| C 120 | 15 | 31.2 | 4809 | 10 | ADE98370 | Ade98370 Cancer-li | 193 | 14 | 29.2 | 285   | 2  | AAT94614  | Aat94614 Human pen  |
| C 121 | 15 | 31.2 | 4814 | 2  | AAQ32956 | Aaq32956 PPI gene  | 194 | 14 | 29.2 | 311   | 12 | ADK60244  | Adk60244 Antisense  |
| C 122 | 15 | 31.2 | 4825 | 10 | ADE98366 | Ade98366 Cancer-li | 195 | 14 | 29.2 | 311   | 12 | ADK60545  | Adk60545 Antisense  |
| C 123 | 15 | 31.2 | 4830 | 10 | ADE98345 | Ade98345 Cancer-li | 196 | 14 | 29.2 | 311   | 12 | ADP73168  | Adp73168 Angiogene  |
| C 124 | 15 | 31.2 | 4876 | 10 | ADE98376 | Ade98376 Cancer-li | 197 | 14 | 29.2 | 313   | 5  | ABA12797  | Abal2797 Human ner  |
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| C 127 | 15 | 31.2 | 4906 | 10 | ADE98369 | Ade98369 Cancer-li | 200 | 14 | 29.2 | 359   | 2  | AAT22137  | Aat22137 Human gen  |
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| C 132 | 15 | 31.2 | 4976 | 10 | ADE98326 | Ade98326 Cancer-li | 205 | 14 | 29.2 | 468   | 9  | ACH38754  | Ach38754 Human foe  |
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| C 146 | 15 | 31.2 | 5094 | 10 | ADE98309 | Ade98309 Cancer-li | 219 | 14 | 29.2 | 818   | 3  | AAA95781  | Aaa95781 Human imm  |
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| C 153 | 15 | 31.2 | 5185 | 10 | ADE98347 | Ade98347 Cancer-li | 226 | 14 | 29.2 | 978   | 8  | ACF73711  | Acf73711 Staphyloc  |
| C 154 | 15 | 31.2 | 5190 | 10 | ADE98335 | Ade98335 Cancer-li | 227 | 14 | 29.2 | 981   | 8  | ACA20302  | Ac20302 Prokaryot   |
| C 155 | 15 | 31.2 | 5232 | 10 | ADE98337 | Ade98337 Cancer-li | 228 | 14 | 29.2 | 1049  | 8  | ACA48612  | Aca48612 Prokaryot  |
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| C 157 | 15 | 31.2 | 5264 | 10 | ADE98382 | Ade98382 Cancer-li | 230 | 14 | 29.2 | 1242  | 4  | AAS56263  | Aas56263 Salmonell  |
| C 158 | 15 | 31.2 | 5271 | 10 | ADE98329 | Ade98329 Cancer-li | 231 | 14 | 29.2 | 1242  | 8  | ACA51807  | Aca51807 Prokaryot  |
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| C 163 | 15 | 31.2 | 5339 | 8  | ACC42351 | Acc42351 Human MAP | 236 | 14 | 29.2 | 1492  | 2  | AAZ00814  | Aaz00814 Human sec  |
| C 164 | 15 | 31.2 | 5359 | 8  | ACC42351 | Acc42351 Human MAP | 237 | 14 | 29.2 | 1492  | 8  | ADA39903  | Ada39903 Human sec  |
| C 165 | 15 | 31.2 | 5361 | 10 | ADE98381 | Ade98381 Cancer-li | 238 | 14 | 29.2 | 1492  | 8  | ACC50492  | Acc50492 Human sec  |
| C 166 | 15 | 31.2 | 5366 | 10 | ADE98351 | Ade98351 Cancer-li | 239 | 14 | 29.2 | 1492  | 8  | ABZ71274  | Abz71274 Human sec  |

|       |    |      |      |    |           |                    |       |    |      |        |    |             |                     |
|-------|----|------|------|----|-----------|--------------------|-------|----|------|--------|----|-------------|---------------------|
| C 240 | 14 | 29.2 | 1492 | 9  | ADB91180  | Adb91180 Human sec | C 313 | 14 | 29.2 | 5765   | 12 | ADO20387    | Ado20387 Human PRO  |
| C 241 | 14 | 29.2 | 1492 | 10 | ADC73557  | Adc73557 Human sec | 314   | 14 | 29.2 | 5771   | 12 | ADK60290    | Adk60290 Angiogene  |
| C 242 | 14 | 29.2 | 1492 | 10 | ADD37614  | Add37614 Human sec | 315   | 14 | 29.2 | 5771   | 12 | ADK60591    | Adk60591 Angiogene  |
| C 243 | 14 | 29.2 | 1492 | 10 | ADA56093  | Ada56093 Gene enco | 316   | 14 | 29.2 | 5771   | 12 | ADP73214    | Adp73214 Angiogene  |
| C 244 | 14 | 29.2 | 1508 | 11 | ADM02282  | Adm02282 Human cDN | C 317 | 14 | 29.2 | 5943   | 10 | ADE53846    | Ades53846 Human pro |
| C 245 | 14 | 29.2 | 1584 | 10 | ACC60774  | Acc60774 Gene sequ | C 318 | 14 | 29.2 | 5955   | 5  | ABA20275    | Abas20275 Human ner |
| C 246 | 14 | 29.2 | 1584 | 10 | ADK61973  | Adk61973 Disease t | C 319 | 14 | 29.2 | 5987   | 11 | ACN89038    | Acn89038 Breat ca   |
| C 247 | 14 | 29.2 | 1584 | 13 | ADT47333  | Adt47333 Bacterial | C 320 | 14 | 29.2 | 5987   | 5  | ABA20274    | Abas20274 Human ner |
| C 248 | 14 | 29.2 | 1619 | 6  | ABL61992  | AbL61992 Colon ade | 321   | 14 | 29.2 | 6871   | 13 | ADR84323    | Adr84323 Aspergill  |
| C 249 | 14 | 29.2 | 1635 | 11 | ABD00187  | Abd00187 Klebsiell | 322   | 14 | 29.2 | 7120   | 4  | ABL04480    | AbL04480 Drosophil  |
| C 250 | 14 | 29.2 | 1662 | 8  | ACA35379  | AcA35379 Prokaryot | 323   | 14 | 29.2 | 7376   | 4  | ABL29946    | AbL29946 Drosophil  |
| C 251 | 14 | 29.2 | 1731 | 10 | ADD47838  | Add47838 Human gen | 324   | 14 | 29.2 | 7751   | 4  | ABL16582    | AbL16582 Drosophil  |
| C 252 | 14 | 29.2 | 1736 | 10 | ADB63042  | AdB63042 Human cDN | 325   | 14 | 29.2 | 8296   | 12 | ADO10003    | Ado10003 Human SIM  |
| C 253 | 14 | 29.2 | 1778 | 4  | AAK84200  | Aak84200 Human imm | C 326 | 14 | 29.2 | 9096   | 2  | AAT88015    | Aat88015 Human int  |
| C 254 | 14 | 29.2 | 1824 | 6  | ABN90694  | Abn90694 Staphyloc | C 327 | 14 | 29.2 | 9404   | 6  | AAD25318    | Aad25318 Human HSD  |
| C 255 | 14 | 29.2 | 1824 | 13 | ADS03917  | Ads03917 Staphyloc | C 328 | 14 | 29.2 | 9404   | 6  | AAD25261    | Aad25261 Human HSD  |
| C 256 | 14 | 29.2 | 1968 | 9  | ADB09644  | AdB09644 Alloiococ | C 329 | 14 | 29.2 | 9500   | 4  | AAH57414    | Aah57414 Human ova  |
| C 257 | 14 | 29.2 | 1968 | 9  | ADB09642  | AdB09642 Alloiococ | 330   | 14 | 29.2 | 17310  | 2  | AAV74334    | Aav74334 Staphyloc  |
| C 258 | 14 | 29.2 | 1968 | 12 | ADJ27112  | Adj27112 Alloiococ | 331   | 14 | 29.2 | 20001  | 13 | ACN37237    | Acn37237 Human per  |
| C 259 | 14 | 29.2 | 2000 | 6  | ABZ17521  | Abz17521 Arabidops | C 332 | 14 | 29.2 | 21045  | 4  | AAS26721    | Aas26721 Human gen  |
| C 260 | 14 | 29.2 | 2024 | 10 | AD121894  | Adi21894 Novel hum | C 333 | 14 | 29.2 | 21045  | 8  | ABX74070    | Abx74070 Human nov  |
| C 261 | 14 | 29.2 | 2066 | 4  | AAK52372  | Aak52372 Human pol | C 334 | 14 | 29.2 | 23307  | 4  | AAI02958    | Aai02958 Human rep  |
| C 262 | 14 | 29.2 | 2123 | 6  | AAK53356  | Aak53356 Human pol | C 335 | 14 | 29.2 | 23307  | 4  | AAI02842    | Aai02842 Human rep  |
| C 263 | 14 | 29.2 | 2166 | 6  | ABL55863  | AbL55863 Human oxi | 336   | 14 | 29.2 | 23307  | 8  | ADA41565    | Ada41565 Human sec  |
| C 264 | 14 | 29.2 | 2232 | 8  | ADA69632  | Ada69632 Rice gene | C 337 | 14 | 29.2 | 23307  | 10 | ADC74654    | Adc74654 Human sec  |
| C 265 | 14 | 29.2 | 2533 | 4  | AAH15617  | Aah15617 Drosophil | C 338 | 14 | 29.2 | 23307  | 10 | ADD38122    | Add38122 cDNA clon  |
| C 266 | 14 | 29.2 | 2623 | 4  | AAH15617  | Aah15617 Human cDN | 339   | 14 | 29.2 | 23307  | 10 | ADA57698    | Ada57698 BAC fragm  |
| C 267 | 14 | 29.2 | 2623 | 6  | ABK09777  | Abk09777 Human ova | C 340 | 14 | 29.2 | 23333  | 4  | ABL14260    | AbL14260 Drosophil  |
| C 268 | 14 | 29.2 | 2638 | 13 | ADS48658  | Ads48658 Bacterial | 341   | 14 | 29.2 | 23694  | 11 | ACN45138    | Acn45138 Human gen  |
| C 269 | 14 | 29.2 | 2709 | 4  | AAK82737  | Aak82737 Human imm | 342   | 14 | 29.2 | 32502  | 4  | AAS59542    | Aas59542 Propionib  |
| C 270 | 14 | 29.2 | 2757 | 2  | AAK06821  | Aax06821 Chlamydia | 343   | 14 | 29.2 | 32502  | 8  | ACF64471    | Acf64471 Propionib  |
| C 271 | 14 | 29.2 | 2823 | 12 | ADO10008  | Ado10008 Human SIM | 344   | 14 | 29.2 | 35048  | 4  | ABL06102    | AbL06102 Drosophil  |
| C 272 | 14 | 29.2 | 2859 | 6  | AAD30523  | Aad30523 Human sin | 345   | 14 | 29.2 | 3676   | 13 | ABD32930    | Abd32930 Human can  |
| C 273 | 14 | 29.2 | 2859 | 4  | AAH14490  | Aah14490 Human cDN | C 346 | 14 | 29.2 | 37004  | 13 | ABD33353    | Abd33353 Human can  |
| C 274 | 14 | 29.2 | 2957 | 3  | AAZ61509  | Aaz61509 DNA encod | C 347 | 14 | 29.2 | 44147  | 6  | ABK84481    | Abk84481 Human cDN  |
| C 275 | 14 | 29.2 | 2957 | 8  | ACC47249  | Acc47249 Human sca | C 348 | 14 | 29.2 | 44147  | 10 | ABD14691    | Abd14691 Human src  |
| C 276 | 14 | 29.2 | 3048 | 2  | AAQ75343  | Aaq75343 Soybean p | 349   | 14 | 29.2 | 47322  | 13 | ADD33395    | Add33395 Murine ca  |
| C 277 | 14 | 29.2 | 3129 | 13 | ACN40913  | Acn40913 Tumour-as | C 350 | 14 | 29.2 | 51256  | 10 | ADB85543    | AdB85543 Human sen  |
| C 278 | 14 | 29.2 | 3130 | 6  | ABL69700  | AbL69700 Prostate  | C 351 | 14 | 29.2 | 51256  | 10 | ADK66161    | Adk66161 Human pro  |
| C 279 | 14 | 29.2 | 3130 | 8  | ABL67710  | AbL67710 Oesophagu | C 352 | 14 | 29.2 | 51719  | 6  | ADK31365    | Adk31365 52Kb gene  |
| C 280 | 14 | 29.2 | 3210 | 6  | ABT32158  | Abt32158 Human neu | 353   | 14 | 29.2 | 53458  | 13 | ABD32806_5  | Continuation (7 of  |
| C 281 | 14 | 29.2 | 3211 | 2  | AAQ75344  | Aaq75344 Soybean p | C 354 | 14 | 29.2 | 58822  | 9  | ADA02540    | Ada02540 Human TCO  |
| C 282 | 14 | 29.2 | 3294 | 13 | ACN40914  | Acn40914 Tumour-as | C 355 | 14 | 29.2 | 58822  | 10 | ADB72278    | AdB72278 Human TCO  |
| C 283 | 14 | 29.2 | 3295 | 12 | ADQ87105  | Adq87105 Human tum | C 356 | 14 | 29.2 | 58822  | 10 | ADE95788    | AdE95788 Human TCO  |
| C 284 | 14 | 29.2 | 3295 | 13 | ADG86058  | AdG86058 Human tum | C 357 | 14 | 29.2 | 59065  | 6  | ABL42416    | AbL42416 Human ser  |
| C 285 | 14 | 29.2 | 3312 | 12 | ADK67724  | Adk67724 Human sim | C 358 | 14 | 29.2 | 59065  | 6  | ABD41839    | Abd41839 Human LIM  |
| C 286 | 14 | 29.2 | 3334 | 4  | AAK82796  | Aak82796 Human imm | C 359 | 14 | 29.2 | 59065  | 10 | ADG98727    | AdG98727 Human kin  |
| C 287 | 14 | 29.2 | 3405 | 12 | AD161914  | Adi61914 Fiber exp | C 360 | 14 | 29.2 | 59065  | 13 | ADR44808    | Adr44808 Human kin  |
| C 288 | 14 | 29.2 | 3405 | 12 | AAI56402  | Aai56402 Cotton fi | 361   | 14 | 29.2 | 79329  | 12 | ADQ97506    | Adq97506 Mouse can  |
| C 289 | 14 | 29.2 | 3560 | 11 | ADM02910  | Adm02910 Human cDN | C 362 | 14 | 29.2 | 92139  | 6  | ADA031364   | Ada031364 92Kb gene |
| C 290 | 14 | 29.2 | 3621 | 11 | ACN89500  | Acn89500 Breast ca | C 363 | 14 | 29.2 | 96587  | 9  | ADA02984    | Ada02984 Human MAP  |
| C 291 | 14 | 29.2 | 3828 | 12 | ADQ22517  | Adq22517 Human eof | C 364 | 14 | 29.2 | 96587  | 10 | ADB72722    | AdB72722 Human MAP  |
| C 292 | 14 | 29.2 | 3885 | 6  | ABK922169 | Abk922169 Prostate | C 365 | 14 | 29.2 | 96587  | 10 | ADC85464    | Adc85464 Human Map  |
| C 293 | 14 | 29.2 | 3885 | 12 | ADO10007  | Ado10007 Human SIM | C 366 | 14 | 29.2 | 96587  | 12 | ADM74579    | Adm74579 Human car  |
| C 294 | 14 | 29.2 | 3920 | 6  | AAD30522  | Aad30522 Human sin | C 367 | 14 | 29.2 | 99957  | 9  | ADA03032    | Ada03032 Human mCG  |
| C 295 | 14 | 29.2 | 3936 | 12 | ADK60411  | Adk60411 Angiogene | C 368 | 14 | 29.2 | 99957  | 10 | ADB72770    | AdB72770 Human CA   |
| C 296 | 14 | 29.2 | 3936 | 12 | ADK60712  | Adk60712 Angiogene | C 369 | 14 | 29.2 | 99957  | 10 | ADC85512    | Adc85512 Human gen  |
| C 297 | 14 | 29.2 | 3936 | 12 | ADP73335  | Adp73335 Human RIN | C 370 | 14 | 29.2 | 99957  | 12 | ADM74627    | Adm74627 Human car  |
| C 298 | 14 | 29.2 | 3937 | 4  | AAH15767  | Aah15767 Human cDN | 371   | 14 | 29.2 | 101169 | 12 | ADQ97584    | Adq97584 Mouse can  |
| C 299 | 14 | 29.2 | 3937 | 12 | ADK60444  | Adk60444 Angiogene | C 372 | 14 | 29.2 | 105184 | 6  | ABK24122    | Abk24122 Bacterial  |
| C 300 | 14 | 29.2 | 3937 | 12 | ADK60745  | Adk60745 Angiogene | C 373 | 14 | 29.2 | 110000 | 2  | AAK91990_00 | Aak91990 Nucleotid  |
| C 301 | 14 | 29.2 | 4493 | 8  | ADR08436  | Adr08436 Full leng | C 374 | 14 | 29.2 | 110000 | 5  | AAI61373_3  | Continuation (4 of  |
| C 302 | 14 | 29.2 | 4679 | 13 | ACC44335  | Acc44335 Gene enco | C 375 | 14 | 29.2 | 110000 | 6  | ABA03041_22 | Continuation (23 o  |
| C 303 | 14 | 29.2 | 4954 | 13 | ADR08350  | Adr08350 Full leng | C 376 | 14 | 29.2 | 110000 | 9  | ADB12064_09 | Continuation (10 o  |
| C 304 | 14 | 29.2 | 4978 | 10 | ADP74208  | Adp74208 Human nov | C 377 | 14 | 29.2 | 110000 | 9  | ADB12064_10 | Continuation (11 o  |
| C 305 | 14 | 29.2 | 5022 | 6  | ABK84067  | Abk84067 Human cDN | 378   | 14 | 29.2 | 110000 | 10 | ADG70447_3  | Continuation (4 of  |
| C 306 | 14 | 29.2 | 5022 | 10 | ADD14628  | AdD14628 Human src | 379   | 14 | 29.2 | 110000 | 10 | ABZ79565_3  | Continuation (4 of  |
| C 307 | 14 | 29.2 | 5022 | 10 | ADH28889  | Adh28889 Human chr | 380   | 14 | 29.2 | 110000 | 12 | ADN46845_14 | Continuation (15 o  |
| C 308 | 14 | 29.2 | 4679 | 13 | ADR08350  | Adr08350 Full leng | C 381 | 14 | 29.2 | 110000 | 12 | ADN47591_06 | Continuation (7 of  |
| C 309 | 14 | 29.2 | 4978 | 10 | ADP74208  | Adp74208 Human nov | C 382 | 14 | 29.2 | 110000 | 12 | ADN46123_14 | Continuation (15 o  |
| C 310 | 14 | 29.2 | 5022 | 6  | ABK84067  | Abk84067 Human cDN | C 383 | 14 | 29.2 | 110000 | 12 | ADN47209_06 | Continuation (7 of  |
| C 311 | 14 | 29.2 | 5022 | 10 | ADD14628  | AdD14628 Human src | 384   | 14 | 29.2 | 110000 | 12 | ADN46464_14 | Continuation (15 o  |
| C 312 | 14 | 29.2 | 5022 | 10 | ADH28889  | Adh28889 Human chr | C 385 | 14 | 29.2 | 110000 | 12 | ADN47960_06 | Continuation (7 of  |

|     |    |      |        |    |          |                    |    |      |     |    |          |                    |
|-----|----|------|--------|----|----------|--------------------|----|------|-----|----|----------|--------------------|
| 386 | 14 | 29.2 | 118951 | 8  | ABT17385 | Abt17385 Human IG  | 13 | 27.1 | 288 | 12 | ADL83774 | Adl83774 DNA up-re |
| 387 | 14 | 29.2 | 123920 | 11 | ACN44816 | Acn44816 Mouse gen | 13 | 27.1 | 289 | 5  | ABV60671 | Abv60671 Human pro |
| 388 | 14 | 29.2 | 128978 | 6  | ABK83459 | Abk83459 Human cDN | 13 | 27.1 | 291 | 5  | ABV60616 | Abv60616 Human pro |
| 389 | 14 | 29.2 | 128978 | 8  | AAD54587 | Aad54587 Human LIM | 13 | 27.1 | 291 | 5  | ABV60425 | Abv60425 Human pro |
| 390 | 14 | 29.2 | 128978 | 13 | ADR52994 | Adr52994 Drug ther | 13 | 27.1 | 293 | 8  | ACA14435 | ACA14435 Prokaryot |
| 391 | 14 | 29.2 | 130320 | 10 | ADF11613 | Adf11613 Human scl | 13 | 27.1 | 293 | 8  | ACA14435 | ACA14435 Prokaryot |
| 392 | 14 | 29.2 | 133893 | 9  | AAD54538 | Aad54538 Human pho | 13 | 27.1 | 295 | 5  | ABV60518 | Abv60518 Human pro |
| 393 | 14 | 29.2 | 134442 | 13 | ABD32824 | Abd32824 Mouse can | 13 | 27.1 | 295 | 5  | ABV60582 | Abv60582 Human pro |
| 394 | 14 | 29.2 | 135995 | 13 | ABD33534 | Abd33534 Murine ca | 13 | 27.1 | 299 | 5  | ABV60557 | Abv60557 Human pro |
| 395 | 14 | 29.2 | 185695 | 8  | ABQ77405 | Abq77405 Human THB | 13 | 27.1 | 300 | 11 | ACH94504 | Ach94504 Klebsiell |
| 396 | 14 | 29.2 | 185695 | 8  | AAD55693 | Aad55693 Human THB | 13 | 27.1 | 301 | 5  | ABV60513 | Abv60513 Human pro |
| 397 | 14 | 29.2 | 192427 | 10 | ADL13825 | Adl13825 Osteoarth | 13 | 27.1 | 301 | 5  | ABV60513 | Abv60513 Human pro |
| 398 | 14 | 29.2 | 200000 | 12 | ADQ47190 | Adq47190 DNA seque | 13 | 27.1 | 302 | 5  | ABV60381 | Abv60381 Human pro |
| 399 | 14 | 29.2 | 210528 | 11 | ACN44040 | Acn44040 Mouse gen | 13 | 27.1 | 303 | 5  | ABV60615 | Abv60615 Human pro |
| 400 | 14 | 29.2 | 222821 | 11 | ACN44754 | Acn44754 Human gen | 13 | 27.1 | 304 | 8  | ACA15490 | ACA15490 Prokaryot |
| 401 | 14 | 29.2 | 228006 | 12 | ADQ97143 | Adq97143 Mouse can | 13 | 27.1 | 304 | 10 | ABX88536 | Abx88536 Corn ear- |
| 402 | 14 | 29.2 | 256157 | 11 | ACN44650 | Acn44650 Human gen | 13 | 27.1 | 305 | 5  | ABV60474 | Abv60474 Human pro |
| 403 | 14 | 29.2 | 256157 | 13 | ABD33570 | Abd33570 Human can | 13 | 27.1 | 307 | 5  | ABV60417 | Abv60417 Human pro |
| 404 | 14 | 29.2 | 256190 | 13 | ABD33276 | Abd33276 Human can | 13 | 27.1 | 308 | 5  | ABV60598 | Abv60598 Human pro |
| 405 | 14 | 29.2 | 302603 | 11 | ADP75187 | Adp75187 Human end | 13 | 27.1 | 311 | 5  | ABV60437 | Abv60437 Human pro |
| 406 | 14 | 29.2 | 337022 | 12 | ADQ59416 | Adq59416 Human can | 13 | 27.1 | 311 | 5  | ABV60437 | Abv60437 Human pro |
| 407 | 14 | 29.2 | 347001 | 12 | ADP43517 | Adp43517 Human MAD | 13 | 27.1 | 315 | 3  | AAC09617 | Aac09617 Human sec |
| 408 | 13 | 27.1 | 17     | 6  | ACN03370 | Acn03370 MNV Inozy | 13 | 27.1 | 315 | 3  | AAC09617 | Aac09617 Human sec |
| 409 | 13 | 27.1 | 17     | 6  | ACN09611 | Acn09611 MNV minus | 13 | 27.1 | 320 | 10 | ADF81163 | Adf81163 Leukaemia |
| 410 | 13 | 27.1 | 18     | 2  | AAV08120 | Aav08120 Primer Vb | 13 | 27.1 | 321 | 8  | ACA14847 | ACA14847 Prokaryot |
| 411 | 13 | 27.1 | 20     | 2  | AAT15131 | Aat15131 Hypermuta | 13 | 27.1 | 321 | 8  | ACA14282 | ACA14282 Prokaryot |
| 412 | 13 | 27.1 | 20     | 2  | AAT15111 | Aat15111 Hypermuta | 13 | 27.1 | 321 | 13 | ACN47162 | Acn47162 Cotton pr |
| 413 | 13 | 27.1 | 20     | 2  | AAV21003 | Aav21003 Microsate | 13 | 27.1 | 324 | 5  | ABV60585 | Abv60585 Human pro |
| 414 | 13 | 27.1 | 20     | 2  | AAV21035 | Aav21035 Microsate | 13 | 27.1 | 324 | 5  | ABV60524 | Abv60524 Human pro |
| 415 | 13 | 27.1 | 20     | 2  | AAV36433 | Aav36433 Primer IA | 13 | 27.1 | 327 | 8  | ACA33375 | ACA33375 Prokaryot |
| 416 | 13 | 27.1 | 20     | 2  | AAZ21659 | Aaz21659 Exemplary | 13 | 27.1 | 327 | 8  | ACA33375 | ACA33375 Prokaryot |
| 417 | 13 | 27.1 | 20     | 2  | AAZ21691 | Aaz21691 Exemplary | 13 | 27.1 | 330 | 5  | ADL36309 | Adl36309 Human ova |
| 418 | 13 | 27.1 | 20     | 2  | AAH42021 | Aah42021 Disease t | 13 | 27.1 | 330 | 5  | ADL36309 | Adl36309 Human ova |
| 419 | 13 | 27.1 | 25     | 9  | ACK12719 | Ack12719 Human mic | 13 | 27.1 | 332 | 6  | ABK76318 | Abk76318 Bacillus  |
| 420 | 13 | 27.1 | 31     | 2  | AAQ72252 | Aaq72252 Chloramph | 13 | 27.1 | 341 | 8  | ABX37643 | Abx37643 Bovine ES |
| 421 | 13 | 27.1 | 32     | 2  | AAQ31901 | Aaq31901 PCR prime | 13 | 27.1 | 345 | 6  | ABK78754 | Abk78754 Bacillus  |
| 422 | 13 | 27.1 | 38     | 12 | ADJ63902 | Adj63902 Plant lip | 13 | 27.1 | 345 | 8  | ACA35241 | ACA35241 Prokaryot |
| 423 | 13 | 27.1 | 60     | 13 | ADG53324 | Adg53324 Eucalyptu | 13 | 27.1 | 353 | 4  | AA337145 | Aa337145 Novel hum |
| 424 | 13 | 27.1 | 64     | 12 | ADN02062 | Adn02062 Primer ml | 13 | 27.1 | 353 | 4  | AA337145 | Aa337145 Novel hum |
| 425 | 13 | 27.1 | 65     | 6  | ABN51566 | Abn51566 Mouse spl | 13 | 27.1 | 363 | 3  | AAC08176 | Aac08176 Human sec |
| 426 | 13 | 27.1 | 81     | 12 | ADF99890 | Adf99890 Nicotiana | 13 | 27.1 | 363 | 3  | AAC08176 | Aac08176 Human sec |
| 427 | 13 | 27.1 | 100    | 8  | ACD75393 | AcD75393 E. coli K | 13 | 27.1 | 366 | 5  | ABV60488 | Abv60488 Human pro |
| 428 | 13 | 27.1 | 100    | 8  | ACD75392 | AcD75392 E. coli K | 13 | 27.1 | 366 | 5  | ABV60488 | Abv60488 Human pro |
| 429 | 13 | 27.1 | 186    | 9  | ADA30667 | Ada30667 DNA encod | 13 | 27.1 | 375 | 8  | ABX45584 | Abx45584 Bovine ES |
| 430 | 13 | 27.1 | 201    | 4  | AAI25931 | Aai25931 Probe #15 | 13 | 27.1 | 377 | 4  | AAI23951 | Aai23951 Probe #13 |
| 431 | 13 | 27.1 | 201    | 4  | ABR72821 | Ab72821 Human foe  | 13 | 27.1 | 377 | 4  | ABX69070 | Abx69070 Human foe |
| 432 | 13 | 27.1 | 201    | 4  | AAI53247 | Aai53247 Probe #21 | 13 | 27.1 |     |    |          |                    |
| 433 | 13 | 27.1 | 201    | 4  | ABA38439 | Ab38439 Probe #16  | 13 | 27.1 |     |    |          |                    |
| 434 | 13 | 27.1 | 201    | 4  | AAK47409 | Aak47409 Human bon | 13 | 27.1 |     |    |          |                    |
| 435 | 13 | 27.1 | 201    | 4  | AAK21252 | Aak21252 Human bra | 13 | 27.1 |     |    |          |                    |
| 436 | 13 | 27.1 | 201    | 4  | AB947150 | Ab947150 Human liv | 13 | 27.1 |     |    |          |                    |
| 437 | 13 | 27.1 | 201    | 6  | AB921547 | Ab921547 Human gen | 13 | 27.1 |     |    |          |                    |
| 438 | 13 | 27.1 | 207    | 8  | ABZ20336 | Abz20336 Group III | 13 | 27.1 |     |    |          |                    |
| 439 | 13 | 27.1 | 210    | 8  | ACA15334 | Ac15334 Prokaryot  | 13 | 27.1 |     |    |          |                    |
| 440 | 13 | 27.1 | 231    | 8  | ACA15310 | Ac15310 Prokaryot  | 13 | 27.1 |     |    |          |                    |
| 441 | 13 | 27.1 | 231    | 8  | ACA15262 | Ac15262 Prokaryot  | 13 | 27.1 |     |    |          |                    |
| 442 | 13 | 27.1 | 231    | 11 | ACH98322 | Ach98322 Klebsiell | 13 | 27.1 |     |    |          |                    |
| 443 | 13 | 27.1 | 259    | 7  | AD565726 | Ad565726 Corn seed | 13 | 27.1 |     |    |          |                    |
| 444 | 13 | 27.1 | 261    | 8  | ACA14491 | Ac14491 Prokaryot  | 13 | 27.1 |     |    |          |                    |
| 445 | 13 | 27.1 | 266    | 5  | ABV60668 | Abv60668 Human pro | 13 | 27.1 |     |    |          |                    |
| 446 | 13 | 27.1 | 267    | 8  | ACA14036 | Ac14036 Prokaryot  | 13 | 27.1 |     |    |          |                    |
| 447 | 13 | 27.1 | 270    | 5  | ABV60479 | Abv60479 Human pro | 13 | 27.1 |     |    |          |                    |
| 448 | 13 | 27.1 | 270    | 6  | ABK15986 | Abk15986 Human lun | 13 | 27.1 |     |    |          |                    |
| 449 | 13 | 27.1 | 270    | 10 | ADB95249 | Adb95249 Human lun | 13 | 27.1 |     |    |          |                    |
| 450 | 13 | 27.1 | 272    | 5  | ABV60436 | Abv60436 Human pro | 13 | 27.1 |     |    |          |                    |
| 451 | 13 | 27.1 | 276    | 5  | ABV60618 | Abv60618 Human pro | 13 | 27.1 |     |    |          |                    |
| 452 | 13 | 27.1 | 277    | 5  | ABV60395 | Abv60395 Human pro | 13 | 27.1 |     |    |          |                    |
| 453 | 13 | 27.1 | 278    | 5  | ABV60480 | Abv60480 Human pro | 13 | 27.1 |     |    |          |                    |
| 454 | 13 | 27.1 | 281    | 5  | ABV60566 | Abv60566 Human pro | 13 | 27.1 |     |    |          |                    |
| 455 | 13 | 27.1 | 282    | 3  | AAA87497 | Aa87497 Rat hepat  | 13 | 27.1 |     |    |          |                    |
| 456 | 13 | 27.1 | 282    | 5  | ABV60532 | Abv60532 Human pro | 13 | 27.1 |     |    |          |                    |
| 457 | 13 | 27.1 | 286    | 5  | ABV60363 | Abv60363 Human pro | 13 | 27.1 |     |    |          |                    |
| 458 | 13 | 27.1 | 288    | 12 | ADL83775 | Adl83775 DNA up-re | 13 | 27.1 |     |    |          |                    |

## ALIGNMENTS

RESULT 1  
ADN36751  
ID ADN36751 standard; DNA; 48 BP.  
XX AC ADN36751;  
XX AC  
XX 15-JUL-2004 (first entry)  
XX DT  
XX DE West Nile virus detection-related oligonucleotide probe SeqID73.  
XX KW hybridisation assay probe; nucleic acid detection;  
XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;  
XX KW RNA virus; infection; meningitis; encephalitis;  
XX XX high throughput screening; probe; ss.  
OS West Nile virus.  
XX XX  
XX PN WO2004036190-A2.  
XX XX  
XX PD  
XX XX  
XX PF 10-OCT-2003; 2003WO-US033639.  
XX XX  
XX PR 16-OCT-2002; 2002US-0418991P.  
XX PR 25-NOV-2002; 2002US-0429006P.  
XX PR 24-FEB-2003; 2003US-0449810P.

XX (GENP-) GEN-PROBE INC.  
 XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;  
 XX WPI; 2004-389590/36.  
 XX New hybridization assay probe comprising target-complementary sequence of  
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
 XX Claim 18; SEQ ID NO 73; 135pp; English.  
 XX This invention relates to a novel hybridisation assay probe, for  
 CC detecting a nucleic acid, which is a probe sequence that comprises a  
 CC target-complementary sequence of bases, and optionally one or more base  
 CC sequences that are not complementary to the nucleic acid that is to be  
 CC detected. The hybridisation assay probes and the kits are useful in  
 CC detecting and amplifying a target nucleic acid sequence, for example  
 CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC birds and culex mosquitoes, with humans and horses serving as incidental  
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
 CC invention may allow for accurate and efficient high throughput screening.  
 CC The present sequence is that of an oligonucleotide probe which is related  
 CC to the invention.  
 XX Sequence 48 BP; 8 A; 12 C; 13 G; 15 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 48; DB 12; Length 48;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-17;  
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGAGACGGTTCTGAGGCGTTACATGGATCGATCTTCGACGCTTTGTTTC 48  
 DB 1 TCCGAGACGGTTCTGAGGCGTTACATGGATCGATCTTCGACGCTTTGTTTC 48  
 RESULT 2  
 ID ADN36750  
 ADN36750 standard; DNA; 70 BP.  
 XX  
 AC ADN36750;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE West Nile virus detection-related oligonucleotide probe SeqID72.  
 XX  
 KW hybridisation assay probe; nucleic acid detection;  
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;  
 KW RNA virus; infection; meningitis; encephalitis;  
 KW high throughput screening; probe; ss.  
 XX  
 OS West Nile virus.  
 XX  
 PN WO2004036190-A2.  
 XX  
 PD 29-APR-2004.  
 XX  
 PF 10-OCT-2003; 2003WO-US033639.  
 XX  
 PR 16-OCT-2002; 2002US-0418891P.  
 PR 25-NOV-2002; 2002US-0429006P.  
 PR 24-FEB-2003; 2003US-0449810P.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;  
 XX WPI; 2004-389590/36.  
 XX New hybridization assay probe comprising target-complementary sequence of  
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
 XX

PS Disclosure; SEQ ID NO 72; 135pp; English.  
 XX  
 XX This invention relates to a novel hybridisation assay probe, for  
 CC detecting a nucleic acid, which is a probe sequence that comprises a  
 CC target-complementary sequence of bases, and optionally one or more base  
 CC sequences that are not complementary to the nucleic acid that is to be  
 CC detected. The hybridisation assay probes and the kits are useful in  
 CC detecting and amplifying a target nucleic acid sequence, for example  
 CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC birds and culex mosquitoes, with humans and horses serving as incidental  
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
 CC invention may allow for accurate and efficient high throughput screening.  
 CC The present sequence is that of an oligonucleotide probe which is related  
 CC to the invention.  
 XX Sequence 70 BP; 11 A; 19 C; 20 G; 20 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 48; DB 12; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-17;  
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGAGACGGTTCTGAGGCGTTACATGGATCGATCTTCGACGCTTTGTTTC 48  
 DB 1 TCCGAGACGGTTCTGAGGCGTTACATGGATCGATCTTCGACGCTTTGTTTC 48  
 RESULT 3  
 ADR32078/c  
 ID ADR32078 standard; DNA; 10945 BP.  
 XX  
 AC ADR32078;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Genomic DNA of a West Nile virus.  
 XX  
 KW analysis; target; real time PCR; ds; genomic.  
 XX  
 OS West Nile virus.  
 XX  
 PN WO2004072230-A2.  
 XX  
 PD 26-AUG-2004.  
 XX  
 PF 10-FEB-2004; 2004WO-US002012.  
 XX  
 PR 10-FEB-2003; 2003US-00361004.  
 XX  
 PA (CLEA-) CLEARANT INC.  
 XX  
 PI Mckenney K, Gillmeister L, Marlowe K, Armistead D;  
 XX WPI; 2004-625843/60.  
 DR  
 DR Analyzing a target nucleic acid sequence in a biological material by real  
 PT time PCR using nucleic acid primers that are separated by at least 750  
 PT nucleic acid residues in the target sequence.  
 XX  
 PS Disclosure; SEQ ID NO 5; 96pp; English.  
 XX  
 XX The invention relates to a novel method for analysing a target nucleic  
 CC acid sequence in a biological material. The method comprises adding at  
 CC least two nucleic acid primers that hybridise under stringent conditions  
 CC to predetermined nucleic acid sequences of the target nucleic acid  
 CC sequence that are separated by at least 750 nucleic acid residues,  
 CC amplifying the target nucleic acid sequence by PCR, and detecting and  
 CC quantifying the target nucleic acid sequence. The methods and  
 CC compositions of the present invention are useful for analysing a target  
 CC nucleic acid sequence in a biological material by real time PCR using  
 CC nucleic acid primers that are separated by at least 750 nucleic acid  
 CC residues in the target sequence. This polynucleotide sequence represents  
 CC the genomic DNA of a West Nile virus used in the target analysis method

CC of the invention.  
 XX Sequence 10945 BP; 2999 A; 2457 C; 3143 G; 2346 T; 0 U; 0 Other;  
 SQ Query Match 79.2%; Score 38; DB 13; Length 10945;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-11;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTACATGATCACTTCGC 38  
 |||||  
 Db 10587 TCCGAGACGGTTCTGAGGGCTTACATGATCACTTCGC 10550

RESULT 4  
 ADR67768/c  
 ID ADR67768 standard; DNA; 10945 BP.  
 XX ADR67768;  
 AC ADR67768;  
 XX 18-NOV-2004 (first entry)  
 DT West Nile virus DNA detected by novel detection method.  
 DE  
 XX ds; detection; pathogen.  
 KW West Nile virus.  
 OS  
 XX WO2004072231-A2.  
 PN  
 XX 26-AUG-2004.  
 PD  
 XX 10-FEB-2004; 2004WO-US002013.  
 PF  
 XX 10-FEB-2003; 2003US-00361002.  
 PR  
 XX (CLEA-) CLEARANT INC.  
 PA  
 XX Mckenney K, Gillmeister L, Marlowe K, Armistead D;  
 XX WPI; 2004-625844/60.  
 XX  
 DR Determining level of potentially active biological pathogens in  
 PT biological material, by adding nucleic acid primer pairs to biological  
 PT material, amplifying target nucleic acid by PCR, detecting and  
 PT quantifying target nucleic acid.  
 XX  
 PS Disclosure; SEQ ID NO 5; 11pp; English.  
 XX

CC The invention relates to a method of determining (M1) level of  
 CC potentially active biological pathogens in biological material, involves  
 CC adding at least two nucleic acid primer pairs to biological material,  
 CC amplifying target nucleic acid sequences by PCR, and detecting and  
 CC quantifying target nucleic acid sequences, where quantity of the nucleic  
 CC acid sequences is proportional to number of biological pathogens in  
 CC biological material. (M1) is useful for determining level of potentially  
 CC active biological pathogens in a biological material such as cells,  
 CC tissues, blood or blood components, proteins, enzymes, immunoglobulins,  
 CC botanicals, food, ligaments, tendons, nerves, bone, teeth, skin grafts,  
 CC bone marrow, heart valves, cartilage, corneas, arteries, veins, organs,  
 CC lipids, carbohydrates, collagen, chitin and its derivatives, forensic  
 CC samples, mummified material, human or animal remains, stem cells, islet  
 CC of Langerhans cells, cells for transplantation, red blood cells, white  
 CC blood cells or platelets. The biological pathogen is chosen from  
 CC bacteria, viruses, fungi and single cell parasites. The biological  
 CC pathogen is chosen from Aspergillus, Candida, Histoplasma,  
 CC Saccharomyces, Coccidioides, Cryptococcus, Scherichia, Bacillus,  
 CC Campylobacter, Helicobacter, Listeria, Clostridium, Streptococcus,  
 CC Enterococcus, Staphylococcus, Brucella, Haemophilus, Salmonella,  
 CC Yersinia, Pseudomonas, Serratia, Enterobacter, Klebsiella, Proteus,  
 CC Citrobacter, Corynebacterium, Propionibacterium and Coxiella. The  
 CC biological pathogen is chosen from Adeno-associated virus (AAV), The  
 CC California encephalitis virus, Coronavirus, Coxsackievirus-A,  
 CC Coxsackievirus-B, Eastern equine encephalitis virus (EEEV), Echovirus,

CC Hantavirus, Hepatitis A virus (HAV), Hepatitis C virus (HCV), Hepatitis  
 CC delta virus (HDV), Hepatitis E virus (HEV), Hepatitis G virus (HGV), HIV,  
 CC Human T-lymphotropic virus (HTLV), Influenza virus (Flu virus), Measles  
 CC virus (Rubella), Mumps virus, Norwalk virus, Parainfluenza virus, Polio  
 CC virus, Rabies virus, Respiratory Syncytial virus, Rhinovirus, Rubella  
 CC virus, Saint Louis encephalitis virus, Western equine encephalitis virus  
 CC (WEEV), Yellow fever virus, Adenovirus, Cytomegalovirus (CMV), Epstein-  
 CC Barr virus (EBV), Hepatitis B virus (HBV), Herpes simplex virus 1, Herpes  
 CC simplex virus 2, Molluscum contagiosum, Papilloma virus (HPV), Smallpox  
 CC virus (Variola), Vaccinia virus, Venezuelan equine encephalitis virus  
 CC (VEEV), Ebola virus, West Nile virus, Human parvovirus B19 and Rotavirus.  
 CC (M1) is useful for determining the effectiveness of a sterilization  
 CC process applied to a biological material. (M1) is useful in determining  
 CC whether the biological pathogen is inactive or active. (M1) enables  
 CC determination of whether the particular biological pathogen is present in  
 CC a biological material as shown by amplification of first target sequence  
 CC and whether the biological pathogen is inactive or active. (M1) enables  
 CC evaluation of the effectiveness of sterilization processes, and  
 CC determination of both the original level and the residual level of  
 CC potentially active biological pathogens. This sequence corresponds to a  
 CC West Nile virus DNA detected by the method of the invention.  
 XX

SQ Sequence 10945 BP; 2999 A; 2457 C; 3143 G; 2346 T; 0 U; 0 Other;  
 Query Match 79.2%; Score 38; DB 13; Length 10945;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-11;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTACATGATCACTTCGC 38  
 |||||  
 Db 10587 TCCGAGACGGTTCTGAGGGCTTACATGATCACTTCGC 10550

RESULT 5  
 ADR98022/c  
 ID ADR98022 standard; DNA; 10975 BP.  
 XX ADR98022;  
 AC ADR98022;  
 XX 29-JUL-2004 (first entry)  
 DT West Nile Virus isolate 2741 complete genome sequence.  
 DE  
 XX ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;  
 KW Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.  
 XX  
 OS West Nile virus.  
 XX  
 XX WO2004040263-A2.  
 PN  
 XX 13-MAY-2004.  
 PD  
 XX 31-OCT-2003; 2003WO-US034823.  
 PF  
 XX 31-OCT-2002; 2002US-0422755P.  
 PR  
 XX 06-JUN-2003; 2003US-0476513P.  
 XX (HEAL-) HEALTH RES INC.  
 PA  
 XX Wong SY, Pei-Yong S;  
 XX WPI; 2004-400223/37.  
 XX GENBANK; AF206518.  
 XX New diagnostic kit comprising West Nile Virus (WNV) envelope protein  
 PT reactive with antibody against WNV and cross-reactive with antibody  
 PT against a flavivirus, useful in diagnosing flavivirus infection caused by  
 PT DENV, WNV, JEV or SLEV.  
 XX  
 PS Disclosure; Fig 37; 212pp; English.  
 XX  
 XX The invention relates to a diagnostic kit comprising at least one  
 CC isolated and purified polypeptide comprising a West Nile Virus (WNV)

CC envelope (E) protein or its immunogenic fragment having a native  
 CC conformation or non-denatured structure and that is reactive with  
 CC antibodies against WNV and cross-reactive with antibodies against a  
 CC flavivirus. The diagnostic kit is useful in diagnosing flavivirus  
 CC infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to  
 CC the complete nucleotide sequence of the WNV isolate 2741.

SQ Sequence 10975 BP; 3007 A; 2460 C; 3149 G; 2359 T; 0 U; 0 Other;  
 Query Match 79.2%; Score 38; DB 12; Length 10975;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-11;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCCGAGACGGTTCTGAGGGCTTACATGGATCACTTCGC 38  
 |||||  
 DB 10611 TCCGAGACGGTTCTGAGGGCTTACATGGATCACTTCGC 10574

RESULT 6  
 ABZ68481/c  
 ID ABZ68481 standard; DNA; 11029 BP.

AC ABZ68481;

DT 22-APR-2003 (first entry)

XX Nucleotide sequence of the genome of West Nile virus IS-98-ST1.

DE WNV; IS-98-ST1; Flavivirus; infection; encephalitis; gene; ss.

XX West Nile virus.

XX Key Location/Qualifiers

FT CDS 97..10397

FT /\*tag= a

FT /product= "polyprotein"

XX WO200281511-A1.

XX 17-OCT-2002.

XX 04-APR-2002; 2002WO-FR001168.

XX 04-APR-2001; 2001FR-00004599.

XX 06-SEP-2001; 2001FR-00011525.

XX (INSP ) INST PASTEUR.

XX (KIMR-) KIMRON VETERINARY INST.

XX Despres P, Deubel V, Guenet J, Drouet M, Malkinson M, Banet C;

XX Frenkiel M, Courageot M, Coulibaly F, Catteau A, Flamand M, Weber P;

XX Ceccaldi P;

XX WPI; 2003-058498/05.

XX P-PSDB; ABP70647.

XX New neurovirulent strain of West Nile virus, useful in diagnosis and

XX screening for antiviral agents, also related nucleic acids, proteins and

XX antibodies.

XX Claim 1; Page 34-49; 68pp; French.

XX The present sequence represents the genome of a strain of West Nile virus

XX (WNV), designated IS-98-ST1. This strain is a neuroinvasive and

XX neurovirulent strain of WNV. Polynucleotides and polypeptides derived

XX from the IS-98-ST1 genome are useful for diagnosis and prognosis of

SQ Sequence 11029 BP; 3019 A; 2471 C; 3167 G; 2372 T; 0 U; 0 Other;

Query Match 79.2%; Score 38; DB 8; Length 11029;

Best Local Similarity 100.0%; Pred. No. 2.7e-11;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCCGAGACGGTTCTGAGGGCTTACATGGATCACTTCGC 38  
 |||||  
 DB 10629 TCCGAGACGGTTCTGAGGGCTTACATGGATCACTTCGC 10592

RESULT 7

ABV74821/c

ID ABV74821 standard; DNA; 11029 BP.

XX AC ABV74821;

XX DT 28-MAR-2003 (first entry)

XX West Nile virus strain NY99-flamingo 382-99 complete genome.

XX Virucide; hepatotropic; antiinflammatory; antiviral; OAS;

XX 2'-5'-oligoadenylate synthase; Flavivirus infection; gene; ss.

XX West Nile Virus.

XX Key Location/Qualifiers

FT CDS 97..10398

FT /\*tag= a

FT /product= "West Nile Virus protein"

XX WO200281741-A2.

XX 17-OCT-2002.

XX 04-APR-2002; 2002WO-FR001169.

XX 04-APR-2001; 2001FR-00004598.

XX (INSP ) INST PASTEUR.

XX (CNRS ) CNRS CENT NAT RECH SCI.

XX Guenet J, Mashimo T, Simon-Chazottes D, Montagutelli X;

XX Frenkiel M, Despres P, Deubel V, Bonhomme F, Lucas M;

XX WPI; 2003-058566/05.

XX P-PSDB; AB998821.

XX Identifying stimulators of oligoadenylate synthase family genes, useful

XX as antiviral agents against Flavivirus, also mutated genes responsible

XX for sensitivity to virus.

XX Example 1; Page 52-67; 93pp; French.

XX The present invention relates to a method for identifying compounds (I)

XX that can stimulate a gene of the OAS (2'-5'-oligoadenylate synthase)

XX family. The method comprises: (a) inducing expression of the OAS gene in

XX a culture of cells from a non-human mammal (Flvr/Flvr or Flvr/Flva;

XX indicating resistance or sensitivity to Flavivirus infection); (b)

XX treating cells with test compound; and (c) measuring activity of OAS gene

XX relative to a control. (I) are potentially useful as antiviral agents for

XX treating infections by Flaviviruses (e.g. hepatitis C; dengue; yellow

XX fever and various forms of encephalitis). Genomic OAS DNA and derived

XX cDNA, also the encoded proteins, are useful: (a) for treating Flavivirus

XX infection; (b) in screening for anti-Flavivirus agents; and (c) for

XX evaluating sensitivity of subjects to Flavivirus infection and their

XX likely response to interferon treatment, e.g. to identify patients at

XX risk of developing severe forms of such infections. The present sequence

XX is West Nile Virus strain NY99-flamingo 382-99 (IS-98-ST1) complete

XX genome, which was used in an example from the invention. West Nile Virus

XX is one such Flavivirus

XX Sequence 11029 BP; 3019 A; 2471 C; 3167 G; 2372 T; 0 U; 0 Other;



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Query Match      79.2%; Score 38; DB 10; Length 11029;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTTGAGGGCTTACATGGATCACTTCGC 38
   |||||
Db 10629 TCCGAGACGGTCTTGAGGGCTTACATGGATCACTTCGC 10592

RESULT 8
ADN98023/c
ID ADN98023 standard; DNA; 11029 BP.
XX
AC ADN98023;
XX
DT 29-JUL-2004 (first entry)
XX
DE West Nile Virus isolate 3356 complete genome sequence.
XX
KW ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;
KW Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.
XX
OS West Nile virus.
XX
PN WO2004040263-A2.
XX
PD 13-MAY-2004.
XX
PF 31-OCT-2003; 2003WO-US034823.
XX
PR 31-OCT-2002; 2002US-0422755P.
PR 06-JUN-2003; 2003US-0476513P.
XX
XX (HEAL-) HEALTH RES INC.
PA
XX
PI Wong SJ, Pei-Yong S;
XX
XX WPI; 2004-400223/37.
DR GENBANK; AF404756.
XX
XX New diagnostic kit comprising West Nile Virus (WNV) envelope protein
PT reactive with antibody against WNV and cross-reactive with antibody
PT against a flavivirus, useful in diagnosing flavivirus infection caused by
PT DENV, WNV, JEV or SLEV.
XX
PS Disclosure; Fig 38; 212pp; English.
XX
CC The invention relates to a diagnostic kit comprising at least one
CC isolated and purified polypeptide comprising a West Nile Virus (WNV)
CC envelope (E) protein or its immunogenic fragment having a native
CC conformation or non-denatured structure and that is reactive with
CC antibodies against WNV and cross-reactive with antibodies against a
CC flavivirus. The diagnostic kit is useful in diagnosing flavivirus
CC infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to
CC the complete nucleotide sequence of the WNV isolate 3356.
XX
SQ Sequence 11029 BP; 3017 A; 2466 C; 3172 G; 2374 T; 0 U; 0 Other;

Query Match      79.2%; Score 38; DB 12; Length 11029;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTTGAGGGCTTACATGGATCACTTCGC 38
   |||||
Db 10629 TCCGAGACGGTCTTGAGGGCTTACATGGATCACTTCGC 10592

RESULT 9
ADN36779/c
ID ADN36779 standard; DNA; 87 BP.
XX
AC ADN36779;
XX

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XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID101.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX
OS West Nile virus.
XX
PN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
XX
XX (GENP-) GEN-PROBE INC.
PA
XX
PI Linmen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX
XX WPI; 2004-389590/36.
XX
XX New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS Claim 1; SEQ ID NO 101; 135pp; English.
XX
CC This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.
XX
SQ Sequence 87 BP; 23 A; 25 C; 26 G; 13 T; 0 U; 0 Other;

Query Match      68.8%; Score 33; DB 12; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACGGTTCTGAGGGCTTACATGGATCACTTCGC 38
   |||||
Db 87 GACGGTTCTGAGGGCTTACATGGATCACTTCGC 55

RESULT 10
ADN36752
ID ADN36752 standard; DNA; 24 BP.
XX
AC ADN36752;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID74.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX

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OS West Nile virus.
PN WO2004036190-A2.
XX
XX
PD 29-APR-2004.
XX
XX 10-OCT-2003; 2003WO-US033639.
XX
XX 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX WPI; 2004-389590/36.
XX
XX New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
PT
XX Claim 27; SEQ ID NO 74; 135pp; English.
XX
XX This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.
XX
XX Sequence 24 BP; 4 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
SQ
Query Match 50.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTAC 24
Db 1 TCCGAGACGGTCTGAGGGCTTAC 24

RESULT 11
ADN36753
ID ADN36753 standard; DNA; 24 BP.
XX
XX ADN36753;
XX
XX 15-JUL-2004 (first entry)
XX
XX West Nile virus detection-related oligonucleotide probe SeqID75.
XX
XX hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX
XX West Nile virus.
OS Enterobacteria phage T7.
XX
XX Key Location/Qualifiers
FH misc_feature 1..27
FT /tag= a
FT /note= "T7 promoter sequence"
FT misc_feature 28..51
FT /tag= b
FT /note= "WNV-complimentary sequence"
XX
XX WO2004036190-A2.
XX
XX 29-APR-2004.
XX
XX 10-OCT-2003; 2003WO-US033639.
XX
XX 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR

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PR 24-FEB-2003; 2003US-0449810P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX WPI; 2004-389590/36.
XX
XX New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
PT
XX Claim 26; SEQ ID NO 75; 135pp; English.
XX
XX This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.
XX
XX Sequence 24 BP; 4 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
SQ
Query Match 50.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTAC 24
Db 1 TCCGAGACGGTCTGAGGGCTTAC 24

RESULT 12
ADN36762
ID ADN36762 standard; DNA; 51 BP.
XX
XX ADN36762;
XX
XX 15-JUL-2004 (first entry)
XX
XX West Nile virus detection-related oligonucleotide probe SeqID84.
XX
XX hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX
XX West Nile virus.
OS Enterobacteria phage T7.
XX
XX Key Location/Qualifiers
FH misc_feature 1..27
FT /tag= a
FT /note= "T7 promoter sequence"
FT misc_feature 28..51
FT /tag= b
FT /note= "WNV-complimentary sequence"
XX
XX WO2004036190-A2.
XX
XX 29-APR-2004.
XX
XX 10-OCT-2003; 2003WO-US033639.
XX
XX 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
PR

```

XX (GENP-) GEN-PROBE INC.  
XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;  
XX WPI; 2004-389590/36.  
XX  
XX New hybridization assay probe comprising target-complementary sequence of  
PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
PT  
XX Disclosure; SEQ ID NO 84; 135pp; English.  
XX  
XX This invention relates to a novel hybridisation assay probe, for  
CC detecting a nucleic acid, which is a probe sequence that comprises a  
CC target-complementary sequence of bases, and optionally one or more base  
CC sequences that are not complementary to the nucleic acid that is to be  
CC detected. The hybridisation assay probes and the kits are useful in  
CC detecting and amplifying a target nucleic acid sequence, for example  
CC flavivirus like West Nile virus, that may be present in a biological  
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
CC birds and culex mosquitoes, with humans and horses serving as incidental  
CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
CC invention may allow for accurate and efficient high throughput screening.  
CC The present sequence is that of an oligonucleotide probe which is related  
CC to the invention.  
XX  
XX Sequence 51 BP; 15 A; 10 C; 13 G; 13 T; 0 U; 0 Other;  
SQ  
Query Match 50.0%; Score 24; DB 12; Length 51;  
Best Local Similarity 100.0%; Pred. No. 0.002;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGAGACGGTCTCGAGGCTTAC 24  
DB 28 TCCGAGACGGTCTCGAGGCTTAC 51  
RESULT 13  
ADK13681/c  
ID ADK13681 standard; DNA; 10962 BP.  
XX  
XX AC ADK13681;  
XX  
XX 20-MAY-2004 (first entry)  
XX  
XX West Nile virus DNA sequence, SEQ ID 1.  
XX  
XX Virucide; Immunostimulant; flavivirus;  
KW envelope protein domain III polypeptide; envelope protein; gene; ss.  
XX  
XX West Nile virus.  
XX  
XX Key Location/Qualifiers  
FH CDS 97..10389  
FT /\*tag= a  
FT /product= "West Nile Virus protein"  
XX  
XX WO2004016586-A2.  
XX  
XX 26-FEB-2004.  
XX  
XX 18-AUG-2003; 2003WO-US025681.  
XX  
XX 16-AUG-2002; 2002US-0403893P.  
XX  
XX 06-FEB-2003; 2003US-0445581P.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX  
XX Barrett A, Beasley D, Holbrook M;  
XX  
XX WPI; 2004-203756/19.  
XX  
XX P-PSDB; ADK13682.  
XX

PT Diagnosing flavivirus infection by contacting a sample from a human or  
PT animal with a flavivirus envelope protein domain III polypeptide, and  
PT detecting formation of an immunocomplex between the envelope protein and  
PT antibodies in the sample.  
XX  
XX PS Disclosure; SEQ ID NO 1; 110pp; English.  
XX  
XX The present invention relates to a method for screening for a flavivirus  
CC in a subject or animal host. The method comprises: contacting a sample  
CC from the subject with a composition comprising a flavivirus envelope  
CC protein domain III polypeptide (ADK13683-ADK13701) under conditions that  
CC permit formation of specific immunocomplex between an antibody in the  
CC sample and the envelope protein domain III polypeptide; and detecting  
CC whether a specific immunocomplex is formed. The present sequence is the  
CC coding sequence for West Nile Virus protein, from which E protein  
CC envelope protein domain III polypeptide (ADK13683) is derived.  
XX  
XX Sequence 10962 BP; 2997 A; 2497 C; 3100 G; 2368 T; 0 U; 0 Other;  
SQ  
Query Match 50.0%; Score 24; DB 12; Length 10962;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGAGACGGTCTCGAGGCTTAC 24  
DB 10564 TCCGAGACGGTCTCGAGGCTTAC 10541  
RESULT 14  
ADN36827  
ID ADN36827 standard; RNA; 23 BP.  
XX  
XX AC ADN36827;  
XX  
XX 15-JUL-2004 (first entry)  
XX  
XX West Nile virus detection-related oligonucleotide probe SeqID149.  
XX  
XX hybridisation assay probe; nucleic acid detection;  
KW target-complementary sequence; flavivirus; West Nile virus; WNV;  
KW RNA virus; infection; meningitis; encephalitis;  
KW high throughput screening; probe; ss.  
XX  
XX West Nile virus.  
XX  
XX Key Location/Qualifiers  
FH modified\_base 1..23  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= 2'-methoxyethoxy (2'-MOE) nucleotides"  
XX  
XX WO2004036190-A2.  
XX  
XX 29-APR-2004.  
XX  
XX 10-OCT-2003; 2003WO-US033639.  
XX  
XX 16-OCT-2002; 2002US-0418891P.  
XX  
XX 25-NOV-2002; 2002US-0429006P.  
XX  
XX 24-FEB-2003; 2003US-0449810P.  
XX  
XX (GENP-) GEN-PROBE INC.  
XX  
XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;  
XX  
XX WPI; 2004-389590/36.  
XX  
XX New hybridization assay probe comprising target-complementary sequence of  
PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
XX  
XX Example 1; SEQ ID NO 149; 135pp; English.  
XX  
XX This invention relates to a novel hybridisation assay probe, for



```
CC invention.
XX
SQ Sequence 50 BP; 15 A; 9 C; 13 G; 13 T; 0 U; 0 Other;

Query Match      47.9%; Score 23; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTT 23
    |||||
Db 28 TCCGAGACGGTTCTGAGGGCTT 50

RESULT 17
ADN36755
ID ADN36755 standard; DNA; 22 BP.
XX
AC ADN36755;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID77.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX
OS West Nile virus.
XX
PN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX WPI; 2004-389590/36.
XX
DR
XX
PT New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS Claim 26; SEQ ID NO 77; 135pp; English.
XX
CC This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.
XX
SQ Sequence 22 BP; 3 A; 5 C; 8 G; 6 T; 0 U; 0 Other;

Query Match      45.8%; Score 22; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTT 22
    |||||
Db 28 TCCGAGACGGTTCTGAGGGCTT 49

CC This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.
XX
SQ Sequence 49 BP; 14 A; 9 C; 13 G; 13 T; 0 U; 0 Other;

Query Match      45.8%; Score 22; DB 12; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTT 22
    |||||
Db 28 TCCGAGACGGTTCTGAGGGCTT 49
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RESULT 19
ADO07431/c
ID ADO07431 standard; DNA; 10818 BP.
XX
XX
AC ADO07431;
XX
XX 15-JUL-2004 (first entry)
XX
XX Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 9.
XX
XX antinflammatory; neuroprotective; gene therapy;
KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;
KW Japanese encephalitis.
XX
XX OS Japanese encephalitis virus.
XX
XX WO2004033690-A1.
XX
XX 22-APR-2004.
XX
XX PF 09-OCT-2003; 2003WO-KR002081.
XX
XX PR 09-OCT-2002; 2002KR-00061589.
XX
XX (CIDC-) CID CO LTD.
XX (LEES/) LEE S H.
XX
XX PI Lee SH, Lee Y, Yun S;
XX
XX WPI; 2004-340933/31.
XX
XX New Japanese encephalitis virus genomic RNA, useful in developing
PT vaccines for and in diagnosing and treating Japanese encephalitis.
XX
XX Example 2; Page 145-152; 265pp; English.
XX
XX The present invention relates to a genomic RNA of the Korean Japanese
CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
CC JEV cDNA and reagents are useful in developing vaccines for and in
CC diagnosing and treating Japanese encephalitis. The present sequence is a
CC sequence of the invention.
XX
XX SQ Sequence 10818 BP; 2991 A; 2491 C; 3075 G; 2361 T; 0 U; 0 Other;
XX
XX Query Match 45.8%; Score 22; DB 12; Length 10818;
XX Best Local Similarity 100.0%; Pred. No. 0.021;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TCCGAGACGGTTCGTGAGGGCTT 22
XX |||||||||||||||||||
XX Db 10523 TCCGAGACGGTTCGTGAGGGCTT 10502
XX
XX RESULT 20
ADO07437/c
ID ADO07437 standard; DNA; 10968 BP.
XX
XX AC ADO07437;
XX
XX XX 15-JUL-2004 (first entry)
XX
XX XX Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 15.
XX
XX antinflammatory; neuroprotective; gene therapy;
KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;
KW Japanese encephalitis.
XX
XX OS Japanese encephalitis virus.
XX
XX WO2004033690-A1.
XX
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XX
XX 22-APR-2004.
XX
XX PF 09-OCT-2003; 2003WO-KR002081.
XX
XX PR 09-OCT-2002; 2002KR-00061589.
XX
XX (CIDC-) CID CO LTD.
XX (LEES/) LEE S H.
XX
XX PI Lee SH, Lee Y, Yun S;
XX
XX WPI; 2004-340933/31.
XX
XX New Japanese encephalitis virus genomic RNA, useful in developing
PT vaccines for and in diagnosing and treating Japanese encephalitis.
XX
XX Claim 3; Page 154-161; 265pp; English.
XX
XX The present invention relates to a genomic RNA of the Korean Japanese
CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
CC JEV cDNA and reagents are useful in developing vaccines for and in
CC diagnosing and treating Japanese encephalitis. The present sequence is a
CC sequence of the invention.
XX
XX SQ Sequence 10968 BP; 3032 A; 2518 C; 3117 G; 2301 T; 0 U; 0 Other;
XX
XX Query Match 45.8%; Score 22; DB 12; Length 10968;
XX Best Local Similarity 100.0%; Pred. No. 0.021;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TCCGAGACGGTTCGTGAGGGCTT 22
XX |||||||||||||||||||
XX Db 10573 TCCGAGACGGTTCGTGAGGGCTT 10552
XX
XX RESULT 21
ADO07466/c
ID ADO07466 standard; DNA; 18563 BP.
XX
XX AC ADO07466;
XX
XX DT 15-JUL-2004 (first entry)
XX
XX DE Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 44.
XX
XX antinflammatory; neuroprotective; gene therapy;
KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;
KW Japanese encephalitis.
XX
XX OS Japanese encephalitis virus.
XX
XX PN WO2004033690-A1.
XX
XX PD 22-APR-2004.
XX
XX PF 09-OCT-2003; 2003WO-KR002081.
XX
XX PR 09-OCT-2002; 2002KR-00061589.
XX
XX (CIDC-) CID CO LTD.
XX (LEES/) LEE S H.
XX
XX PI Lee SH, Lee Y, Yun S;
XX
XX WPI; 2004-340933/31.
XX
XX New Japanese encephalitis virus genomic RNA, useful in developing
PT vaccines for and in diagnosing and treating Japanese encephalitis.
XX
XX Claim 12; Page 193-206; 265pp; English.
XX
```

CC The present invention relates to a genomic RNA of the Korean Japanese  
 CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated  
 CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,  
 CC JEV cDNA and reagents are useful in developing vaccines for and in  
 CC diagnosing and treating Japanese encephalitis. The present sequence is a  
 CC sequence of the invention.  
 XX

SQ Sequence 18563 BP; 4943 A; 4211 C; 4929 G; 4480 T; 0 U; 0 Other;  
 Query Match 45.8%; Score 22; DB 12; Length 18563;  
 Best Local Similarity 100.0%; Pred. No. 0.02;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCGAGGGCTT 22  
 |||||  
 Db 10573 TCCGAGACGGTTCGAGGGCTT 10552

## RESULT 22

ADO07465/c  
 ID ADO07465 standard; DNA; 18563 BP.

XX  
 AC ADO07465;

XX 15-JUL-2004 (first entry)

XX Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 43.

XX antiinflammatory; neuroprotective; gene therapy;  
 XX Japanese Encephalitis virus; JEV; ds; gene; vaccine;  
 XX Japanese encephalitis.

XX Japanese encephalitis virus.

XX WO2004033690-A1.

XX 22-APR-2004.

XX 09-OCT-2003; 2003WO-KR002081.

XX 09-OCT-2002; 2002KR-00061589.

XX (CIDC-) CID CO LTD.

XX (LEES/) LEE S H.

XX Lee SH, Lee Y, Yun S;

XX WPI; 2004-340933/31.

XX New Japanese encephalitis virus genomic RNA, useful in developing  
 PT vaccines for and in diagnosing and treating Japanese encephalitis.

XX Claim 12; Page 180-193; 265pp; English.

XX The present invention relates to a genomic RNA of the Korean Japanese  
 CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated  
 CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,  
 CC JEV cDNA and reagents are useful in developing vaccines for and in  
 CC diagnosing and treating Japanese encephalitis. The present sequence is a  
 CC sequence of the invention.  
 XX

SQ Sequence 18563 BP; 4944 A; 4211 C; 4929 G; 4479 T; 0 U; 0 Other;

Query Match 45.8%; Score 22; DB 12; Length 18563;  
 Best Local Similarity 100.0%; Pred. No. 0.02;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCGAGGGCTT 22  
 |||||  
 Db 10573 TCCGAGACGGTTCGAGGGCTT 10552

## RESULT 23

ADO07467/c

ID ADO07467 standard; DNA; 18565 BP.

XX ADO07467;

XX 15-JUL-2004 (first entry)

XX Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 45.

XX antiinflammatory; neuroprotective; gene therapy;

XX Japanese Encephalitis virus; JEV; ds; gene; vaccine;  
 XX Japanese encephalitis.

XX Japanese encephalitis virus.

XX WO2004033690-A1.

XX 22-APR-2004.

XX 09-OCT-2003; 2003WO-KR002081.

XX 09-OCT-2002; 2002KR-00061589.

XX (CIDC-) CID CO LTD.

XX (LEES/) LEE S H.

XX Lee SH, Lee Y, Yun S;

XX WPI; 2004-340933/31.

XX New Japanese encephalitis virus genomic RNA, useful in developing  
 PT vaccines for and in diagnosing and treating Japanese encephalitis.

XX Claim 12; Page 206-219; 265pp; English.

XX The present invention relates to a genomic RNA of the Korean Japanese  
 CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated  
 CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,  
 CC JEV cDNA and reagents are useful in developing vaccines for and in  
 CC diagnosing and treating Japanese encephalitis. The present sequence is a  
 CC sequence of the invention.  
 XX

SQ Sequence 18565 BP; 4944 A; 4211 C; 4929 G; 4481 T; 0 U; 0 Other;

Query Match 45.8%; Score 22; DB 12; Length 18565;  
 Best Local Similarity 100.0%; Pred. No. 0.02;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCGAGGGCTT 22  
 |||||  
 Db 10573 TCCGAGACGGTTCGAGGGCTT 10552

## RESULT 24

ADO07468/c

ID ADO07468 standard; DNA; 19038 BP.

XX ADO07468;

XX 15-JUL-2004 (first entry)

XX Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 46.

XX antiinflammatory; neuroprotective; gene therapy;

XX Japanese Encephalitis virus; JEV; ds; gene; vaccine;  
 XX Japanese encephalitis.

XX Japanese encephalitis virus.

XX WO2004033690-A1.

XX 22-APR-2004.

PF 09-OCT-2003; 2003WO-KR002081.  
XX  
PR 09-OCT-2002; 2002KR-00061589.  
XX  
PA (CIDC-) CID CO LTD.  
PA (LEES/) LEE S H.  
XX  
PI Lee SH, Lee Y, Yun S;  
XX WPI; 2004-340933/31.  
XX  
DR New Japanese encephalitis virus genomic RNA, useful in developing  
PT vaccines for and in diagnosing and treating Japanese encephalitis.  
XX  
PS Claim 12; Page 219-232; 265pp; English.  
XX  
CC The present invention relates to a genomic RNA of the Korean Japanese  
CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated  
CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,  
CC JEV cDNA and reagents are useful in developing vaccines for and in  
CC diagnosing and treating Japanese encephalitis. The present sequence is a  
CC sequence of the invention.  
XX  
SQ Sequence 19038 BP; 5060 A; 4310 C; 5055 G; 4613 T; 0 U; 0 Other;  
Query Match 45.8%; Score 22; DB 12; Length 19038;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGAGACGGTTCGTGAGGGCTT 22  
DB 10573 TCCGAGACGGTTCGTGAGGGCTT 10552  
RESULT 25  
AD007469/C  
ID ADO07469 standard; DNA; 19038 BP.  
XX  
AC ADO07469;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 47.  
XX  
KW antiinflammatory; neuroprotective; gene therapy;  
KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;  
KW Japanese encephalitis.  
XX  
OS Japanese encephalitis virus.  
XX  
PN WO2004033690-A1.  
XX  
PD 22-APR-2004.  
XX  
PF 09-OCT-2003; 2003WO-KR002081.  
XX  
PR 09-OCT-2002; 2002KR-00061589.  
XX  
PA (CIDC-) CID CO LTD.  
PA (LEES/) LEE S H.  
XX  
PI Lee SH, Lee Y, Yun S;  
XX WPI; 2004-340933/31.  
XX  
DR New Japanese encephalitis virus genomic RNA, useful in developing  
PT vaccines for and in diagnosing and treating Japanese encephalitis.  
XX  
PS Claim 12; Page 232-245; 265pp; English.  
XX  
CC The present invention relates to a genomic RNA of the Korean Japanese  
CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated  
CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,  
CC JEV cDNA and reagents are useful in developing vaccines for and in  
CC diagnosing and treating Japanese encephalitis. The present sequence is a  
CC sequence of the invention.  
XX  
SQ Sequence 19038 BP; 5060 A; 4310 C; 5055 G; 4613 T; 0 U; 0 Other;  
Query Match 45.8%; Score 22; DB 12; Length 19038;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGAGACGGTTCGTGAGGGCTT 22  
DB 10573 TCCGAGACGGTTCGTGAGGGCTT 10552

CC JEV cDNA and reagents are useful in developing vaccines for and in  
CC diagnosing and treating Japanese encephalitis. The present sequence is a  
CC sequence of the invention.  
XX  
SQ Sequence 19038 BP; 5059 A; 4310 C; 5055 G; 4614 T; 0 U; 0 Other;  
Query Match 45.8%; Score 22; DB 12; Length 19038;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGAGACGGTTCGTGAGGGCTT 22  
DB 10573 TCCGAGACGGTTCGTGAGGGCTT 10552  
RESULT 26  
AD007470/C  
ID ADO07470 standard; DNA; 19040 BP.  
XX  
AC ADO07470;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 48.  
XX  
KW antiinflammatory; neuroprotective; gene therapy;  
KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;  
KW Japanese encephalitis.  
XX  
OS Japanese encephalitis virus.  
XX  
PN WO2004033690-A1.  
XX  
PD 22-APR-2004.  
XX  
PF 09-OCT-2003; 2003WO-KR002081.  
XX  
PR 09-OCT-2002; 2002KR-00061589.  
XX  
PA (CIDC-) CID CO LTD.  
PA (LEES/) LEE S H.  
XX  
PI Lee SH, Lee Y, Yun S;  
XX WPI; 2004-340933/31.  
XX  
DR New Japanese encephalitis virus genomic RNA, useful in developing  
PT vaccines for and in diagnosing and treating Japanese encephalitis.  
XX  
PS Claim 12; Page 245-258; 265pp; English.  
XX  
CC The present invention relates to a genomic RNA of the Korean Japanese  
CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated  
CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,  
CC JEV cDNA and reagents are useful in developing vaccines for and in  
CC diagnosing and treating Japanese encephalitis. The present sequence is a  
CC sequence of the invention.  
XX  
SQ Sequence 19040 BP; 5060 A; 4310 C; 5055 G; 4615 T; 0 U; 0 Other;  
Query Match 45.8%; Score 22; DB 12; Length 19040;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGAGACGGTTCGTGAGGGCTT 22  
DB 10573 TCCGAGACGGTTCGTGAGGGCTT 10552  
RESULT 27  
ADN36873  
ID ADN36873 standard; RNA; 36 BP.  
XX





KW RNA virus; infection; meningitis; encephalitis;  
 XX high throughput screening; probe; ss.  
 OS West Nile virus.  
 XX  
 PH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= 2'-methoxyethoxy (2'-MOE) nucleotides"  
 XX  
 XX WO2004036190-A2.  
 XX  
 XX 29-APR-2004.  
 XX  
 XX 10-OCT-2003; 2003WO-US033639.  
 XX  
 XX 16-OCT-2002; 2002US-0418891P.  
 PR 25-NOV-2002; 2002US-0429006P.  
 PR 24-FEB-2003; 2003US-0449810P.  
 XX  
 XX (GENP-) GEN-PROBE INC.  
 XX  
 XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;  
 PI WPI; 2004-389590/36.  
 DR  
 XX New hybridization assay probe comprising target-complementary sequence of  
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
 PT  
 XX Claim 17; SEQ ID NO 114; 135pp; English.  
 PS  
 XX This invention relates to a novel hybridisation assay probe, for  
 CC detecting a nucleic acid, which is a probe sequence that comprises a  
 CC target-complementary sequence of bases, and optionally one or more base  
 CC sequences that are not complementary to the nucleic acid that is to be  
 CC detected. The hybridisation assay probes and the kits are useful in  
 CC detecting and amplifying a target nucleic acid sequence, for example  
 CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC birds and culex mosquitoes, with humans and horses serving as incidental  
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
 CC invention may allow for accurate and efficient high throughput screening.  
 CC The present sequence is that of an oligonucleotide probe which is related  
 CC to the invention.  
 XX  
 SQ Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;  
 Query Match 37.5%; Score 18; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.5;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 31 CACTTCGCAGCTTGTTC 48  
 DB 20 CACTTCGCAGCTTGTTC 3  
 RESULT 30  
 ACN03369/c  
 ID ACN03369 standard; RNA; 17 BP.  
 XX  
 XX ACN03369;  
 AC  
 DT 22-APR-2004 (first entry)  
 XX  
 DE WNV Inozyme substrate SEQ ID NO 3372.  
 XX  
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX

OS West Nile Virus.  
 XX  
 PN WO200268637-A2.  
 XX  
 PD 06-SEP-2002.  
 XX  
 PF 19-OCT-2001; 2001WO-US048350.  
 XX  
 PR 20-OCT-2000; 2000US-0242411P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX  
 XX Blatt L, Mcswiggen JA;  
 PI WPI; 2002-706994/76.  
 DR  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX  
 PS Claim 23; SEQ ID NO 3372; 495pp; English.  
 XX  
 CC The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX  
 SQ Sequence 17 BP; 4 A; 6 C; 4 G; 0 T; 3 U; 0 Other;  
 Query Match 35.4%; Score 17; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGAGACGGTCTGAG 17  
 DB 17 TCCGAGACGGTCTGAG 1  
 RESULT 31  
 ACN03364/c  
 ID ACN03364 standard; RNA; 17 BP.  
 XX  
 XX ACN03364;  
 AC  
 DT 22-APR-2004 (first entry)  
 XX  
 DE WNV Inozyme substrate SEQ ID NO 3367.  
 XX  
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX  
 XX West Nile Virus.  
 XX  
 PN WO200268637-A2.  
 XX  
 PD 06-SEP-2002.  
 XX  
 PF 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.  
 PR (RIBO-) RIBOZYME PHARM INC.  
 XX (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX Blatt L, Mcswiggen JA;  
 PI WPI; 2002-706994/76.  
 XX  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX  
 PS Claim 23; SEQ ID NO 3367; 495pp; English.  
 XX  
 XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX  
 SQ Sequence 17 BP; 5 A; 4 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 18 GCCTTACATGGATCACT 34  
 Db 17 GCCTTACATGGATCACT 1

RESULT 32  
 ACN05430/c  
 ID ACN05430 standard; RNA; 17 BP.  
 XX ACN05430;  
 AC  
 XX 22-APR-2004 (first entry)  
 DT  
 XX WNV DNazyme substrate SEQ ID NO 5433.  
 DE  
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX  
 XX West Nile Virus.  
 OS  
 XX WO200268637-A2.  
 PN  
 XX 06-SEP-2002.  
 PD  
 XX 19-OCT-2001; 2001WO-US048350.  
 PF  
 XX 20-OCT-2000; 2000US-0242411P.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX Blatt L, Mcswiggen JA;  
 PI WPI; 2002-706994/76.  
 XX  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX

PI Blatt L, Mcswiggen JA;  
 XX WPI; 2002-706994/76.  
 XX  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX  
 PS Claim 23; SEQ ID NO 5433; 495pp; English.  
 XX  
 XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX  
 SQ Sequence 17 BP; 5 A; 3 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 22 TACATGGATCACTTCGC 38  
 Db 17 TACATGGATCACTTCGC 1

RESULT 33  
 ACN09609  
 ID ACN09609 standard; RNA; 17 BP.  
 XX ACN09609;  
 AC  
 XX 22-APR-2004 (first entry)  
 DT  
 XX WNV minus strand Inozyme substrate SEQ ID NO 9612.  
 DE  
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX  
 XX West Nile Virus.  
 OS  
 XX WO200268637-A2.  
 PN  
 XX 06-SEP-2002.  
 PD  
 XX 19-OCT-2001; 2001WO-US048350.  
 PF  
 XX 20-OCT-2000; 2000US-0242411P.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX Blatt L, Mcswiggen JA;  
 PI WPI; 2002-706994/76.  
 XX  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX

XX Claim 23; SEQ ID NO 9612; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication

CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for

CC treating a condition related to WNV infection e.g. pancreatitis,

CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

CC molecule is selected from the group of ribozymes consisting of

CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The

CC nucleic acid molecules further comprise at least five ribose residues, at

CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at

CC least three of the 5' terminal nucleotides and a 3' end modification of a

CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

CC in the specification. The present sequence is that of a nucleic acid

CC molecule of the invention

XX SQ Sequence 17 BP; 4 A; 4 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;

Best Local Similarity 76.5%; Pred. No. 16;

Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 17 GGCTTACATGGATCAC 33

DB 1 GGCGUACAGGAUCAC 17

RESULT 34

ACN13634

ID ACN13634 standard; RNA; 17 BP.

XX ACN13634;

XX 22-APR-2004 (first entry)

XX WNV minus strand DNazyme substrate SEQ ID NO 13637.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;

KW virucide; neuroprotective; antibacterial; replication; pancreatitis;

KW encephalitis; myocarditis; meningitis; infection; hepatitis;

KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;

KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus

PT (WNV), useful for treating a condition related to WNV infection e.g.

PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 13637; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication

CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for

CC treating a condition related to WNV infection e.g. pancreatitis,

CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

CC molecule is selected from the group of ribozymes consisting of

CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The

CC nucleic acid molecules further comprise at least five ribose residues, at

CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at

CC least three of the 5' terminal nucleotides and a 3' end modification of a

CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

CC in the specification. The present sequence is that of a nucleic acid

CC molecule of the invention

XX SQ Sequence 17 BP; 4 A; 4 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;

Best Local Similarity 76.5%; Pred. No. 16;

Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 17 GGCTTACATGGATCAC 33

DB 1 GGCGUACAGGAUCAC 17

RESULT 35

ACN14220

ID ACN14220 standard; RNA; 17 BP.

XX ACN14220;

XX 22-APR-2004 (first entry)

XX WNV minus strand Amberzyme substrate SEQ ID NO 14223.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;

KW virucide; neuroprotective; antibacterial; replication; pancreatitis;

KW encephalitis; myocarditis; meningitis; infection; hepatitis;

KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;

KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus

PT (WNV), useful for treating a condition related to WNV infection e.g.

PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 14223; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication

CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for

CC treating a condition related to WNV infection e.g. pancreatitis,

CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

CC molecule is selected from the group of ribozymes consisting of

CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The

CC nucleic acid molecules further comprise at least five ribose residues, at

CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at

CC least three of the 5' terminal nucleotides and a 3' end modification of a

CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

CC in the specification. The present sequence is that of a nucleic acid

CC molecule of the invention

XX SQ Sequence 17 BP; 4 A; 4 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;

Best Local Similarity 64.7%; Pred. No. 16;

Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 21 TTACATGGATCACTTCG 37

DB 1 UUACAUGGAUCACUUCG 17

CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

CC molecule is selected from the group of ribozymes consisting of

CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The

CC nucleic acid molecules further comprise at least five ribose residues, at

CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at

CC least three of the 5' terminal nucleotides and a 3' end modification of a

CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

CC in the specification. The present sequence is that of a nucleic acid

CC molecule of the invention

XX SQ Sequence 17 BP; 4 A; 4 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;

Best Local Similarity 64.7%; Pred. No. 16;

Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 21 TTACATGGATCACTTCG 37

DB 1 UUACAUGGAUCACUUCG 17

RESULT 35

ACN14220

ID ACN14220 standard; RNA; 17 BP.

XX ACN14220;

XX 22-APR-2004 (first entry)

XX WNV minus strand Amberzyme substrate SEQ ID NO 14223.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;

KW virucide; neuroprotective; antibacterial; replication; pancreatitis;

KW encephalitis; myocarditis; meningitis; infection; hepatitis;

KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;

KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus

PT (WNV), useful for treating a condition related to WNV infection e.g.

PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 14223; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication

CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for

CC treating a condition related to WNV infection e.g. pancreatitis,

CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

CC molecule is selected from the group of ribozymes consisting of

CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The

CC nucleic acid molecules further comprise at least five ribose residues, at

CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at

CC least three of the 5' terminal nucleotides and a 3' end modification of a

CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

CC in the specification. The present sequence is that of a nucleic acid

CC molecule of the invention



```

RESULT 38
ACN14217
ID ACN14217 standard; RNA; 17 BP.
XX
XX
AC ACN14217;
XX
XX
DT 22-APR-2004 (first entry)
XX
XX
WNV minus strand Amberzyme substrate SEQ ID NO 14220.
DE
XX
XX
WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
XX
OS West Nile Virus.
XX
XX
WO200268637-A2.
PN
XX
XX
06-SEP-2002.
PD
XX
XX
19-OCT-2001; 2001WO-US048350.
PF
XX
XX
20-OCT-2000; 2000US-0242411P.
PR
XX
XX
(RIBO-) RIBOZYME PHARM INC.
PA
PA
(BLAT/) BLATT L.
PA
(MCSW/) MCSWIGGEN J A.
XX
XX
Blatt L, Mcswiggen JA;
PI
XX
XX
WPI; 2002-706994/76.
DR
XX
XX
New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX
Claim 23; SEQ ID NO 14220; 495pp; English.
XX
XX
The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-Cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX
Sequence 17 BP; 3 A; 3 C; 6 G; 0 T; 5 U; 0 Other;
SQ
Query Match 35.4%; Score 17; DB 6; Length 17;
Best Local Similarity 70.6%; Pred. No. 16;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACGGTTCTGAGGGCTTA 23
|||||:|||||:|
Db 1 ACGGUUCUGAGGGCUUA 17

RESULT 39
ACN04659/C
ID ACN04659 standard; RNA; 17 BP.
XX
XX
AC ACN04659;
XX
XX
QY 7 ACGGTTCTGAGGGCTTA 23
|||||:|||||:|
Db 1 ACGGUUCUGAGGGCUUA 17

RESULT 38
ACN14217
ID ACN14217 standard; RNA; 17 BP.
XX
XX
AC ACN14217;
XX
XX
DT 22-APR-2004 (first entry)
XX
XX
WNV minus strand Amberzyme substrate SEQ ID NO 14220.
DE
XX
XX
WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
XX
OS West Nile Virus.
XX
XX
WO200268637-A2.
PN
XX
XX
06-SEP-2002.
PD
XX
XX
19-OCT-2001; 2001WO-US048350.
PF
XX
XX
20-OCT-2000; 2000US-0242411P.
PR
XX
XX
(RIBO-) RIBOZYME PHARM INC.
PA
PA
(BLAT/) BLATT L.
PA
(MCSW/) MCSWIGGEN J A.
XX
XX
Blatt L, Mcswiggen JA;
PI
XX
XX
WPI; 2002-706994/76.
DR
XX
XX
New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX
Claim 23; SEQ ID NO 14220; 495pp; English.
XX
XX
The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-Cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX
Sequence 17 BP; 3 A; 3 C; 6 G; 0 T; 5 U; 0 Other;
SQ
Query Match 35.4%; Score 17; DB 6; Length 17;
Best Local Similarity 70.6%; Pred. No. 16;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACGGTTCTGAGGGCTTA 23
|||||:|||||:|
Db 1 ACGGUUCUGAGGGCUUA 17

RESULT 39
ACN04659/C
ID ACN04659 standard; RNA; 17 BP.
XX
XX
AC ACN04659;
XX
XX
QY 7 ACGGTTCTGAGGGCTTA 23
|||||:|||||:|
Db 1 ACGGUUCUGAGGGCUUA 17

RESULT 39
ACN04659/C
ID ACN04659 standard; RNA; 17 BP.
XX
XX
AC ACN04659;
XX
XX
QY 7 ACGGTTCTGAGGGCTTA 23
|||||:|||||:|
Db 1 ACGGUUCUGAGGGCUUA 17

```

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DT 22-APR-2004 (first entry)
XX
XX
WNV Zinzyme substrate SEQ ID NO 4662.
XX
XX
WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
XX
OS West Nile Virus.
XX
XX
WO200268637-A2.
PN
XX
XX
06-SEP-2002.
PD
XX
XX
19-OCT-2001; 2001WO-US048350.
PF
XX
XX
20-OCT-2000; 2000US-0242411P.
PR
XX
XX
(RIBO-) RIBOZYME PHARM INC.
PA
PA
(BLAT/) BLATT L.
PA
(MCSW/) MCSWIGGEN J A.
XX
XX
Blatt L, Mcswiggen JA;
PI
XX
XX
WPI; 2002-706994/76.
DR
XX
XX
New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX
Claim 23; SEQ ID NO 4662; 495pp; English.
XX
XX
The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-Cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX
Sequence 17 BP; 4 A; 5 C; 3 G; 0 T; 5 U; 0 Other;
SQ
Query Match 35.4%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ACGGCTTACATGATCA 32
|||||:|||||:|
Db 17 ACGGCTTACATGATCA 1

RESULT 40
ACN14221
ID ACN14221 standard; RNA; 17 BP.
XX
XX
AC ACN14221;
XX
XX
22-APR-2004 (first entry)
XX
XX
WNV minus strand Amberzyme substrate SEQ ID NO 14224.
XX
XX
WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;

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KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 XX Amberzyme; Zinzyne; ss.  
 OS West Nile Virus.  
 XX  
 XX  
 XX  
 XX WO200268637-A2.  
 XX  
 XX  
 PD  
 PD  
 PF 19-OCT-2001; 2001WO-US048350.  
 XX  
 XX 20-OCT-2000; 2000US-0242411P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX  
 XX Blatt L, Mcswiggen JA;  
 XX WPI; 2002-706994/76.  
 DR  
 XX  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX  
 XX Claim 23; SEQ ID NO 14224; 495pp; English.  
 XX  
 XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX  
 SQ Sequence 17 BP; 4 A; 5 C; 2 G; 0 T; 6 U; 0 Other;  
 Query Match 35.4%; Score 17; DB 6; Length 17;  
 Best Local Similarity 64.7%; Pred. No. 16;  
 Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
 QY 20 CTTACATGGATCACTTC 36  
 Db ::::||||:|  
 1 CUUACAUGGACUACUUC 17  
 RESULT 41  
 ACN03363/C  
 ID ACN03363 standard; RNA; 17 BP.  
 AC  
 AC ACN03363;  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX  
 XX WNV Inozyme substrate SEQ ID NO 3366.  
 DE  
 XX  
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX  
 XX West Nile Virus.  
 OS  
 XX WO200268637-A2.  
 PN  
 XX

PD 06-SEP-2002.  
 XX  
 PF 19-OCT-2001; 2001WO-US048350.  
 XX  
 XX 20-OCT-2000; 2000US-0242411P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX  
 XX Blatt L, Mcswiggen JA;  
 XX WPI; 2002-706994/76.  
 DR  
 XX  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX  
 XX Claim 23; SEQ ID NO 3366; 495pp; English.  
 XX  
 XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX  
 SQ Sequence 17 BP; 6 A; 3 C; 4 G; 0 T; 4 U; 0 Other;  
 Query Match 35.4%; Score 17; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 19 GCTTACATGGATCACTT 35  
 Db :|||||  
 17 GCTTACATGGATCACTT 1  
 RESULT 42  
 ACN14216  
 ID ACN14216 standard; RNA; 17 BP.  
 XX  
 XX ACN14216;  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX  
 XX WNV minus strand Amberzyme substrate SEQ ID NO 14219.  
 DE  
 XX  
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX  
 XX West Nile Virus.  
 OS  
 XX WO200268637-A2.  
 PN  
 XX 06-SEP-2002.  
 PD  
 XX 19-OCT-2001; 2001WO-US048350.  
 PF  
 XX 20-OCT-2000; 2000US-0242411P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA

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PA (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX Blatt L, Mcswiggen JA;
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (WNV), useful for treating a condition related to WNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 14219; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX treating a condition related to WNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention
XX
XX Sequence 17 BP; 3 A; 4 C; 6 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 35.4%; Score 17; DB 6; Length 17;
XX Best Local Similarity 76.5%; Pred. No. 16;
XX Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCCGAGACGGTTCTGAG 17
DB 1 UCCGAGACGGUUCUGAG 17

RESULT 43
ACN01375/C
ID ACN01375 standard; RNA; 17 BP.
XX
XX ACN01375;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV Hammerhead Ribozyme substrate SEQ ID NO 1365.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX
XX Blatt L, Mcswiggen JA;
XX
XX WPI; 2002-706994/76.
XX

New nucleic acid molecule that modulates replication of West Nile Virus
(WNV), useful for treating a condition related to WNV infection e.g.
pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
Claim 23; SEQ ID NO 1365; 495pp; English.
The invention relates to nucleic acid molecules that modulate replication
of the West Nile Virus (WNV). The nucleic acid molecules are useful for
treating a condition related to WNV infection e.g. pancreatitis,
encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
molecule is selected from the group of ribozymes consisting of
Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
nucleic acid molecules further comprise at least five ribose residues, at
least ten 2'-O-methyl modifications, phosphorothioate linkages on at
least three of the 5' terminal nucleotides and a 3' end modification of a
3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
in the specification. The present sequence is that of a nucleic acid
molecule of the invention
Sequence 17 BP; 6 A; 2 C; 5 G; 0 T; 4 U; 0 Other;
Query Match 35.4%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 CTTACATGGATCACTTC 36
DB 17 CTTACATGGATCACTTC 1

RESULT 44
ACN07449
ID ACN07449 standard; RNA; 17 BP.
XX
XX ACN07449;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7452.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX
XX Blatt L, Mcswiggen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (WNV), useful for treating a condition related to WNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 7452; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication

```

CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages, at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

XX SQ Sequence 17 BP; 4 A; 3 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;  
 Best Local Similarity 76.5%; Pred. No. 16;  
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 15 GAGGGCTTACATGGATC 31  
 Db 1 GAGGGCUUACUUGAUC 17

RESULT 45  
 ACN03368/c  
 ID ACN03368 standard; RNA; 17 BP.

AC ACN03368;

XX 22-APR-2004 (first entry)

DE WNV Inozyme substrate SEQ ID NO 3371.

WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 encephalitis; myocarditis; meningitis; infection; hepatitis;  
 liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNzyme;  
 Amberzyme; Zinzyme; ss.

OS West Nile Virus.

PN WO200268637-A2.

PD 06-SEP-2002.

PF 19-OCT-2001; 2001WO-US048350.

PR 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

PI Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 23; SEQ ID NO 3371; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at

CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

XX SQ Sequence 17 BP; 5 A; 7 C; 3 G; 0 T; 2 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACGGTTCGAGGGCTT 22  
 Db 17 GACGGTTCGAGGGCTT 1

RESULT 46

ACN12333  
 ID ACN12333 standard; RNA; 17 BP.

XX ACN12333;

XX 22-APR-2004 (first entry)

DE WNV minus strand Zinzyme substrate SEQ ID NO 12336.

WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 encephalitis; myocarditis; meningitis; infection; hepatitis;  
 liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNzyme;  
 Amberzyme; Zinzyme; ss.

OS West Nile Virus.

PN WO200268637-A2.

PD 06-SEP-2002.

PF 19-OCT-2001; 2001WO-US048350.

PR 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

PI Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 23; SEQ ID NO 12336; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention



SQ Sequence 17 BP; 3 A; 4 C; 7 G; 0 T; 3 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;  
Best Local Similarity 82.4%; Pred. No. 16;  
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGAGACGGTTCGAGG 18  
DB 1 CCGAGACGGUUCUGAGG 17

RESULT 47

ACN01376/c  
ID ACN01376 standard; RNA; 17 BP.

XX ACN01376;

XX 22-APR-2004 (first entry)

XX WNV Hammerhead Ribozyme substrate SEQ ID NO 1366.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
XX viricide; neuroprotective; antibacterial; replication; pancreatitis;  
XX encephalitis; myocarditis; meningitis; infection; hepatitis;  
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
XX Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus

(WNV), useful for treating a condition related to WNV infection e.g.  
pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 1366; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication  
of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
treating a condition related to WNV infection e.g. pancreatitis,  
encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
molecule is selected from the group of ribozymes consisting of  
Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
nucleic acid molecules further comprise at least five ribose residues, at  
least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
least three of the 5' terminal nucleotides and a 3' end modification of a  
3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
in the specification. The present sequence is that of a nucleic acid  
molecule of the invention

XX Sequence 17 BP; 5 A; 6 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TGAGGGCTTACATGGAT 30

DB 17 TGAGGGCTTACATGGAT 1

RESULT 48

ACN03365/c  
ID ACN03365 standard; RNA; 17 BP.

XX ACN03365;

XX 22-APR-2004 (first entry)

XX WNV Inozyme substrate SEQ ID NO 3368.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
XX viricide; neuroprotective; antibacterial; replication; pancreatitis;  
XX encephalitis; myocarditis; meningitis; infection; hepatitis;  
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
XX Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus  
(WNV), useful for treating a condition related to WNV infection e.g.  
pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 3368; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication  
of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
treating a condition related to WNV infection e.g. pancreatitis,  
encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
molecule is selected from the group of ribozymes consisting of  
Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
nucleic acid molecules further comprise at least five ribose residues, at  
least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
least three of the 5' terminal nucleotides and a 3' end modification of a  
3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
in the specification. The present sequence is that of a nucleic acid  
molecule of the invention

XX Sequence 17 BP; 6 A; 5 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCTGAGGGCTTACAT 26

DB 17 GTTCTGAGGGCTTACAT 1

RESULT 49

ACN03366/c  
ID ACN03366 standard; RNA; 17 BP.

```

XX AC ACN03366;
XX DT 22-APR-2004 (first entry)
XX DE WNV Inozyme substrate SEQ ID NO 3369.
XX KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX KW encephalitis; myocarditis; meningitis; infection; hepatitis;
XX KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX KW Amberzyme; Zinzyme; ss.
XX OS West Nile Virus.
XX PN WO200268637-A2.
XX PD 06-SEP-2002.
XX PF 19-OCT-2001; 2001WO-US048350.
XX PR 20-OCT-2000; 2000US-0242411P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PI Blatt L, Mcswiggen JA;
XX PS WPI; 2002-706994/76.
XX CC New nucleic acid molecule that modulates replication of West Nile Virus
XX CC (WNV), useful for treating a condition related to WNV infection e.g.
XX CC pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX PS Claim 23; SEQ ID NO 3369; 495pp; English.
XX CC The invention relates to nucleic acid molecules that modulate replication
XX CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX CC treating a condition related to WNV infection e.g. pancreatitis,
XX CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX CC molecule is selected from the group of ribozymes consisting of
XX CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
XX CC nucleic acid molecules further comprise at least five ribose residues, at
XX CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX CC least three of the 5' terminal nucleotides and a 3' end modification of a
XX CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX CC in the specification. The present sequence is that of a nucleic acid
XX CC molecule of the invention
XX SQ Sequence 17 BP; 5 A; 6 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGTTCGTGAGGCTTACA 25
DB 17 GGTTCGTGAGGCTTACA 1

RESULT 50
ACN04660/c
ID ACN04660 standard; RNA; 17 BP.
XX AC ACN04660;
XX DT 22-APR-2004 (first entry)
XX DE WNV Zinzyme substrate SEQ ID NO 4663.
XX

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KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX OS West Nile Virus.
XX PN WO200268637-A2.
XX PD 06-SEP-2002.
XX PF 19-OCT-2001; 2001WO-US048350.
XX PR 20-OCT-2000; 2000US-0242411P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PI Blatt L, Mcswiggen JA;
XX PS WPI; 2002-706994/76.
XX CC New nucleic acid molecule that modulates replication of West Nile Virus
XX CC (WNV), useful for treating a condition related to WNV infection e.g.
XX CC pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX PS Claim 23; SEQ ID NO 4663; 495pp; English.
XX CC The invention relates to nucleic acid molecules that modulate replication
XX CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX CC treating a condition related to WNV infection e.g. pancreatitis,
XX CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX CC molecule is selected from the group of ribozymes consisting of
XX CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
XX CC nucleic acid molecules further comprise at least five ribose residues, at
XX CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX CC least three of the 5' terminal nucleotides and a 3' end modification of a
XX CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX CC in the specification. The present sequence is that of a nucleic acid
XX CC molecule of the invention
XX SQ Sequence 17 BP; 5 A; 6 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TCTGAGGCTTACATGG 28
DB 17 TCTGAGGCTTACATGG 1

Search completed: March 25, 2005, 08:13:37
Job time : 284.253 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 04:27:15 ; Search time 1913.92 Seconds  
(without alignments)  
954.628 Million cell updates/sec

Title: US-10-688-489-73

Perfect score: 48

Sequence: 1 tcgcagacgttctgaggc.....atcacttcgagctttgttc 48

Scoring table: OLIGO NUC

Gapop\_60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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| C 9        | 17    | 35.4        | 381    | 9  | CE717260    |
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| C 105 | 16 | 33.3 | 641 | 8 | BH996029 | oeh20H05_1 | 178 | 15 | 31.2 | 257 | 9 | CE482232 | CE482232 | tigr-g88-   |
| C 106 | 16 | 33.3 | 642 | 7 | CL176655 | 104_383_1  | 179 | 15 | 31.2 | 258 | 9 | CE677702 | CE677702 | tigr-g88-   |
| C 107 | 16 | 33.3 | 643 | 7 | CU176655 | oeh20H05_1 | 180 | 15 | 31.2 | 260 | 9 | CE008552 | CE008552 | tigr-g88-   |
| C 108 | 16 | 33.3 | 644 | 7 | CU176655 | oeh20H05_1 | 181 | 15 | 31.2 | 260 | 9 | CE432060 | CE432060 | tigr-g88-   |
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| C 139 | 16 | 33.3 | 675 | 7 | BZ676878 | PUBHE50TD  | 212 | 15 | 31.2 | 317 | 9 | CE821716 | CE821716 | tigr-g88-   |
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| C 151 | 16 | 33.3 | 687 | 7 | BZ676878 | PUBHE50TD  | 224 | 15 | 31.2 | 334 | 6 | CD584966 | CD584966 | RK028A4F0   |
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| C 162 | 16 | 33.3 | 698 | 7 | BZ676878 | PUBHE50TD  | 235 | 15 | 31.2 | 358 | 9 | CE672729 | CE672729 | tigr-g88-   |
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| C 164 | 16 | 33.3 | 700 | 7 | BZ676878 | PUBHE50TD  | 237 | 15 | 31.2 | 365 | 8 | CE069331 | CE069331 | tigr-g88-   |
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| C 170 | 16 | 33.2 | 706 | 7 | BZ676878 | PUBHE50TD  | 243 | 15 | 31.2 | 379 | 9 | CE193502 | CE193502 | tigr-g88-   |

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| C 256 | 15 | 31.2 | 401 | 4 | BM269931 | 8ak22d05.   | C 329 | 15 | 31.2 | 467 | 1 | BJ485368 | BJ485368  |            |
| 257   | 15 | 31.2 | 402 | 9 | CE426537 | tigr-g88-   | C 330 | 15 | 31.2 | 469 | 1 | AI629999 | ASMTAG74  |            |
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| 259   | 15 | 31.2 | 405 | 5 | BP137897 | BP137897    | 332   | 15 | 31.2 | 469 | 9 | CE281508 | tigr-g88- |            |
| 260   | 15 | 31.2 | 405 | 9 | CE506039 | tigr-g88-   | C 333 | 15 | 31.2 | 473 | 9 | CE047479 | tigr-g88- |            |
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| 267   | 15 | 31.2 | 415 | 9 | CE203570 | tigr-g88-   | C 340 | 15 | 31.2 | 480 | 1 | AA537612 | AA537612  |            |
| 268   | 15 | 31.2 | 418 | 1 | AA745862 | ny93f12.8   | 341   | 15 | 31.2 | 480 | 9 | CE078290 | tigr-g88- |            |
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| C 273 | 15 | 31.2 | 424 | 1 | AI585329 | vj98q07.y   | 346   | 15 | 31.2 | 489 | 9 | CE814198 | tigr-g88- |            |
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|-------|----|------|-----|---|-----------|-----------|-----------|-------|----|------|-----|---|----------|----------|-----------|
| 390   | 15 | 31.2 | 515 | 7 | CE136813  | CE136813  | UI-HP-BNO | 463   | 15 | 31.2 | 556 | 9 | CE167158 | CE167158 | tigr-g8s- |
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| C 399 | 15 | 31.2 | 524 | 9 | CE654543  | tigr-g8s- |           | C 472 | 15 | 31.2 | 559 | 9 | CE801758 | CE801758 | tigr-g8s- |
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| 413   | 15 | 31.2 | 538 | 9 | CE603585  | tigr-g8s- |           | C 486 | 15 | 31.2 | 567 | 9 | CE722614 | CE722614 | tigr-g8s- |
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| C 428 | 15 | 31.2 | 553 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 429 | 15 | 31.2 | 554 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 430 | 15 | 31.2 | 555 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
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| C 433 | 15 | 31.2 | 558 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 434 | 15 | 31.2 | 559 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 435 | 15 | 31.2 | 560 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 436 | 15 | 31.2 | 561 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 437 | 15 | 31.2 | 562 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 438 | 15 | 31.2 | 563 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 439 | 15 | 31.2 | 564 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 440 | 15 | 31.2 | 565 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 441 | 15 | 31.2 | 566 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 442 | 15 | 31.2 | 567 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 443 | 15 | 31.2 | 568 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 444 | 15 | 31.2 | 569 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 445 | 15 | 31.2 | 570 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 446 | 15 | 31.2 | 571 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 447 | 15 | 31.2 | 572 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 448 | 15 | 31.2 | 573 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 449 | 15 | 31.2 | 574 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 450 | 15 | 31.2 | 575 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 451 | 15 | 31.2 | 576 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 452 | 15 | 31.2 | 577 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 453 | 15 | 31.2 | 578 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 454 | 15 | 31.2 | 579 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 455 | 15 | 31.2 | 580 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 456 | 15 | 31.2 | 581 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 457 | 15 | 31.2 | 582 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 458 | 15 | 31.2 | 583 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 459 | 15 | 31.2 | 584 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 460 | 15 | 31.2 | 585 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 461 | 15 | 31.2 | 586 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |
| C 462 | 15 | 31.2 | 587 | 9 | CE244433  | tigr-g8s- |           |       |    |      |     |   |          |          |           |

ALIGNMENTS

BI100670 916 bp mRNA linear EST 26-JUN-2001  
602885941F1 NCI\_CGAP\_Kid14 Mus musculus cDNA clone IMAGE:5041067  
5', mRNA sequence.

BI100670  
BI100670.1 GI:14551563  
EST.  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 916)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-romail.nih.gov](mailto:cgabbs-romail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1AM1113 row: b column: 12  
High quality sequence stop: 513.  
Location/Qualifiers  
1. .916  
/organism="Mus musculus"

FEATURES  
source

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/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5041067"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Kid14"
/notes="Organ: Kidney; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

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## ORIGIN

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Query Match      39.6%; Score 19; DB 4; Length 916;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 10 GTTCTGAGGCTTACATGG 28
    |||||
Db 514 GTTCTGAGGCTTACATGG 496

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## RESULT 2

```

CN226960      413 bp mRNA linear EST 09-APR-2004
LOCUS RUB008B11.ab1 RJtestis Gallus gallus cDNA 5', mRNA sequence.
ACCESSION CN226960
VERSION CN226960.1 GI:46330704
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

```

## REFERENCE

```

1 (bases 1 to 413)
Savolainen,P., Fitzsimmons,C.J., Arvestad,L., Andersson,L. and
Lundberg,J.

```

```

EST analysis of brain and testis cDNA libraries from White leghorn
and Red Jungle Fowl

```

## JOURNAL

```

Unpublished (2004)
Contact: Peter Savolainen
Department of Biotechnology
Royal Institute of Technology, KTH
SE-106 91 Stockholm, SWEDEN
Tel: +46 (0)8 5537 8481
Fax: +46 (0)8 5537 8335
Email: Peter.Savolainen@biotech.kth.se
Seq primer: M13 reverse primer.

```

## FEATURES

```

source
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    Location/Qualifiers
        /organism="Gallus gallus"
        /mol_type="mRNA"
        /strain="Red junglefowl"
        /db_xref="taxon:9031"
        /sex="male"
        /lab_host="ElectroMAX DH10B (Invitrogen)"
        /clone_lib="RJtestis"
        /notes="Organ: testis; Vector: pSPORT-1; Site 1: Hind III; Site 2: EcoRI; The cDNA libraries were created with the Superscript Plasmid System (Invitrogen)."
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## ORIGIN

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Query Match      37.5%; Score 18; DB 7; Length 413;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 26 TGGATCACTTCGAGCTT 43
    |||||
Db 137 TGGATCACTTCGAGCTT 154

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## RESULT 3

```

CE067576      154 bp DNA linear GSS 24-SEP-2003
LOCUS

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## DEFINITION

tigr-gss-dog-17000322656173 Dog Library Canis familiaris genomic, genomic survey sequence.

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ACCESSION CE067576
VERSION CE067576.1 GI:35125996
KEYWORDS GSS.
SOURCE Canis familiaris (dog)

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## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

## REFERENCE

1 (bases 1 to 154)
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K., Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and Venter,J.C.

## AUTHORS

The dog genome: survey sequencing and comparative analysis

## TITLE

Science 301 (5641), 1898-1903 (2003)

## MEDLINE

22875432

## PUBMED

14512627

## COMMENT

Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org  
Class: shotgun.

## FEATURES

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source
1..154
    Location/Qualifiers
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        /mol_type="genomic DNA"
        /strain="Standard Poodle"
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        /clone_lib="Dog Library"
        /note="Site 1: BstXI; Libraries were prepared from peripheral blood"
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## ORIGIN

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Query Match      35.4%; Score 17; DB 9; Length 154;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 4 GAGACGGTTCTGAGGCG 20
    |||||
Db 28 GAGACGGTTCTGAGGCG 44

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## RESULT 4

```

AW839969      193 bp mRNA linear EST 18-MAY-2000
LOCUS MR4-LT0077-150200-101-h10 LT0077 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW839969
VERSION AW839969.1 GI:7933943
KEYWORDS EST.
SOURCE Homo sapiens (human)

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## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 193)
Dias Neto,B., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,P.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baig,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.P., de Souza,S.J. and Simpson,A.J.

## AUTHORS

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

## TITLE

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

## JOURNAL

20202663

## MEDLINE

10737800

## PUBMED

10737800

## COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimponeludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=et5=MR4-LR0077-150  
 200-101-h10&t3=2000-02-15&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 19  
 High quality sequence stop: 193.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="LR0077"  
 /note="Organ: leiomyos; Vector: puc18; Site 1: SmaI;  
 Site 2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

FEATURES  
source

ORIGIN  
 Query Match 35.4%; Score 17; DB 2; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 ACTTCGAGCTTTGTTTC 48  
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 Db 1 ACTTCGAGCTTTGTTTC 17

RESULT 5  
 CE600009/c  
 LOCUS  
 DEFINITION tigr-gss-dog-1700036646390 Dog Library Canis familiaris genomic,  
 genomic survey sequence.  
 ACCESSION CE600009  
 VERSION CE600009.1 GI:36916848  
 KEYWORDS GSS.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 REFERENCE 1 (bases 1 to 222)  
 AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
 Venter,J.C.  
 TITLE The dog genome: survey sequencing and comparative analysis  
 JOURNAL Science 301 (5641), 1898-1903 (2003)  
 MEDLINE 22875432  
 PUBMED 14512627  
 COMMENT Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirknes@tigr.org  
 Class: shotgun.

ORIGIN  
 Query Match 35.4%; Score 17; DB 2; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 1. .222  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
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 /clone\_lib="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"

## ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 222;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 GAGACGGTTCTGAGGCG 20  
 |||||  
 Db 213 GAGACGGTTCTGAGGCG 197

RESULT 6  
 CE381828/c

LOCUS  
 DEFINITION tigr-gss-dog-17000334214632 Dog Library Canis familiaris genomic,  
 genomic survey sequence.  
 ACCESSION CE381828  
 VERSION CE381828.1 GI:36613404  
 KEYWORDS GSS.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 REFERENCE 1 (bases 1 to 235)  
 AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
 Venter,J.C.  
 TITLE The dog genome: survey sequencing and comparative analysis  
 JOURNAL Science 301 (5641), 1898-1903 (2003)  
 MEDLINE 22875432  
 PUBMED 14512627  
 COMMENT Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirknes@tigr.org  
 Class: shotgun.

ORIGIN  
 Query Match 35.4%; Score 17; DB 9; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES  
 source

1. .235  
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 /db\_xref="taxon:9615"  
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 peripheral blood"

ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCTGAGGCG 20  
 |||||  
 Db 131 GAGACGGTTCTGAGGCG 115

RESULT 7  
 CE403157

LOCUS  
 DEFINITION tigr-gss-dog-17000334744718 Dog Library Canis familiaris genomic,  
 genomic survey sequence.  
 ACCESSION CE403157  
 VERSION CE403157.1 GI:36652971  
 KEYWORDS GSS.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 REFERENCE 1 (bases 1 to 278)  
 AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and

FEATURES  
 source

1. .278  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"

## ORIGIN



Venter, J.C.  
 The dog genome: survey sequencing and comparative analysis  
 Science 301 (5641), 1898-1903 (2003)  
 MEDLINE 22875432  
 PUBMED 14512627  
 COMMENT Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirknes@tigr.org  
 Class: shotgun.

FEATURES  
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 1. .278  
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 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:9615"  
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 peripheral Blood"

ORIGIN  
 Query Match 35.4%; Score 17; DB 9; Length 278;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCTGAGGCG 20  
 |||||  
 DB 138 GAGACGGTTCTGAGGCG 154

RESULT 8  
 CE621983/c  
 LOCUS tigr-gss-dog-17000313638114 353 bp DNA linear GSS 29-SEP-2003  
 DEFINITION genomic survey sequence.  
 ACCESSION CE621983  
 VERSION CE621983.1 GI:36939358  
 KEYWORDS GSS.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 REFERENCE 1 (bases 1 to 353)  
 AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,  
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
 Venter, J.C.  
 TITLE The dog genome: survey sequencing and comparative analysis  
 JOURNAL Science 301 (5641), 1898-1903 (2003)  
 MEDLINE 22875432  
 PUBMED 14512627  
 COMMENT Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirknes@tigr.org  
 Class: shotgun.

FEATURES  
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 /clone\_lib="Dog Library"  
 /notes="Site 1: BstXI; Libraries were prepared from  
 peripheral Blood"

ORIGIN  
 Query Match 35.4%; Score 17; DB 9; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCTGAGGCG 20  
 |||||  
 DB 162 GAGACGGTTCTGAGGCG 146

RESULT 9  
 CE737260  
 LOCUS tigr-gss-dog-17000315462536 381 bp DNA linear GSS 30-SEP-2003  
 DEFINITION genomic survey sequence.  
 ACCESSION CE737260  
 VERSION CE737260.1 GI:37077455  
 KEYWORDS GSS.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 REFERENCE 1 (bases 1 to 381)  
 AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,  
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
 Venter, J.C.  
 TITLE The dog genome: survey sequencing and comparative analysis  
 JOURNAL Science 301 (5641), 1898-1903 (2003)  
 MEDLINE 22875432  
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 The Institute for Genomic Research  
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 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirknes@tigr.org  
 Class: shotgun.

FEATURES  
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 /notes="Site 1: BstXI; Libraries were prepared from  
 peripheral Blood"

ORIGIN  
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 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCTGAGGCGTTACAT 26  
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 DB 213 GTTCTGAGGCGTTACAT 229

RESULT 10  
 CE052353  
 LOCUS tigr-gss-dog-17000358219219 401 bp DNA linear GSS 24-SEP-2003  
 DEFINITION genomic survey sequence.  
 ACCESSION CE052353  
 VERSION CE052353.1 GI:35095839  
 KEYWORDS GSS.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 REFERENCE 1 (bases 1 to 401)  
 AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,  
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
 Venter, J.C.  
 TITLE The dog genome: survey sequencing and comparative analysis

```

JOURNAL      Science 301 (5641), 1898-1903 (2003)
MEDLINE      22875432
PUBMED       14512627
COMMENT      Contact: Kirkness EF
              The Institute for Genomic Research
              Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
              Rockville, MD 20850, USA
              Tel: 301-838-0200
              Fax: 301-838-0208
              Email: ekirknes@tigr.org
              Class: shotgun.
FEATURES     Location/Qualifiers
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             /organism="Canis familiaris"
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             /strain="Standard Poodle"
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             /note="Site 1: BstXI; Libraries were prepared from
             peripheral Blood"
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Best Local Similarity 100.0%; Pred. No. 42;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GAGACGGTTCTGAGGC 20
        |||||
Db      262 GAGACGGTTCTGAGGC 278

RESULT 11
CE025163
LOCUS      tigr-gss-dog-17000322362916 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
ACCESSION  CE025163
VERSION     1 GI:35041644
KEYWORDS   GSS.
SOURCE     Canis familiaris (dog)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE  1 (bases 1 to 406)
AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
            The dog genome: survey sequencing and comparative analysis
            Science 301 (5641), 1898-1903 (2003)
            22875432
            14512627
            Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES     Location/Qualifiers
             1..406
             /organism="Canis familiaris"
             /mol_type="genomic DNA"
             /strain="Standard Poodle"
             /db_xref="taxon:9615"
             /clone_lib="Dog Library"
             /note="Site 1: BstXI; Libraries were prepared from
             peripheral Blood"
ORIGIN
Query Match      35.4%; Score 17; DB 9; Length 406;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

JOURNAL      Science 301 (5641), 1898-1903 (2003)
MEDLINE      22875432
PUBMED       14512627
COMMENT      Contact: Kirkness EF
              The Institute for Genomic Research
              Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
              Rockville, MD 20850, USA
              Tel: 301-838-0200
              Fax: 301-838-0208
              Email: ekirknes@tigr.org
              Class: shotgun.
FEATURES     Location/Qualifiers
             1..406
             /organism="Canis familiaris"
             /mol_type="genomic DNA"
             /strain="Standard Poodle"
             /db_xref="taxon:9615"
             /clone_lib="Dog Library"
             /note="Site 1: BstXI; Libraries were prepared from
             peripheral Blood"
ORIGIN
Query Match      35.4%; Score 17; DB 9; Length 406;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      4 GAGACGGTTCTGAGGC 20
        |||||
Db      302 GAGACGGTTCTGAGGC 318

RESULT 12
CE778541/c
LOCUS      tigr-gss-dog-17000317030140 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
ACCESSION  CE778541
VERSION     1 GI:37119304
KEYWORDS   GSS.
SOURCE     Canis familiaris (dog)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE  1 (bases 1 to 409)
AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
            The dog genome: survey sequencing and comparative analysis
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            22875432
            14512627
            Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES     Location/Qualifiers
             1..409
             /organism="Canis familiaris"
             /mol_type="genomic DNA"
             /strain="Standard Poodle"
             /db_xref="taxon:9615"
             /clone_lib="Dog Library"
             /note="Site 1: BstXI; Libraries were prepared from
             peripheral Blood"
ORIGIN
Query Match      35.4%; Score 17; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GAGACGGTTCTGAGGC 20
        |||||
Db      301 GAGACGGTTCTGAGGC 285

RESULT 13
CE468568
LOCUS      tigr-gss-dog-17000363678786 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
ACCESSION  CE468568
VERSION     1 GI:36772018
KEYWORDS   GSS.
SOURCE     Canis familiaris (dog)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE  1 (bases 1 to 410)
AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
            The dog genome: survey sequencing and comparative analysis
            Science 301 (5641), 1898-1903 (2003)
            22875432

```

```

PUBMED 14512627
COMMENT Contact: Kirkness EF
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Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
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    1..410
    /organism="Canis familiaris"
    /mol_type="genomic DNA"
    /strain="Standard Poodle"
    /db_xref="taxon:9615"
    /clone_lib="Dog Library"
    /notes="Site 1: BatXI; Libraries were prepared from
    peripheral blood"

ORIGIN
Query Match 35.4%; Score 17; DB 9; Length 410;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGACGGTTCTGAGGC 20
|||||
Db 372 GAGACGGTTCTGAGGC 388

RESULT 14
LOCUS CE206168/c 413 bp DNA linear GSS 25-SEP-2003
DEFINITION tigr-gss-dog-17000372648258 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE206168
VERSION CE206168.1 GI:35361823
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 413)
AUTHORS Kirkness,E.F., Batna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
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Rockville, MD 20850, USA
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Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
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    1..413
    /organism="Canis familiaris"
    /mol_type="genomic DNA"
    /strain="Standard Poodle"
    /db_xref="taxon:9615"
    /clone_lib="Dog Library"
    /notes="Site 1: BatXI; Libraries were prepared from
    peripheral blood"

ORIGIN
Query Match 35.4%; Score 17; DB 9; Length 413;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGACGGTTCTGAGGC 20
|||||
Db 372 GAGACGGTTCTGAGGC 388

RESULT 15
LOCUS CE267316/c 426 bp DNA linear GSS 26-SEP-2003
DEFINITION tigr-gss-dog-17000359912254 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE267316
VERSION CE267316.1 GI:35992555
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 426)
AUTHORS Kirkness,E.F., Batna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
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COMMENT Contact: Kirkness EF
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Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
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    1..426
    /organism="Canis familiaris"
    /mol_type="genomic DNA"
    /strain="Standard Poodle"
    /db_xref="taxon:9615"
    /clone_lib="Dog Library"
    /notes="Site 1: BatXI; Libraries were prepared from
    peripheral blood"

ORIGIN
Query Match 35.4%; Score 17; DB 9; Length 426;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGACGGTTCTGAGGC 20
|||||
Db 277 GAGACGGTTCTGAGGC 261

RESULT 16
LOCUS CE218594 431 bp DNA linear GSS 25-SEP-2003
DEFINITION tigr-gss-dog-17000326860586 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE218594
VERSION CE218594.1 GI:35374263
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 431)
AUTHORS Kirkness,E.F., Batna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF

```

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Class: shotgun.

# FEATURES

source  
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Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: BstXI; Libraries were prepared from  
peripheral blood"

## ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 431;  
Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GAGACGGTCTCAGGGC 20  
|||||  
Db 330 GAGACGGTCTCAGGGC 346

## RESULT 17

CE111389  
LOCUS  
DEFINITION tigr-gss-dog-17000324922150 Dog Library Canis familiaris genomic,  
genomic survey sequence.

ACCESSION CE111389.1 GI:35178274  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Canis familiaris (dog)

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
Venter,J.C.

TITLE The dog genome: survey sequencing and comparative analysis  
JOURNAL Science 301 (5641), 1898-1903 (2003)  
MEDLINE  
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## COMMENT

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Fax: 301-838-0208  
Email: ekirknes@tigr.org  
Class: shotgun.

## FEATURES

source  
1. .460  
Location/Qualifiers  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: BstXI; Libraries were prepared from  
peripheral blood"

## ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 460;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GAGACGGTCTCAGGGC 20  
|||||  
Db 322 GAGACGGTCTCAGGGC 338

RESULT 18  
CE015704/c  
LOCUS  
DEFINITION tigr-gss-dog-17000321327472 Dog Library Canis familiaris genomic,  
genomic survey sequence.

ACCESSION CE015704.1 GI:35022697  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Canis familiaris (dog)

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
Venter,J.C.

TITLE The dog genome: survey sequencing and comparative analysis  
JOURNAL Science 301 (5641), 1898-1903 (2003)  
MEDLINE  
PUBMED 14512627  
COMMENT Contact: Kirkness EF  
The Institute for Genomic Research  
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Fax: 301-838-0208  
Email: ekirknes@tigr.org  
Class: shotgun.

## FEATURES

source  
1. .462  
Location/Qualifiers  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: BstXI; Libraries were prepared from  
peripheral blood"

## ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 462;  
Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GAGACGGTCTCAGGGC 20  
|||||  
Db 267 GAGACGGTCTCAGGGC 251

RESULT 19  
CE235142  
LOCUS  
DEFINITION tigr-gss-dog-1700033378589 Dog Library Canis familiaris genomic,  
genomic survey sequence.

ACCESSION CE235142.1 GI:35390900  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Canis familiaris (dog)

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
Venter,J.C.

TITLE The dog genome: survey sequencing and comparative analysis  
JOURNAL Science 301 (5641), 1898-1903 (2003)  
MEDLINE  
PUBMED 14512627  
COMMENT Contact: Kirkness EF  
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Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirknes@tigr.org  
Class: shotgun.

# FEATURES

source

Location/Qualifiers  
1. .468  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/notes="Site 1: BstXI; Libraries were prepared from peripheral blood"

## ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 468;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCGAGGC 20  
|||||  
DB 329 GAGACGGTTCGAGGC 345

## RESULT 20

CE724068 471 bp DNA linear GSS 30-SEP-2003  
LOCUS tigr-gss-dog-17000315207540 Dog Library Canis familiaris genomic,  
DEFINITION genomic survey sequence.

ACCESSION CE724068  
VERSION CE724068.1 GI:37064093  
KEYWORDS GSS.

## SOURCE

ORGANISM Canis familiaris (dog)  
Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

## REFERENCE

AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,  
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
Venter, J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)

14512627

## TITLE

JOURNAL The Institute for Genomic Research  
MEDLINE Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
PUBMED Rockville, MD 20850, USA  
KEYWORDS Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirknes@tigr.org  
Class: shotgun.

## FEATURES

source

Location/Qualifiers  
1. .471  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/notes="Site 1: BstXI; Libraries were prepared from peripheral blood"

## ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 471;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCGAGGC 20  
|||||  
DB 211 GAGACGGTTCGAGGC 227

## RESULT 21

CE788674/c

## LOCUS

DEFINITION tigr-gss-dog-17000317779733 Dog Library Canis familiaris genomic,  
genomic survey sequence.

## ACCESSION

VERSION CE788674.1 GI:37129437

## KEYWORDS

SOURCE GSS.

## ORGANISM

Canis familiaris (dog)  
Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

## REFERENCE

AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,  
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
Venter, J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)

22875432

## PUBMED

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## COMMENT

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Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirknes@tigr.org  
Class: shotgun.

## FEATURES

source

Location/Qualifiers  
1. .498  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/notes="Site 1: BstXI; Libraries were prepared from peripheral blood"

## ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 498;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCGAGGC 20  
|||||

DB 135 GAGACGGTTCGAGGC 119

## RESULT 22

CE679750/c

## LOCUS

DEFINITION tigr-gss-dog-17000314411471 Dog Library Canis familiaris genomic,  
genomic survey sequence.

## ACCESSION

VERSION CE679750.1 GI:36998750

## KEYWORDS

SOURCE GSS.

## ORGANISM

Canis familiaris (dog)  
Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

## REFERENCE

AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,  
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
Venter, J.C.  
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Science 301 (5641), 1898-1903 (2003)

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## PUBMED

14512627

## COMMENT

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Rockville, MD 20850, USA  
Tel: 301-838-0200

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FEATURES
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        /strain="Standard Poodle"
        /db_xref="taxon:9615"
        /clone_lib="Dog Library"
        /note="Site 1: BstXI; Libraries were prepared from
        peripheral blood"
ORIGIN
  Query Match      35.4%; Score 17; DB 9; Length 544;
  Best Local Similarity 100.0%; Pred. No. 43;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY      4 GAGACGGTTCTGAGGCG 20
          |||||
  Db      253 GAGACGGTTCTGAGGCG 237

RESULT 23
CE411475/c
LOCUS
DEFINITION
  tigr-gss-dog-17000362273066 Dog Library Canis familiaris genomic,
  genomic survey sequence.
ACCESSION
  CE411475
VERSION
  CE411475.1 GI:36668289
KEYWORDS
  GSS.
SOURCE
  Canis familiaris (dog)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
  1 (bases 1 to 556)
  Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
  Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
  Venter,J.C.
  The dog genome: survey sequencing and comparative analysis
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  14512627
  PUBMED
  COMMENT
  Contact: Kirkness EF
  The Institute for Genomic Research
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  Rockville, MD 20850, USA
  Tel: 301-838-0200
  Fax: 301-838-0208
  Email: ekirknes@tigr.org
  Class: shotgun.
  Location/Qualifiers
    1..556
      /organism="Canis familiaris"
      /mol_type="genomic DNA"
      /strain="Standard Poodle"
      /db_xref="taxon:9615"
      /clone_lib="Dog Library"
      /note="Site 1: BstXI; Libraries were prepared from
      peripheral blood"
ORIGIN
  Query Match      35.4%; Score 17; DB 9; Length 556;
  Best Local Similarity 100.0%; Pred. No. 43;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY      4 GAGACGGTTCTGAGGCG 20
          |||||
  Db      113 GAGACGGTTCTGAGGCG 97

RESULT 24
CE274341/c
LOCUS
DEFINITION
  tigr-gss-dog-17000333595430 Dog Library Canis familiaris genomic,
  genomic survey sequence.
ACCESSION
  CE274341
VERSION
  CE274341.1 GI:36012978
KEYWORDS
  GSS.
SOURCE
  Canis familiaris (dog)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
  1 (bases 1 to 565)
  Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
  Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
  Venter,J.C.
  The dog genome: survey sequencing and comparative analysis
  Science 301 (5641), 1898-1903 (2003)
  14512627
  PUBMED
  COMMENT
  Contact: Kirkness EF
  The Institute for Genomic Research
  Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
  Rockville, MD 20850, USA
  Tel: 301-838-0200
  Fax: 301-838-0208
  Email: ekirknes@tigr.org
  Class: shotgun.
  Location/Qualifiers
    1..565
      /organism="Canis familiaris"
      /mol_type="genomic DNA"
      /strain="Standard Poodle"
      /db_xref="taxon:9615"
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      /note="Site 1: BstXI; Libraries were prepared from
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  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY      4 GAGACGGTTCTGAGGCG 20
          |||||
  Db      113 GAGACGGTTCTGAGGCG 97

RESULT 25
CE671584/c
LOCUS
DEFINITION
  tigr-gss-dog-17000313756475 Dog Library Canis familiaris genomic,
  genomic survey sequence.
ACCESSION
  CE671584
VERSION
  CE671584.1 GI:36990584
KEYWORDS
  GSS.
SOURCE
  Canis familiaris (dog)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
  1 (bases 1 to 566)
  Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
  Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
  Venter,J.C.
  The dog genome: survey sequencing and comparative analysis
  Science 301 (5641), 1898-1903 (2003)
  14512627
  PUBMED
  COMMENT
  Contact: Kirkness EF
  The Institute for Genomic Research
  Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
  Rockville, MD 20850, USA
  Tel: 301-838-0200
  Fax: 301-838-0208
  Email: ekirknes@tigr.org
  Class: shotgun.
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    1..556
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      /strain="Standard Poodle"
      /db_xref="taxon:9615"
      /clone_lib="Dog Library"
      /note="Site 1: BstXI; Libraries were prepared from
      peripheral blood"
ORIGIN
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  Best Local Similarity 100.0%; Pred. No. 43;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY      4 GAGACGGTTCTGAGGCG 20
          |||||
  Db      113 GAGACGGTTCTGAGGCG 97

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FEATURES
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    Class: shotgun.
    Location/Qualifiers
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        /mol_type="genomic DNA"
        /strain="Standard Poodle"
        /db_xref="taxon:9615"
        /clone_lib="Dog Library"
        /notes="Site 1: BstXI; Libraries were prepared from
        peripheral Blood"
ORIGIN
  Query Match      35.4%; Score 17; DB 9; Length 566;
  Best Local Similarity 100.0%; Pred. No. 43;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4 GAGACGGTTCTGAGGGC 20
      |||||||
Db      181 GAGACGGTTCTGAGGGC 165
      |||||||
RESULT 26
CE371722/c      582 bp DNA linear GSS 27-SEP-2003
LOCUS CE371722
DEFINITION tigr-gss-dog-17000362071090 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE371722
VERSION CE371722.1 GI:36594536
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
  1..589
    /organism="Canis familiaris"
    /mol_type="genomic DNA"
    /strain="Standard Poodle"
    /db_xref="taxon:9615"
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    /notes="Site 1: BstXI; Libraries were prepared from
    peripheral Blood"
ORIGIN
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  Best Local Similarity 100.0%; Pred. No. 43;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4 GAGACGGTTCTGAGGGC 20
      |||||||
Db      372 GAGACGGTTCTGAGGGC 356
      |||||||
RESULT 28
CE683680
LOCUS CE683680
DEFINITION tigr-gss-dog-17000314487053 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE683680
VERSION CE683680.1 GI:37002716
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
  1..582
    /organism="Canis familiaris"
    /mol_type="genomic DNA"
    /strain="Standard Poodle"
    /db_xref="taxon:9615"
    /clone_lib="Dog Library"
    /notes="Site 1: BstXI; Libraries were prepared from
    peripheral Blood"
ORIGIN
  Query Match      35.4%; Score 17; DB 9; Length 582;
  Best Local Similarity 100.0%; Pred. No. 43;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4 GAGACGGTTCTGAGGGC 20
      |||||||
Db      243 GAGACGGTTCTGAGGGC 227
      |||||||
RESULT 27
CE076080/c      589 bp DNA linear GSS 24-SEP-2003
LOCUS CE076080
DEFINITION tigr-gss-dog-17000324332391 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE076080
VERSION CE076080.1 GI:35142780
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
  1..589
    /organism="Canis familiaris"
    /mol_type="genomic DNA"
    /strain="Standard Poodle"
    /db_xref="taxon:9615"
    /clone_lib="Dog Library"
    /notes="Site 1: BstXI; Libraries were prepared from
    peripheral Blood"
ORIGIN
  Query Match      35.4%; Score 17; DB 9; Length 589;
  Best Local Similarity 100.0%; Pred. No. 43;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4 GAGACGGTTCTGAGGGC 20
      |||||||
Db      372 GAGACGGTTCTGAGGGC 356
      |||||||

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source
1. .598
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BtXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 35.4%; Score 17; DB 9; Length 598;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCGAGGCG 20
|||||
Db 432 GAGACGGTTCGAGGCG 448

RESULT 29
CA229401
LOCUS CA229401 600 bp mRNA linear EST 25-SBP-2003
DEFINITION SCAGFL3025C06.g Saccharum officinarum FL3 Saccharum officinarum
cDNA clone SCAGFL3025C06 5', mRNA sequence.
ACCESSION CA229401
VERSION CA229401
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE 1 (bases 1 to 600)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bccccenter.fcav.unesp.br
Plate: 025 row: C column: 06
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1. .600
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCAGFL3025C06"
/lab_host="DH10B"
/clone_lib="Saccharum officinarum FL3"
Vector: pSport1; Site 1: SalI; Site 2: NotI; An
unidirectional cDNA library generated from [base of
developing inflorescence (5cm-long)]. cDNA was prepared
from polyA+ mRNA using Superscript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"

ORIGIN
Query Match 35.4%; Score 17; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 18 GGCTTACATGGATCACT 34
|||||
Db 142 GGCTTACATGGATCACT 158

RESULT 30
CE237342/c
LOCUS CE237342 605 bp DNA linear GSS 25-SEP-2003
DEFINITION tigr-gss-dog-1700033398507 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE237342
VERSION CE237342.1 GI:35393100
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 605)
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1. 605
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BtXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 35.4%; Score 17; DB 9; Length 605;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCGAGGCG 20
|||||
Db 345 GAGACGGTTCGAGGCG 329

RESULT 31
CE069149
LOCUS CE069149 612 bp DNA linear GSS 24-SEP-2003
DEFINITION tigr-gss-dog-17000322919379 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE069149
VERSION CE069149.1 GI:35129037
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 612)
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1. 605
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BtXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 35.4%; Score 17; DB 9; Length 605;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```





The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirknes@tigr.org  
Class: shotgun.

# FEATURES

source  
1. .649  
/location/Qualifiers  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: BstXI; Libraries were prepared from  
peripheral blood"

# ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 649;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCGAGGC 20  
|||||  
Db 405 GAGACGGTTCGAGGC 421

# RESULT 35

AW422619 660 bp mRNA linear EST 09-FEB-2000  
LOCUS f144f06.y1 Sugano Kawakami zebrafish DRA Danio rerio cDNA clone  
DEFINITION IMAGE:2640515.5' similar to SW:BTEL\_HUMAN Q13886 TRANSCRIPTION  
FACTOR BTEBI ; mRNA sequence.

# ACCESSION

VERSION AW422619.1 GI:6950551  
KEYWORDS EST.

# SOURCE

ORGANISM Danio rerio (zebrafish)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 660)  
Sugano, S., Kawakami, K., Johnson, S., Li, F., Marra, M., Eddy, S.,  
Hillier, L., Clifton, S., Allen, M., Gibbons, M., Jost, S., Kucaba, T.,  
Martin, J., Pape, D., Stepien, M., Underwood, K., Theising, B.,  
Ritter, E., Bowers, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU Zebrafish EST Project 1999  
Unpublished (1999)  
Contact: S.L. Johnson  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 9501, St. Louis, MO 63109, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA  
Sequencing by: Washington University Genome Sequencing Center  
Seq primer: T3 ET from Amersham  
High quality sequence stop: 455.

# TITLE

# JOURNAL

# COMMENT

# FEATURES

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1. .660  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/strain="AB"  
/db\_xref="taxon:7955"  
/clone\_lib="IMAGE:2640515"  
/sex="mixed (one male and one female, including  
unfertilized eggs)"  
/dev\_stage="adult"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Sugano Kawakami zebrafish DRA"  
/note="Vector: pME18S-FL3; Site\_1: DraIII (CACTGTGTC);  
Site\_2: DraIII (CACCATGTG); 1st strand cDNA was primed  
with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT];

double-stranded cDNA was ligated to a DraIII adaptor  
[GTGTGGCTACTGG], digested and cloned into distinct DraIII  
sites of the pME18S-FL3 vector (5' site CACTGTGTC, 3' site  
CACCATGTG). XhoI should be used to isolate the cDNA  
insert. Size selection was performed to exclude fragments  
<1.5kb. Library constructed by Dr. Sumio Sugano  
(University of Tokyo Institute of Medical Science) and  
kindly donated by Dr. Koichi Kawakami. Custom primers for  
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGG and 3' end  
primer CGACCTGCAGCTCGAGCAC. "

# ORIGIN

Query Match 35.4%; Score 17; DB 2; Length 660;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 ATGGATCACTTCGAGC 41  
|||||  
Db 226 ATGGATCACTTCGAGC 242

# RESULT 36

CE844747 668 bp DNA linear GSS 01-OCT-2003  
LOCUS tigr-gss-dog-17000332719174 Dog Library Canis familiaris genomic,  
DEFINITION genomic survey sequence.  
ACCESSION CE844747  
VERSION CE844747.1 GI:37207016  
KEYWORDS GSS.

# SOURCE

# ORGANISM

Canis familiaris (dog)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
1 (bases 1 to 668)  
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,  
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
Venter, J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)  
MEDLINE 22875432  
PUBMED 14512627  
COMMENT Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirknes@tigr.org  
Class: shotgun.

# FEATURES

# source

1. .668  
/location/Qualifiers  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: BstXI; Libraries were prepared from  
peripheral blood"

# ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 668;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCGAGGC 20  
|||||  
Db 428 GAGACGGTTCGAGGC 444

# RESULT 37

BH014887/c  
LOCUS TDGBR95TH cTOG Lycopersicon esculentum genomic clone cTOG11P22,  
DEFINITION

```

ACCESSION      BH014887
VERSION        BH014887.1 GI:14145925
KEYWORDS       GSS.
SOURCE         Lycopersicon esculentum (tomato)
ORGANISM       Lycopersicon esculentum
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE      1 (bases 1 to 672)
AUTHORS        van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Ronning,C. and
               Tanksley,S.
TITLE          Tomato Demethylated Genomic DNA Sequences
JOURNAL        Unpublished (2001)
COMMENT        Contact: CUGI
               Clemson University
               Clemson University Genomics Institute
               100 Jordan Hall, Clemson, SC 29634, USA
               Email: http://www.genome.clemson.edu/orders/index.html
               tomato demethylated genomic DNA
               Seq primer: M13F-R
               Class: shotgun.
FEATURES       Location/Qualifiers
               source
               1..672
               /organism="Lycopersicon esculentum"
               /mol_type="genomic DNA"
               /cultivar="E6203"
               /db_xref="taxon:4081"
               /clone="CTOG11P22"
               /tissue_type="young leaves"
               /dev_stage="12-14 weeks post harvest"
               /lab_host="E.coli JM109"
               /clone_lib="CTOG"
               /notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
               XhoI; This library was made from short EcoRI digested
               fragments of the genome of Lycopersicon esculentum ligated
               into pBS (SK-). The fragments were cloned into the
               methylation restrictive E.coli strain JM109 with the
               purpose of enriching the library for non-methylated DNA
               fragments. This procedure may enrich the pool of cloned
               fragments in JM109 cells for sequences representing
               expressed genes. Average insert size 1.27 Kb."
ORIGIN
Query Match      35.4%; Score 17; DB 8; Length 672;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GGGCTTACATGGATCAC 33
      |||||
DB 248 GGGCTTACATGGATCAC 232

RESULT 38
BH012308
LOCUS          BH012308      673 bp      DNA      linear      GSS 18-MAY-2001
DEFINITION    TGM474TH cTOG Lycopersicon esculentum genomic clone cTOG2N4,
               genomic survey sequence.
ACCESSION     BH012308
VERSION       BH012308.1 GI:14142497
KEYWORDS      GSS.
SOURCE        Lycopersicon esculentum (tomato)
ORGANISM      Lycopersicon esculentum
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE     1 (bases 1 to 673)
AUTHORS        van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Ronning,C. and
               Tanksley,S.
TITLE          Tomato Demethylated Genomic DNA Sequences
JOURNAL        Unpublished (2001)
COMMENT        Contact: CUGI
               Clemson University Genomics Institute

```

```

Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
tomato demethylated genomic DNA
Seq primer: M13F-R
Class: shotgun.
FEATURES       Location/Qualifiers
               source
               1..673
               /organism="Lycopersicon esculentum"
               /mol_type="genomic DNA"
               /cultivar="E6203"
               /db_xref="taxon:4081"
               /clone="CTOG2N4"
               /tissue_type="young leaves"
               /dev_stage="12-14 weeks post harvest"
               /lab_host="E.coli JM109"
               /clone_lib="CTOG"
               /notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
               XhoI; This library was made from short EcoRI digested
               fragments of the genome of Lycopersicon esculentum ligated
               into pBS (SK-). The fragments were cloned into the
               methylation restrictive E.coli strain JM109 with the
               purpose of enriching the library for non-methylated DNA
               fragments. This procedure may enrich the pool of cloned
               fragments in JM109 cells for sequences representing
               expressed genes. Average insert size 1.27 Kb."
ORIGIN
Query Match      35.4%; Score 17; DB 8; Length 673;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GGGCTTACATGGATCAC 33
      |||||
DB 420 GGGCTTACATGGATCAC 436

RESULT 39
BH145540
LOCUS          BH145540      673 bp      DNA      linear      GSS 16-AUG-2001
DEFINITION    TDGEX60TH cTOG Lycopersicon esculentum genomic clone cTOG32J24,
               genomic survey sequence.
ACCESSION     BH145540
VERSION       BH145540.1 GI:15201636
KEYWORDS      GSS.
SOURCE        Lycopersicon esculentum (tomato)
ORGANISM      Lycopersicon esculentum
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE     1 (bases 1 to 673)
AUTHORS        van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Ronning,C. and
               Tanksley,S.
TITLE          Tomato Demethylated Genomic DNA Sequences
JOURNAL        Unpublished (2001)
COMMENT        Contact: CUGI
               Clemson University Genomics Institute
               Clemson University
               100 Jordan Hall, Clemson, SC 29634, USA
               Email: http://www.genome.clemson.edu/orders/index.html
               tomato demethylated genomic DNA
               Insert Length: 1270 Std Error: 0.00
               Seq primer: M13F-R
               Class: shotgun.
FEATURES       Location/Qualifiers
               source
               1..673
               /organism="Lycopersicon esculentum"
               /mol_type="genomic DNA"
               /cultivar="E6203"
               /db_xref="taxon:4081"
               /clone="cTOG32J24"
               /dev_stage="12-14 weeks post harvest"

```

/lab host="E.coli JM109"  
 /clone lib="cTGG"  
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:  
 XhoI; This library was made from short EcoRI digested  
 fragments of the genome of Lycopersicon esculentum ligated  
 into pBS (SK-). The fragments were cloned into the  
 methylation restrictive E.coli strain JM109 with the  
 purpose of enriching the library for non-methylated DNA  
 fragments. This procedure may enrich the pool of cloned  
 fragments in JM109 cells for sequences representing  
 expressed genes. Average insert size 1.27 kb."

## ORIGIN

Query Match 35.4%; Score 17; DB 8; Length 673;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 GGGCTTACATGGATCAC 33  
 Db 419 GGGCTTACATGGATCAC 435

## RESULT 40

CE552243/c  
 LOCUS  
 DEFINITION tigr-gss-dog-17000312313299 Dog Library Canis familiaris genomic,  
 genomic survey sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE

CE552243.1 GI:36869024  
 GSS.

## ORGANISM

Canis familiaris (dog)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

## REFERENCE

AUTHORS  
 Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
 Venter,J.C.

## TITLE

The dog genome: survey sequencing and comparative analysis

## JOURNAL

Medline  
 PUBMED  
 COMMENT

The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirknes@tigr.org  
 Class: shotgun.

## FEATURES

source  
 Location/Qualifiers  
 1..689  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /notes="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"

## ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 689;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGACGGTCTGAGGCG 20  
 Db 360 GAGACGGTCTGAGGCG 344

## RESULT 41

CE667057/c  
 LOCUS

## DEFINITION

tigr-gss-dog-17000313695737 Dog Library Canis familiaris genomic,  
 genomic survey sequence.

## ACCESSION

CE667057  
 VERSION  
 KEYWORDS  
 SOURCE

## ORGANISM

Canis familiaris (dog)  
 Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

## REFERENCE

AUTHORS  
 Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
 Venter,J.C.

## TITLE

The dog genome: survey sequencing and comparative analysis

## JOURNAL

Medline  
 PUBMED  
 COMMENT

Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirknes@tigr.org  
 Class: shotgun.

## FEATURES

source  
 Location/Qualifiers  
 1..709  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"

## ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 709;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGACGGTCTGAGGCG 20  
 Db 330 GAGACGGTCTGAGGCG 314

## RESULT 42

CE322509/c  
 LOCUS

## DEFINITION

tigr-gss-dog-17000360493114 Dog Library Canis familiaris genomic,  
 genomic survey sequence.

## ACCESSION

CE322509  
 VERSION  
 KEYWORDS  
 SOURCE

## ORGANISM

Canis familiaris (dog)  
 Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

## REFERENCE

AUTHORS  
 Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
 Venter,J.C.

## TITLE

The dog genome: survey sequencing and comparative analysis

## JOURNAL

Medline  
 PUBMED  
 COMMENT

Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirknes@tigr.org  
 Class: shotgun.

```

FEATURES
  source
    Location/Qualifiers
      1..712
        /organism="Canis familiaris"
        /mol_type="genomic DNA"
        /strain="Standard Poodle"
        /db_xref="taxon:9615"
        /clone_lib="Dog Library"
        /notes="Site 1: BstXI; Libraries were prepared from
        peripheral blood"

ORIGIN
  Query Match      35.4%; Score 17; DB 9; Length 712;
  Best Local Similarity 100.0%; Pred. No. 43;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTCTGAGGCC 20
    |||||
Db 314 GAGACGGTCTGAGGCC 298

RESULT 43
AG300452
LOCUS
DEFINITION
  Mus musculus molossinus DNA, clone:MSMg01-079F15.TJ, genomic survey
  sequence.
ACCESSION
  AG300452
VERSION
  AG300452.1 GI:47873406
KEYWORDS
  GSS.
SOURCE
  Mus musculus molossinus
ORGANISM
  Mus musculus molossinus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
  1 Hattori M., Toyoda A., Noguchi H., Kojima T. and Sakaki, Y.
  BAC end Sequences of Library MSMg01
  Unpublished
  2 (bases 1 to 716)
  Hattori M., Toyoda A., Noguchi H., Kojima T. and Sakaki, Y.
  Direct Submission
  Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
  and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
  1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
  (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
  Tel:81-45-503-9111, Fax:81-45-503-9170)
  Clones are derived from the mouse BAC library MSMg01. For BAC
  library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
  Tsukuba Institute Bio Resource Center, Research (RIKEN) 3-1-1
  The Institute of Physical and Chemical Research (RIKEN) 3-1-1
  Koyadai, Tsukuba, 305-0074 Japan
  phone: 81-298-36-9189, fax: 81-298-36-9199
  e-mail: abe@rtc.riken.jp
  PRIMERS
  Sequencing : TJ
  LIBRARY
  Vector : pBACe3.6
  R.Site 1 : EcoRI
  R.Site 2 : EcoRI.
FEATURES
  source
    Location/Qualifiers
      1..716
        /organism="Mus musculus molossinus"
        /mol_type="genomic DNA"
        /sub_species="molossinus"
        /db_xref="taxon:57486"
        /clone="MSMg01-079F15.TJ"
        /sex="male"
        /tissue_type="mixture of kidney and spleen"
        /clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
  Query Match      35.4%; Score 17; DB 9; Length 716;
  Best Local Similarity 100.0%; Pred. No. 43;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTCTGAGGCTTACATG 27
    |||||
Db 556 TTCTGAGGCTTACATG 540

RESULT 44
BU466014/c
LOCUS
DEFINITION
  Gallus gallus (chicken)
  sequence.
ACCESSION
  BU466014
VERSION
  BU466014.1 GI:25959591
KEYWORDS
  EST.
SOURCE
  Gallus gallus (chicken)
ORGANISM
  Gallus gallus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
  Phasianinae; Gallus.
REFERENCE
  1 (bases 1 to 815)
  Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
  Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
  A Comprehensive Collection of Chicken cDNAs
  Curr. Biol. 12 (22), 1965-1969 (2002)
  22335534
  PUBMED
COMMENT
  Contact: Simon Hubbard
  Department of Biomolecular Sciences
  University of Manchester Institute of Science and Technology
  (UMIST)
  PO Box 88, Manchester, M60 1QD, UK
  Tel: 01612008930
  Fax: 01612360409
  Email: Simon.Hubbard@umist.ac.uk.
FEATURES
  source
    Location/Qualifiers
      1..815
        /organism="Gallus gallus"
        /mol_type="mRNA"
        /strain="Layer and broiler"
        /db_xref="taxon:9031"
        /clone="ChEST277e5"
        /sex="Male and female"
        /tissue_type="Chondrocytes isolated from growth plate
        cartilage"
        /dev_stage="adult"
        /lab_host="DH10B"
        /clone_lib="CSEQRN20"
        /note="Vector: pBluescript II KS(+); Site_1: EcoRI;
        Site_2: NotI; This normalized library was constructed from
        1 million independent clones. cDNA synthesis was initiated
        using an oligo(dT) primer, using methylated C in the first
        strand synthesis reaction. Following this first strand
        reaction, double-stranded cDNA was blunted, ligated to
        NotI adapters, digested with EcoRI, size-selected, and
        cloned into the NotI and EcoRI compatible sites of a
        custom modified MCS of the pBluescript (KS+) vector. The
        library was normalized in 2 rounds using conditions
        adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
        Bonaldo et al., Genome Research 6 (1996): 791, except that
        a significantly longer reannealing hybridization was
        used."
  Query Match      35.4%; Score 17; DB 5; Length 815;
  Best Local Similarity 100.0%; Pred. No. 44;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTCTGAGGCTTACATG 27
    |||||
Db 556 TTCTGAGGCTTACATG 540

RESULT 45
BU466018/c

```

LOCUS BU466018 816 bp mRNA linear EST 30-NOV-2002  
 DEFINITION 603371676F1 CSEQREN20 Gallus gallus CDNA clone CHEST279g20 5', mRNA sequence.  
 ACCESSION BU466018  
 VERSION BU466018.1 GI:25959595  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 1 (bases 1 to 816)  
 REFERENCE Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)  
 22335534  
 MEDLINE PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
 source  
 1..816  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Layer and broiler"  
 /db\_xref="taxon:9031"  
 /clone="CHEST279g20"  
 /sex="Male and female"  
 /tissue\_type="Chondrocytes isolated from growth plate cartilage"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQREN20"

NOTE: Vector: pBluescript II KS(+); Site\_1: EcoRI; Site\_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 35.4%; Score 17; DB 5; Length 816;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTCTGAGGGCTTACATG 27  
 |||||  
 DB 551 TTCTGAGGGCTTACATG 535

RESULT 46  
 CF549567  
 LOCUS  
 DEFINITION AGENCOURT\_15591571 NIH\_ZGC\_4 Danio rerio cDNA clone IMAGE:7013722  
 5', mRNA sequence.  
 ACCESSION CF549567  
 VERSION CF549567.1 GI:34886399  
 KEYWORDS EST.  
 SOURCE Danio rerio (zebrafish)

## ORGANISM

Danio rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 816)  
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL  
 COMMENT Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgabs-r@mail.nih.gov  
 Tissue Procurement: John Ngai, Univ of CA, Berkeley  
 cDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM14725 row: p column: 08  
 High quality sequence start: 15  
 High quality sequence stop: 706.

FEATURES  
 source

1..816  
 /organism="Danio rerio"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7955"  
 /clone="IMAGE:7013722"  
 /lab\_host="DH10B Tona"  
 /clone\_lib="NIH ZGC 4"  
 /note="Organ: brain/CNS; Vector: pME18S-FL3; Site\_1: DraIII; Site\_2: DraIII"

## ORIGIN

Query Match 35.4%; Score 17; DB 7; Length 816;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 ATGGATCATTGGCAGC 41  
 |||||  
 DB 307 ATGGATCATTGGCAGC 323

## RESULT 47

BU467348 821 bp mRNA linear EST 30-NOV-2002  
 603371996F1 CSEQREN20 Gallus gallus CDNA clone CHEST280c23 5', mRNA sequence.  
 ACCESSION BU467348  
 VERSION BU467348.1 GI:25960925  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 1 (bases 1 to 821)

REFERENCE Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)  
 22335534  
 MEDLINE PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers

## FEATURES

```

source
1. .821
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST280c23"
/sex="Male and female"
/tissue_type="Chondrocytes isolated from growth plate cartilage"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSQRBN20"
/notes="Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Ronaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN
Query Match 35.4%; Score 17; DB 5; Length 821;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTCTGAGGGCTTACATG 27
|||||
Db 555 TTCTGAGGGCTTACATG 539

RESULT 48
BU467944/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

FEATURES
source
1. .825
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST28j15"
/sex="Male and female"

BU467944 825 bp mRNA linear EST 30-NOV-2002
603373461F1 CSQRBN20 Gallus gallus cDNA clone CHEST28j15 5', mRNA
sequence.
BU467944
BU467944.1 GI:25961521
EST.
Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 825)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. .825
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST28j15"
/sex="Male and female"

source
1. .825
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN290f03"
/clone_lib="MHPN"

ORIGIN
Query Match 35.4%; Score 17; DB 9; Length 825;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TGAGGGCTTACATGGAT 30
|||||
Db 63 TGAGGGCTTACATGGAT 79

RESULT 50
CN511377/c
LOCUS
DEFINITION
ACCESSION

```

/tissue\_type="Chondrocytes isolated from growth plate cartilage"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSQRBN20"  
/notes="Vector: pBluescript II KS(+); Site\_1: EcoRI; Site\_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Ronaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN  
Query Match 35.4%; Score 17; DB 5; Length 825;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTCTGAGGGCTTACATG 27  
|||||  
Db 556 TTCTGAGGGCTTACATG 540

RESULT 49  
CR241446  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1. .825  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="MHPN290f03"  
/clone\_lib="MHPN"

ORIGIN  
Query Match 35.4%; Score 17; DB 9; Length 825;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TGAGGGCTTACATGGAT 30  
|||||  
Db 63 TGAGGGCTTACATGGAT 79

RESULT 50  
CN511377/c  
LOCUS  
DEFINITION  
ACCESSION

CR241446 825 bp DNA linear GSS 06-JUL-2004  
Reverse strand read from insert in 5'HPRT insertion targeting and  
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Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,  
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,  
Rogers, J. and Bradley, A.  
Direct Submission  
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. http://www.sanger.ac.uk/MICER  
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CN511377

VERSION CN511377.1 GI:46824001  
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 Cypriniformes; Cyprinidae; Danio.  
 REFERENCE 1 (bases 1 to 896)  
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Chi-Bin Chien  
 cDNA Library Preparation: Dr. Sumio Sugano  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
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 and is not amplified. Library constructed by Yutaka Suzuki  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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| c 149 | 13 | 27.1 | 601 | 4 | US-09-949-016-87652  | Sequence 87653, A  | c 222 | 13 | 27.1 | 2799 | 3 | US-09-536-224-5     | Sequence 5, Appli |
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| c 169 | 13 | 27.1 | 666 | 4 | US-09-107-433-1248   | Sequence 1248, Ap  | c 242 | 13 | 27.1 | 2799 | 3 | US-09-536-224-5     | Sequence 5, Appli |
| c 170 | 13 | 27.1 | 729 | 4 | US-09-583-645A-15    | Sequence 15, Appli | c 243 | 13 | 27.1 | 2799 | 3 | US-09-536-224-5     | Sequence 5, Appli |
| c 171 | 13 | 27.1 | 777 | 4 | US-09-489-039A-3793  | Sequence 3793, Ap  | c 244 | 13 | 27.1 | 2799 | 3 | US-09-536-224-5     | Sequence 5, Appli |
| c 172 | 13 | 27.1 | 786 | 3 | US-09-134-001C-2129  | Sequence 2129, Ap  | c 245 | 13 | 27.1 | 2799 | 3 | US-09-536-224-5     | Sequence 5, Appli |
| c 173 | 13 | 27.1 | 897 | 3 | US-09-134-001C-460   | Sequence 460, App  | c 246 | 13 | 27.1 | 2799 | 3 | US-09-536-224-5     | Sequence 5, Appli |

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| C 247 | 13 | 27.1 | 4293  | 4 | US-09-252-991A-1619 | Sequence 1619, Ap  | 320   | 13 | 27.1 | 43333   | 4 | US-09-949-016-15381   | Sequence 15381, A  |
| C 248 | 13 | 27.1 | 4359  | 4 | US-09-252-991A-1547 | Sequence 1547, Ap  | 321   | 13 | 27.1 | 44208   | 4 | US-09-949-016-12240   | Sequence 12240, A  |
| C 249 | 13 | 27.1 | 4376  | 4 | US-09-548-938A-6    | Sequence 6, Appli  | 322   | 13 | 27.1 | 44208   | 4 | US-09-949-016-15941   | Sequence 15941, A  |
| C 250 | 13 | 27.1 | 4411  | 2 | US-08-929-967-5     | Sequence 5, Appli  | 323   | 13 | 27.1 | 44947   | 4 | US-09-949-016-12018   | Sequence 12018, A  |
| C 251 | 13 | 27.1 | 4922  | 2 | US-08-330-272-5     | Sequence 5, Appli  | 324   | 13 | 27.1 | 44947   | 4 | US-09-949-016-13101   | Sequence 13101, A  |
| C 252 | 13 | 27.1 | 4922  | 5 | PCT-US95-13663-5    | Sequence 5, Appli  | C 325 | 13 | 27.1 | 45323   | 4 | US-09-949-016-16142   | Sequence 16142, A  |
| C 253 | 13 | 27.1 | 5082  | 4 | US-09-497-822C-18   | Sequence 18, Appli | C 326 | 13 | 27.1 | 59479   | 4 | US-09-949-016-16910   | Sequence 16910, A  |
| C 254 | 13 | 27.1 | 5201  | 4 | US-09-640-882-2     | Sequence 2, Appli  | C 327 | 13 | 27.1 | 59479   | 4 | US-09-949-016-16910   | Sequence 16910, A  |
| C 255 | 13 | 27.1 | 5201  | 4 | US-09-640-882-2     | Sequence 2, Appli  | C 328 | 13 | 27.1 | 65745   | 4 | US-09-949-016-12591   | Sequence 12591, A  |
| C 256 | 13 | 27.1 | 5641  | 4 | US-09-630-931A-13   | Sequence 13, Appli | C 329 | 13 | 27.1 | 65745   | 4 | US-09-949-016-15871   | Sequence 15871, A  |
| C 257 | 13 | 27.1 | 5670  | 4 | US-09-630-931A-14   | Sequence 14, Appli | C 330 | 13 | 27.1 | 65524   | 4 | US-09-949-001-32      | Sequence 32, Appli |
| C 258 | 13 | 27.1 | 5677  | 1 | US-07-623-953A-14   | Sequence 14, Appli | C 331 | 13 | 27.1 | 65525   | 4 | US-09-949-001-38      | Sequence 38, Appli |
| C 259 | 13 | 27.1 | 5826  | 4 | US-09-630-931A-11   | Sequence 11, Appli | C 332 | 13 | 27.1 | 80332   | 4 | US-09-949-016-12951   | Sequence 12951, A  |
| C 260 | 13 | 27.1 | 5838  | 2 | US-08-850-880-3     | Sequence 3, Appli  | C 333 | 13 | 27.1 | 86213   | 4 | US-09-949-016-17240   | Sequence 17240, A  |
| C 261 | 13 | 27.1 | 5838  | 2 | US-08-850-880-3     | Sequence 3, Appli  | C 334 | 13 | 27.1 | 86213   | 4 | US-09-949-016-17241   | Sequence 17241, A  |
| C 262 | 13 | 27.1 | 5838  | 2 | US-08-814-877-3     | Sequence 3, Appli  | C 335 | 13 | 27.1 | 86213   | 4 | US-09-949-016-17242   | Sequence 17242, A  |
| C 263 | 13 | 27.1 | 5838  | 2 | US-09-272-432A-3    | Sequence 3, Appli  | C 336 | 13 | 27.1 | 86213   | 4 | US-09-949-016-17243   | Sequence 17243, A  |
| C 264 | 13 | 27.1 | 6043  | 4 | US-09-630-929-4     | Sequence 4, Appli  | C 337 | 13 | 27.1 | 88736   | 4 | US-09-949-016-12758   | Sequence 12758, A  |
| C 265 | 13 | 27.1 | 6071  | 4 | US-09-630-931A-12   | Sequence 12, Appli | C 338 | 13 | 27.1 | 88992   | 4 | US-09-949-016-13667   | Sequence 13667, A  |
| C 266 | 13 | 27.1 | 6314  | 1 | US-08-211-430-1     | Sequence 1, Appli  | C 339 | 13 | 27.1 | 94095   | 4 | US-09-949-016-14389   | Sequence 14389, A  |
| C 267 | 13 | 27.1 | 6363  | 2 | US-08-929-967-6     | Sequence 6, Appli  | C 340 | 13 | 27.1 | 100863  | 4 | US-09-949-016-17031   | Sequence 17031, A  |
| C 268 | 13 | 27.1 | 6775  | 4 | US-09-620-312D-289  | Sequence 289, App  | C 341 | 13 | 27.1 | 102053  | 4 | US-09-949-016-13025   | Sequence 13025, A  |
| C 269 | 13 | 27.1 | 7252  | 3 | US-09-238-356-27    | Sequence 27, Appli | C 342 | 13 | 27.1 | 106746  | 4 | US-09-326-402C-1      | Sequence 1, Appli  |
| C 270 | 13 | 27.1 | 7316  | 3 | US-09-289-254-3     | Sequence 3, Appli  | C 343 | 13 | 27.1 | 106746  | 4 | US-09-326-402C-12     | Sequence 12, Appli |
| C 271 | 13 | 27.1 | 7326  | 6 | 5304637-21          | Patent No. 5304637 | C 344 | 13 | 27.1 | 121982  | 4 | US-09-949-016-12085   | Sequence 12085, A  |
| C 272 | 13 | 27.1 | 7326  | 6 | 5304637-21          | Patent No. 5304637 | C 345 | 13 | 27.1 | 121982  | 4 | US-09-949-016-14105   | Sequence 14105, A  |
| C 273 | 13 | 27.1 | 7336  | 2 | US-08-418-085-3     | Sequence 3, Appli  | C 346 | 13 | 27.1 | 126176  | 4 | US-09-949-016-16137   | Sequence 16137, A  |
| C 274 | 13 | 27.1 | 7336  | 3 | US-09-099-011A-3    | Sequence 3, Appli  | C 347 | 13 | 27.1 | 126176  | 4 | US-09-949-016-16138   | Sequence 16138, A  |
| C 275 | 13 | 27.1 | 7336  | 3 | US-08-470-369-21    | Sequence 21, Appli | C 348 | 13 | 27.1 | 135030  | 4 | US-09-949-016-14896   | Sequence 14896, A  |
| C 276 | 13 | 27.1 | 7336  | 4 | US-09-098-877B-3    | Sequence 3, Appli  | C 349 | 13 | 27.1 | 139150  | 4 | US-09-949-016-17398   | Sequence 17398, A  |
| C 277 | 13 | 27.1 | 7408  | 3 | US-09-115-475-13    | Sequence 13, Appli | C 350 | 13 | 27.1 | 139150  | 4 | US-09-949-016-12879   | Sequence 12879, A  |
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| C 279 | 13 | 27.1 | 7496  | 4 | US-09-949-016-17280 | Sequence 17280, A  | C 352 | 13 | 27.1 | 146104  | 4 | US-09-949-016-13239   | Sequence 13239, A  |
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| C 283 | 13 | 27.1 | 8150  | 4 | US-09-949-016-13830 | Sequence 13830, A  | C 356 | 13 | 27.1 | 157866  | 4 | US-09-949-016-12984   | Sequence 12984, A  |
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| C 286 | 13 | 27.1 | 8906  | 3 | US-09-027-169-5     | Sequence 5, Appli  | C 359 | 13 | 27.1 | 173791  | 4 | US-09-949-016-17302   | Sequence 17302, A  |
| C 287 | 13 | 27.1 | 9319  | 4 | US-09-949-016-13044 | Sequence 13044, A  | C 360 | 13 | 27.1 | 187136  | 4 | US-09-949-016-17231   | Sequence 17231, A  |
| C 288 | 13 | 27.1 | 14875 | 4 | US-09-949-016-13929 | Sequence 13929, A  | C 361 | 13 | 27.1 | 187848  | 4 | US-09-949-016-12111   | Sequence 12111, A  |
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| C 294 | 13 | 27.1 | 15108 | 4 | US-10-226-065-1     | Sequence 1, Appli  | C 367 | 13 | 27.1 | 248968  | 4 | US-09-949-016-12614   | Sequence 12614, A  |
| C 295 | 13 | 27.1 | 18554 | 4 | US-09-811-825A-3    | Sequence 3, Appli  | C 368 | 13 | 27.1 | 250958  | 4 | US-09-949-016-16061   | Sequence 16061, A  |
| C 296 | 13 | 27.1 | 18900 | 4 | US-09-949-016-16989 | Sequence 16989, A  | C 369 | 13 | 27.1 | 301828  | 4 | US-09-949-016-13969   | Sequence 13969, A  |
| C 297 | 13 | 27.1 | 21721 | 4 | US-09-269-939A-41   | Sequence 41, Appli | C 370 | 13 | 27.1 | 319608  | 4 | US-09-539-333D-1      | Sequence 1, Appli  |
| C 298 | 13 | 27.1 | 22976 | 4 | US-09-269-939A-19   | Sequence 19, Appli | C 371 | 13 | 27.1 | 319608  | 4 | US-09-679-409-1       | Sequence 1, Appli  |
| C 299 | 13 | 27.1 | 23187 | 4 | US-09-499-522-1     | Sequence 1, Appli  | C 372 | 13 | 27.1 | 323820  | 4 | US-09-949-016-14139   | Sequence 14139, A  |
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| C 301 | 13 | 27.1 | 25260 | 4 | US-09-949-016-11985 | Sequence 11985, A  | C 374 | 13 | 27.1 | 455726  | 4 | US-09-949-016-14157   | Sequence 14157, A  |
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| C 304 | 13 | 27.1 | 27578 | 4 | US-09-949-016-12167 | Sequence 12167, A  | C 377 | 13 | 27.1 | 670690  | 4 | US-09-949-016-14207   | Sequence 14207, A  |
| C 305 | 13 | 27.1 | 27579 | 4 | US-09-949-016-15005 | Sequence 15005, A  | C 378 | 13 | 27.1 | 784019  | 4 | US-09-949-016-14033   | Sequence 14033, A  |
| C 306 | 13 | 27.1 | 27617 | 4 | US-09-949-016-17040 | Sequence 17040, A  | C 379 | 13 | 27.1 | 828152  | 4 | US-09-949-016-12777   | Sequence 12777, A  |
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| C 309 | 13 | 27.1 | 31144 | 4 | US-09-949-016-15993 | Sequence 15993, A  | C 382 | 12 | 25.0 | 20      | 4 | US-09-193-881-22      | Sequence 22, Appli |
| C 310 | 13 | 27.1 | 33519 | 4 | US-09-949-016-17165 | Sequence 17165, A  | C 383 | 12 | 25.0 | 22      | 4 | US-08-857-636-19      | Sequence 19, Appli |
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| C 312 | 13 | 27.1 | 34658 | 4 | US-09-949-016-12629 | Sequence 12629, A  | C 385 | 12 | 25.0 | 25      | 4 | US-09-396-196G-58911  | Sequence 58911, A  |
| C 313 | 13 | 27.1 | 34779 | 4 | US-09-949-016-13787 | Sequence 13787, A  | C 386 | 12 | 25.0 | 25      | 4 | US-09-396-196G-122549 | Sequence 122549, A |
| C 314 | 13 | 27.1 | 36651 | 3 | US-09-738-894A-3    | Sequence 3, Appli  | C 387 | 12 | 25.0 | 28      | 3 | US-08-831-133-12      | Sequence 12, Appli |
| C 315 | 13 | 27.1 | 36651 | 4 | US-09-964-469-3     | Sequence 3, Appli  | C 388 | 12 | 25.0 | 30      | 3 | US-09-416-150-12      | Sequence 12, Appli |
| C 316 | 13 | 27.1 | 40130 | 4 | US-09-949-016-17275 | Sequence 17275, A  | C 389 | 12 | 25.0 | 30      | 3 | US-08-891-292A-76     | Sequence 76, Appli |
| C 317 | 13 | 27.1 | 41125 | 4 | US-09-949-016-12413 | Sequence 12413, A  | C 390 | 12 | 25.0 | 30      | 4 | US-09-927-737C-76     | Sequence 76, Appli |
| C 318 | 13 | 27.1 | 41126 | 4 | US-09-949-016-17273 | Sequence 17273, A  | C 391 | 12 | 25.0 | 37      | 2 | US-08-570-153-4       | Sequence 4, Appli  |
| C 319 | 13 | 27.1 | 41941 | 4 | US-09-949-016-17380 | Sequence 17380, A  | C 392 | 12 | 25.0 | 37      | 5 | PCT-US95-02861-4      | Sequence 4, Appli  |

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| 393 | 12 | 25.0 | 41  | 4 | US-08-495-209-34     | Sequence 34, Appl | C 466 | 12 | 25.0 | 434 | 4 | US-09-270-767-16174  | Sequence 16174, A |
| 394 | 12 | 25.0 | 41  | 5 | PCT-US96-10905-34    | Sequence 34, Appl | C 467 | 12 | 25.0 | 439 | 4 | US-09-621-976-15505  | Sequence 15505, A |
| 395 | 12 | 25.0 | 45  | 3 | US-09-446-504-42     | Sequence 42, Appl | C 468 | 12 | 25.0 | 441 | 4 | US-09-621-976-14488  | Sequence 14488, A |
| 396 | 12 | 25.0 | 45  | 3 | US-09-712-266-42     | Sequence 42, Appl | C 469 | 12 | 25.0 | 448 | 4 | US-09-513-999C-34612 | Sequence 34612, A |
| 397 | 12 | 25.0 | 45  | 3 | US-09-091-889A-6     | Sequence 6, Appl  | C 470 | 12 | 25.0 | 450 | 4 | US-09-252-991A-11234 | Sequence 11234, A |
| 398 | 12 | 25.0 | 47  | 4 | US-09-671-317-495    | Sequence 495, App | C 471 | 12 | 25.0 | 453 | 4 | US-09-621-976-17835  | Sequence 17835, A |
| 399 | 12 | 25.0 | 50  | 4 | US-09-554-329-61     | Sequence 61, Appl | C 472 | 12 | 25.0 | 454 | 4 | US-09-621-976-19159  | Sequence 19159, A |
| 400 | 12 | 25.0 | 50  | 4 | US-09-554-329-61     | Sequence 61, Appl | C 473 | 12 | 25.0 | 454 | 4 | US-09-270-767-8740   | Sequence 8740, Ap |
| 401 | 12 | 25.0 | 60  | 4 | US-08-891-292A-77    | Sequence 77, Appl | C 474 | 12 | 25.0 | 454 | 4 | US-09-270-767-24022  | Sequence 24022, A |
| 402 | 12 | 25.0 | 61  | 4 | US-09-927-737C-77    | Sequence 77, Appl | C 475 | 12 | 25.0 | 456 | 4 | US-09-513-999C-1298  | Sequence 1298, Ap |
| 403 | 12 | 25.0 | 63  | 1 | US-08-387-874-94     | Sequence 94, Appl | C 476 | 12 | 25.0 | 462 | 4 | US-09-270-767-9280   | Sequence 9280, Ap |
| 404 | 12 | 25.0 | 63  | 1 | PCT-US93-08364-94    | Sequence 94, Appl | C 477 | 12 | 25.0 | 462 | 4 | US-09-270-767-24562  | Sequence 24562, A |
| 405 | 12 | 25.0 | 124 | 4 | US-08-956-171E-1451  | Sequence 1451, Ap | C 478 | 12 | 25.0 | 464 | 4 | US-09-270-767-9677   | Sequence 9677, Ap |
| 406 | 12 | 25.0 | 124 | 4 | US-08-781-366A-1451  | Sequence 1451, Ap | C 479 | 12 | 25.0 | 464 | 4 | US-09-270-767-24959  | Sequence 24959, A |
| 407 | 12 | 25.0 | 143 | 3 | US-08-469-318-181    | Sequence 181, App | C 480 | 12 | 25.0 | 472 | 4 | US-09-489-039A-4310  | Sequence 4310, Ap |
| 408 | 12 | 25.0 | 143 | 3 | US-08-468-609A-181   | Sequence 181, App | C 481 | 12 | 25.0 | 472 | 4 | US-09-702-705-868    | Sequence 868, App |
| 409 | 12 | 25.0 | 143 | 3 | US-08-446-872A-181   | Sequence 181, App | C 482 | 12 | 25.0 | 472 | 4 | US-09-736-457-868    | Sequence 868, App |
| 410 | 12 | 25.0 | 143 | 3 | US-08-446-872A-181   | Sequence 181, App | C 483 | 12 | 25.0 | 472 | 4 | US-09-614-124B-868   | Sequence 868, App |
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| 412 | 12 | 25.0 | 143 | 3 | PCT-US95-01185-181   | Sequence 181, App | C 485 | 12 | 25.0 | 472 | 4 | US-09-658-824-868    | Sequence 868, App |
| 413 | 12 | 25.0 | 148 | 4 | US-09-094-207A-4     | Sequence 4, Appl  | C 486 | 12 | 25.0 | 478 | 4 | US-09-205-258-60     | Sequence 60, Appl |
| 414 | 12 | 25.0 | 180 | 4 | US-10-109-725A-4     | Sequence 4, Appl  | C 487 | 12 | 25.0 | 489 | 4 | US-09-328-352-1328   | Sequence 1328, Ap |
| 415 | 12 | 25.0 | 180 | 4 | US-09-270-767-26875  | Sequence 26875, A | C 488 | 12 | 25.0 | 489 | 4 | US-09-621-976-15103  | Sequence 15103, A |
| 416 | 12 | 25.0 | 180 | 3 | US-08-469-318-182    | Sequence 182, App | C 489 | 12 | 25.0 | 490 | 4 | US-09-513-999C-32356 | Sequence 32356, A |
| 417 | 12 | 25.0 | 180 | 3 | US-08-468-609A-182   | Sequence 182, App | C 490 | 12 | 25.0 | 505 | 4 | US-09-270-767-5220   | Sequence 5220, A  |
| 418 | 12 | 25.0 | 180 | 3 | US-08-446-872A-182   | Sequence 182, App | C 491 | 12 | 25.0 | 505 | 4 | US-09-270-767-20502  | Sequence 20502, A |
| 419 | 12 | 25.0 | 180 | 3 | US-08-762-227A-182   | Sequence 182, App | C 492 | 12 | 25.0 | 519 | 3 | US-09-615-192A-364   | Sequence 364, App |
| 420 | 12 | 25.0 | 180 | 3 | PCT-US95-01185-182   | Sequence 182, App | C 493 | 12 | 25.0 | 519 | 3 | US-09-248-796A-7154  | Sequence 7154, Ap |
| 421 | 12 | 25.0 | 212 | 3 | US-09-008-892-8      | Sequence 8, Appl  | C 494 | 12 | 25.0 | 520 | 4 | US-09-621-976-12177  | Sequence 12177, A |
| 422 | 12 | 25.0 | 216 | 4 | US-09-107-532A-729   | Sequence 729, App | C 495 | 12 | 25.0 | 527 | 4 | US-09-702-705-1      | Sequence 1, Appl  |
| 423 | 12 | 25.0 | 242 | 1 | US-08-464-164-3      | Sequence 3, Appl  | C 496 | 12 | 25.0 | 527 | 4 | US-09-736-457-1      | Sequence 1, Appl  |
| 424 | 12 | 25.0 | 242 | 1 | US-08-338-057-3      | Sequence 3, Appl  | C 497 | 12 | 25.0 | 527 | 4 | US-09-614-124B-1     | Sequence 1, Appl  |
| 425 | 12 | 25.0 | 242 | 2 | US-08-668-416-3      | Sequence 2, Appl  | C 498 | 12 | 25.0 | 527 | 4 | US-09-671-325-1      | Sequence 1, Appl  |
| 426 | 12 | 25.0 | 257 | 4 | US-09-193-881-2      | Sequence 2, Appl  | C 499 | 12 | 25.0 | 527 | 4 | US-09-589-184-1      | Sequence 1, Appl  |
| 427 | 12 | 25.0 | 267 | 4 | US-09-270-767-26880  | Sequence 26880, A | C 500 | 12 | 25.0 | 527 | 4 | US-09-658-824-1      | Sequence 1, Appl  |
| 428 | 12 | 25.0 | 270 | 4 | US-09-270-767-29252  | Sequence 29252, A |       |    |      |     |   |                      |                   |
| 429 | 12 | 25.0 | 270 | 4 | US-09-313-294A-216   | Sequence 216, App |       |    |      |     |   |                      |                   |
| 430 | 12 | 25.0 | 274 | 4 | US-09-313-294A-1213  | Sequence 1213, Ap |       |    |      |     |   |                      |                   |
| 431 | 12 | 25.0 | 279 | 4 | US-09-313-294A-3649  | Sequence 3649, Ap |       |    |      |     |   |                      |                   |
| 432 | 12 | 25.0 | 285 | 4 | US-09-313-294A-5090  | Sequence 5090, Ap |       |    |      |     |   |                      |                   |
| 433 | 12 | 25.0 | 285 | 4 | US-09-489-039A-1749  | Sequence 1749, Ap |       |    |      |     |   |                      |                   |
| 434 | 12 | 25.0 | 285 | 4 | US-09-621-976-17225  | Sequence 17225, A |       |    |      |     |   |                      |                   |
| 435 | 12 | 25.0 | 288 | 4 | US-09-252-991A-15424 | Sequence 15424, A |       |    |      |     |   |                      |                   |
| 436 | 12 | 25.0 | 292 | 4 | US-09-497-855A-33    | Sequence 33, Appl |       |    |      |     |   |                      |                   |
| 437 | 12 | 25.0 | 306 | 4 | US-09-513-999C-8327  | Sequence 8327, Ap |       |    |      |     |   |                      |                   |
| 438 | 12 | 25.0 | 312 | 4 | US-09-489-039A-4365  | Sequence 4365, Ap |       |    |      |     |   |                      |                   |
| 439 | 12 | 25.0 | 312 | 4 | US-09-313-294A-3865  | Sequence 3865, Ap |       |    |      |     |   |                      |                   |
| 440 | 12 | 25.0 | 312 | 4 | US-09-513-999C-4377  | Sequence 4377, A  |       |    |      |     |   |                      |                   |
| 441 | 12 | 25.0 | 325 | 4 | US-09-722-377-56     | Sequence 56, Appl |       |    |      |     |   |                      |                   |
| 442 | 12 | 25.0 | 338 | 3 | US-08-928-881-27     | Sequence 27, Appl |       |    |      |     |   |                      |                   |
| 443 | 12 | 25.0 | 338 | 3 | US-09-543-921-27     | Sequence 27, Appl |       |    |      |     |   |                      |                   |
| 444 | 12 | 25.0 | 338 | 4 | US-09-491-759-27     | Sequence 27, Appl |       |    |      |     |   |                      |                   |
| 445 | 12 | 25.0 | 339 | 4 | US-09-270-767-8172   | Sequence 8172, Ap |       |    |      |     |   |                      |                   |
| 446 | 12 | 25.0 | 339 | 4 | US-09-270-767-23454  | Sequence 23454, A |       |    |      |     |   |                      |                   |
| 447 | 12 | 25.0 | 344 | 4 | US-09-651-169A-39    | Sequence 39, Appl |       |    |      |     |   |                      |                   |
| 448 | 12 | 25.0 | 351 | 4 | US-09-513-999C-97    | Sequence 97, Appl |       |    |      |     |   |                      |                   |
| 449 | 12 | 25.0 | 357 | 3 | US-09-712-016-69     | Sequence 69, Appl |       |    |      |     |   |                      |                   |
| 450 | 12 | 25.0 | 357 | 4 | US-08-956-171E-4249  | Sequence 4249, Ap |       |    |      |     |   |                      |                   |
| 451 | 12 | 25.0 | 364 | 4 | US-08-781-986A-4249  | Sequence 4249, Ap |       |    |      |     |   |                      |                   |
| 452 | 12 | 25.0 | 372 | 4 | US-09-902-540-2117   | Sequence 2117, Ap |       |    |      |     |   |                      |                   |
| 453 | 12 | 25.0 | 389 | 4 | US-09-640-211A-343   | Sequence 343, App |       |    |      |     |   |                      |                   |
| 454 | 12 | 25.0 | 390 | 2 | US-09-621-976-14888  | Sequence 14888, A |       |    |      |     |   |                      |                   |
| 455 | 12 | 25.0 | 390 | 2 | US-08-494-907-19     | Sequence 19, Appl |       |    |      |     |   |                      |                   |
| 456 | 12 | 25.0 | 400 | 4 | PCT-US96-10986-19    | Sequence 19, Appl |       |    |      |     |   |                      |                   |
| 457 | 12 | 25.0 | 400 | 4 | US-09-722-377-55     | Sequence 55, Appl |       |    |      |     |   |                      |                   |
| 458 | 12 | 25.0 | 413 | 4 | US-09-949-016-65058  | Sequence 65058, A |       |    |      |     |   |                      |                   |
| 459 | 12 | 25.0 | 416 | 4 | US-09-902-540-1614   | Sequence 1614, Ap |       |    |      |     |   |                      |                   |
| 460 | 12 | 25.0 | 417 | 4 | US-09-107-532A-3252  | Sequence 3252, Ap |       |    |      |     |   |                      |                   |
| 461 | 12 | 25.0 | 421 | 4 | US-09-489-039A-5287  | Sequence 5287, Ap |       |    |      |     |   |                      |                   |
| 462 | 12 | 25.0 | 421 | 4 | US-09-513-999C-11405 | Sequence 11405, A |       |    |      |     |   |                      |                   |
| 463 | 12 | 25.0 | 428 | 4 | US-09-270-767-11842  | Sequence 11842, A |       |    |      |     |   |                      |                   |
| 464 | 12 | 25.0 | 429 | 4 | US-09-902-540-1309   | Sequence 1309, Ap |       |    |      |     |   |                      |                   |
| 465 | 12 | 25.0 | 434 | 4 | US-09-252-991A-11056 | Sequence 11056, A |       |    |      |     |   |                      |                   |
|     |    |      |     |   | US-09-270-767-892    | Sequence 892, App |       |    |      |     |   |                      |                   |

ALIGNMENTS

RESULT 1  
 US-09-949-016-67727/c  
 ; Sequence 67727, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CLO01307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; PRIOR FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 67727  
 ; LENGTH: 601  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-67727  
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 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 22 TACATGATCATTTC 36  
 Db 601 TACATGATCATTTC 587

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RESULT 2
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; Sequence 88593, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88593
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-88593

Query Match          31.2%; Score 15; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 TTACATGGATCACTT 35
Db 36 TTACATGGATCACTT 50

RESULT 3
US-09-949-016-88594
; Sequence 88594, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88594
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-88594

Query Match          31.2%; Score 15; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 TTACATGGATCACTT 35
Db 38 TTACATGGATCACTT 52

RESULT 4
US-09-949-016-88595
; Sequence 88595, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88595
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-88595

Query Match          31.2%; Score 15; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 TTACATGGATCACTT 35
Db 562 CATGGATCACTTCGC 548

RESULT 5
US-09-252-991A-6538/c
; Sequence 6538, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6538
; LENGTH: 726
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6538

Query Match          31.2%; Score 15; DB 4; Length 726;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 CATGGATCACTTCGC 38
Db 562 CATGGATCACTTCGC 548

RESULT 6
US-08-867-087B-54
; Sequence 54, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; Whinston, LLP
```

STREET: One World Trade Center  
STREET: 121 S.W. Salmon Street  
STREET: Suite 1600  
CITY: Portland  
STATE: Oregon  
COUNTRY: United States of America  
ZIP: 97204  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Disk, 3-1/2 inch  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/867,087B  
FILING DATE: June 2, 1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/323,449  
FILING DATE: October 14, 1994  
APPLICATION NUMBER: U.S. 08/485,981  
FILING DATE: June 7, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Alan. E.  
REGISTRATION NUMBER: 35,123  
REFERENCE/DOCKET NUMBER: 4630-47071  
TELEPHONE: (503) 226-7391  
TELEFAX: (503) 228-9446  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1027 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
US-08-867-087B-54

Query Match 31.2%; Score 15; DB 2; Length 1027;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GCTTACATGATCAC 33  
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Db 776 GCTTACATGATCAC 790

RESULT 7  
US-09-252-991A-6495  
; Sequence 6495, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 6495  
; LENGTH: 1521  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-6495

Query Match 31.2%; Score 15; DB 4; Length 1521;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 CATGGATCACTTCGC 38  
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Db 1008 CATGGATCACTTCGC 1022  
RESULT 8  
US-08-861-464-7  
; Sequence 7, Application US/08861464  
; Patent No. 5874210  
; GENERAL INFORMATION:  
; APPLICANT: Guarente, Leonard P.  
; APPLICANT: Austriaco Jr., Nicanor  
; APPLICANT: Kennedy, Brian  
; TITLE OF INVENTION: Genes Determining Cellular Senescence  
; TITLE OF INVENTION: in Yeast  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/861,464  
; FILING DATE: 22-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/396,001  
; FILING DATE: 28-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/09351  
; FILING DATE: 15-AUG-1994  
; APPLICATION NUMBER: US 08/107,408  
; FILING DATE: 16-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: MIT-6408A2Z  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 781-861-6240  
; TELEFAX: 781-861-9540  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5319 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 57..3614  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 57..3614  
US-08-861-464-7

Query Match 31.2%; Score 15; DB 2; Length 5319;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGTTCGAGGCTTA 23  
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Db 1008 GGTTCGAGGCTTA 1022

RESULT 9  
US-08-396-001-7  
; Sequence 7, Application US/08396001

Patent No. 5919618  
GENERAL INFORMATION:  
APPLICANT: Guarente, Leonard P.  
APPLICANT: Austriaco Jr., Nicanor  
APPLICANT: Claus, James  
APPLICANT: Cole, Francesca  
APPLICANT: Kennedy, Brian  
TITLE OF INVENTION: Genes Determining Cellular Senescence in  
TITLE OF INVENTION: Yeast  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/396,001  
FILING DATE: 28-FEB-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: MIT-6408A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5319 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 57..3614  
US-08-396-001-7

Query Match 31.2%; Score 15; DB 2; Length 5319;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGTCTGAGGGCTTA 23  
|||||  
Db 1008 GGTCTGAGGGCTTA 1022

RESULT 10  
US-09-323-433A-7  
Sequence 7, Application US/09323433A  
Patent No. 6218512  
GENERAL INFORMATION:  
APPLICANT: Guarente, Leonard P.  
APPLICANT: Austriaco Jr., Nicanor  
APPLICANT: Claus, James J.  
APPLICANT: Cole, Francesca  
APPLICANT: Kennedy, Brian  
TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE IN  
TITLE OF INVENTION: YEAST  
FILE REFERENCE: 0050.1491-003  
CURRENT APPLICATION NUMBER: US/09/323,433A  
CURRENT FILING DATE: 1999-06-01  
PRIOR APPLICATION NUMBER: US 08/396,001  
PRIOR FILING DATE: 1995-02-28  
PRIOR APPLICATION NUMBER: PCT/US94/09351  
PRIOR FILING DATE: 1994-08-15

PRIOR APPLICATION NUMBER: US 08/107,408  
PRIOR FILING DATE: 1993-08-16  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 7  
LENGTH: 5319  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (57)...(3614)  
OTHER INFORMATION: D43951  
US-09-323-433A-7

Query Match 31.2%; Score 15; DB 3; Length 5319;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGTCTGAGGGCTTA 23  
|||||  
Db 1008 GGTCTGAGGGCTTA 1022

RESULT 11  
US-09-826-752-7  
Sequence 7, Application US/09826752  
Patent No. 6787300  
GENERAL INFORMATION:  
APPLICANT: Guarente, Leonard P.  
APPLICANT: Austriaco Jr., Nicanor  
APPLICANT: Claus, James J.  
APPLICANT: Cole, Francesca  
APPLICANT: Kennedy, Brian  
TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE IN  
TITLE OF INVENTION: YEAST  
FILE REFERENCE: 0050.1491-005  
CURRENT APPLICATION NUMBER: US/09/826,752  
CURRENT FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: US 08/396,001  
PRIOR FILING DATE: 1995-02-28  
PRIOR APPLICATION NUMBER: PCT/US94/09351  
PRIOR FILING DATE: 1994-08-15  
PRIOR APPLICATION NUMBER: US 08/107,408  
PRIOR FILING DATE: 1993-08-16  
PRIOR APPLICATION NUMBER: US 09/323,433  
PRIOR FILING DATE: 1999-06-01  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 5319  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (57)...(3614)  
OTHER INFORMATION: D43951  
US-09-826-752-7

Query Match 31.2%; Score 15; DB 4; Length 5319;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGTCTGAGGGCTTA 23  
|||||  
Db 1008 GGTCTGAGGGCTTA 1022

RESULT 12  
US-09-949-016-12029/c  
Sequence 12029, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.



```

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12029
; LENGTH: 73853
; TYPE: DNA
; ORGANISM: Human
;
US-09-949-016-12029

Query Match      31.2%; Score 15; DB 4; Length 73853;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CGGTTCTGAGGGCTT 22
Db      1324 CGGTTCTGAGGGCTT 1310

RESULT 13
US-09-949-016-13597/c
; Sequence 13597, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13597
; LENGTH: 98439
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(98439)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13597

```

```

Query Match      31.2%; Score 15; DB 4; Length 98439;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GGTTCGAGGGCTTA 23
Db      5385 GGTTCGAGGGCTTA 5371

```

```

RESULT 14
US-09-949-016-13730
; Sequence 13730, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

```

```

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13730
; LENGTH: 163181
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(163181)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13730

```

```

Query Match      31.2%; Score 15; DB 4; Length 163181;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 TACATGGATCACTTC 36
Db      111655 TACATGGATCACTTC 111669

```

```

RESULT 15
US-09-949-016-11968/c
; Sequence 11968, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11968
; LENGTH: 174259
; TYPE: DNA
; ORGANISM: Human
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11968

```

```

Query Match      31.2%; Score 15; DB 4; Length 174259;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 TTACATGGATCACTT 35
Db      36881 TTACATGGATCACTT 36867

```

```

RESULT 16
US-09-949-016-14259/c
; Sequence 14259, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

```



FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14259  
LENGTH: 174262  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-14259

Query Match 31.2%; Score 15; DB 4; Length 174262;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 TTACATGGATCACTT 35

Db 36881 TTACATGGATCACTT 36867

RESULT 17  
US-09-513-999C-17495/c  
Sequence 17495, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
Patent No. 6783961  
FILE REFERENCE: 59.US2.REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 17495  
LENGTH: 110  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-513-999C-17495

Query Match 29.2%; Score 14; DB 4; Length 110;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGTTCTGAGGCT 21

Db 108 CGGTTCTGAGGCT 95

RESULT 18  
US-09-513-999C-18518/c  
Sequence 18518, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
Patent No. 6783961  
FILE REFERENCE: 59.US2.REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 18518  
LENGTH: 110  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 7  
OTHER INFORMATION: s-g or c  
US-09-513-999C-18518

Query Match 29.2%; Score 14; DB 4; Length 110;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGTTCTGAGGCT 21

Db 108 CGGTTCTGAGGCT 95

RESULT 19  
US-09-016-434-461  
Sequence 461, Application US/09016434  
Patent No. 6500938  
GENERAL INFORMATION:  
APPLICANT: Janice Au-Young  
APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HERewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 461:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: PROSNOT16  
CLONE: 2231705  
US-09-016-434-461

Query Match 29.2%; Score 14; DB 4; Length 255;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 23 ACATGGATCACTTC 36
Db 154 ACATGGATCACTTC 167

RESULT 20
US-09-270-767-5714
; Sequence 5714, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5714
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-5714

Query Match 29.2%; Score 14; DB 4; Length 453;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GCTTACATGGATCA 32
Db 347 GCTTACATGGATCA 360

RESULT 21
US-09-270-767-20996
; Sequence 20996, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20996
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-20996

Query Match 29.2%; Score 14; DB 4; Length 453;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GCTTACATGGATCA 32
Db 347 GCTTACATGGATCA 360

RESULT 22
US-09-949-016-84794
; Sequence 84794, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 207012
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
```

```
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84794
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-84794

Query Match 29.2%; Score 14; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 TCGCAGCTTTC 48
Db 466 TCGCAGCTTTC 479

RESULT 23
US-09-949-016-94216/c
; Sequence 94216, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94216
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-94216

Query Match 29.2%; Score 14; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGTTCGAGGGCTT 22
Db 117 GGTTCGAGGGCTT 104

RESULT 24
US-09-949-016-124634/c
; Sequence 124634, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 207012
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
```

; SEQ ID NO 124634  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-124634

Query Match 29.2%; Score 14; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTT 35  
DB 213 TACATGGATCACTT 200

## RESULT 25

US-09-949-016-130860  
; Sequence 130860, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 130860  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-130860

Query Match 29.2%; Score 14; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGTCTCTGAGGGCTT 22  
DB 135 GGTCTCTGAGGGCTT 148

## RESULT 26

US-09-949-016-161379/c  
; Sequence 161379, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 161379  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-161379

Query Match 29.2%; Score 14; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GAGGGCTTACATGG 28  
DB 452 GAGGGCTTACATGG 439

## RESULT 27

US-09-949-016-172387/c  
; Sequence 172387, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 172387  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-172387

Query Match 29.2%; Score 14; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 ACATGGATCACTTC 36  
DB 129 ACATGGATCACTTC 116

## RESULT 28

US-09-489-039A-975/c  
; Sequence 975, Application US/09489039A  
; Patent No. 6610836

; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; PRIOR FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 975  
; LENGTH: 624  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-975

Query Match 29.2%; Score 14; DB 4; Length 624;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 GGATCACTTCGCAG 40  
DB 172 GGATCACTTCGCAG 159

```
RESULT 29
US-09-489-039A-6225/c
; Sequence 6225, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6225
; LENGTH: 831
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6225
Query Match      29.2%; Score 14; DB 4; Length 831;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTCTGAGGGCTTAC 24
Db 609 TTCTGAGGGCTTAC 596

RESULT 30
US-09-489-039A-3317/c
; Sequence 3317, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3317
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3317
Query Match      29.2%; Score 14; DB 4; Length 909;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTCTGAGGGCTTAC 24
Db 609 TTCTGAGGGCTTAC 596

RESULT 31
US-09-807-757C-5
; Sequence 5, Application US/09807757C
; Patent No. 6825035
; GENERAL INFORMATION:
; APPLICANT: Owens, Gary K.
; APPLICANT: Mack, Christopher
; APPLICANT: Blank, Randall
; APPLICANT: University of Virginia Patent Foundation
; TITLE OF INVENTION: Compositions and Methods for Modulating Expression
; FILE REFERENCE: 021258-000500US
; CURRENT APPLICATION NUMBER: US/09/807,757C
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 60/105,330
```

```
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: WO PCT/US99/24972
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: smooth muscle alpha-actin (SM alpha-A) gene
; OTHER INFORMATION: 5' promoter region
US-09-807-757C-5
Query Match      29.2%; Score 14; DB 4; Length 1074;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCTGAGGGCTTA 23
Db 825 GTTCTGAGGGCTTA 838

RESULT 32
US-09-369-247-23/c
; Sequence 23, Application US/09369247
; Patent No. 6569992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/09/369,247
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1492
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-369-247-23
Query Match      29.2%; Score 14; DB 4; Length 1492;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGTTCTGAGGGCT 21
Db 907 CGGTTCTGAGGGCT 894

RESULT 33
US-09-248-796A-2667/c
; Sequence 2667, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
```

|                       |                |               |          |             |
|-----------------------|----------------|---------------|----------|-------------|
| Query Match           | 29.2%          | Score 14      | DB 3     | Length 1824 |
| Best Local Similarity | 100.0%         | Pred. No. 97  |          |             |
| Matches 14            | Conservative 0 | Mismatches 0  | Indels 0 | Gaps 0      |
| Qy                    | 34             | TTGCAGCTTTGTT | 47       |             |
| Db                    | 1763           | TTGCAGCTTTGTT | 1750     |             |

RESULT 36  
US-09-949-016-1271  
: Sequence 1271, Application US/09949016

Patent No. 6812339  
General Information:  
Applicant: VENTER, J. Craig et al.  
Title of Invention: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

```
,
, CURRENT APPLICATION NUMBER: US/09/949,016
,
, CURRENT FILING DATE: 2000-04-14
,
, PRIOR APPLICATION NUMBER: 60/241,755
,
, PRIOR FILING DATE: 2000-10-20
,
, PRIOR APPLICATION NUMBER: 60/237,768
,
, PRIOR FILING DATE: 2000-10-03
,
, PRIOR APPLICATION NUMBER: 60/231,498
,
, PRIOR FILING DATE: 2000-09-08
,
, NUMBER OF SEQ. IDS.: 3,2012
```

```

; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1271
; LENGTH: 1390
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1271

```

```

Query Match      29.2%; Score 14; DB 4; Length 1990;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      23  ACATGGATCACTTC 36
          |||||
Db      841 ACATGGATCACTTC 854

```

RESULT 37  
US-09-221-017B-885

sequence 003, Application 0070322101010  
Patent No. 6444799  
GENERAL INFORMATION:  
APPLICANT: ROSS, BRUCE C.

NUMBER OF SEQUENCES: 1120  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:

COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: Fastseq for Windows Version 2.0.b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/221.017B  
FILING DATE: 23-DEC-1998  
CLASSIFICATION:

; PRIOR APPLICATION DATA: PP1182  
 ; APPLICATION NUMBER: PP1182  
 ; FILING DATE: 31-DEC-1997  
 ; PRIOR APPLICATION DATA: PP1546  
 ; APPLICATION NUMBER: PP1546  
 ;

FILING DATE: 30-JAN-1998

```

; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: MONROY, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 885:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2165 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..2165
US-09-221-017B-885

Query Match 29.2%; Score 14; DB 3; Length 2165;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 ACATGGATCACTTC 36
Db 109 ACATGGATCACTTC 122

RESULT 38
US-09-923-684-2
; Sequence 2, Application US/09923684
; Patent No. 6780642
; GENERAL INFORMATION:
; APPLICANT: Narayanan, Ramaswamy
; TITLE OF INVENTION: ASSOCIATION OF SIM2 WITH CANCER
; FILE REFERENCE: 6818-24
; CURRENT APPLICATION NUMBER: US/09/923,684
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2859
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-923-684-2

Query Match 29.2%; Score 14; DB 4; Length 2859;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ATCACTTCGCAGCT 42
Db 189 ATCACTTCGCAGCT 202

RESULT 39
US-09-949-016-3231/c
; Sequence 3231, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3231
; LENGTH: 3619
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3231

Query Match 29.2%; Score 14; DB 4; Length 3619;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTCTGAGGGCTTAC 24
Db 2816 TTCTGAGGGCTTAC 2803

RESULT 40
US-09-923-684-1
; Sequence 1, Application US/09923684
; Patent No. 6780642
; GENERAL INFORMATION:
; APPLICANT: Narayanan, Ramaswamy
; TITLE OF INVENTION: ASSOCIATION OF SIM2 WITH CANCER
; FILE REFERENCE: 6818-24
; CURRENT APPLICATION NUMBER: US/09/923,684
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3920
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-923-684-1

Query Match 29.2%; Score 14; DB 4; Length 3920;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ATCACTTCGCAGCT 42
Db 189 ATCACTTCGCAGCT 202

RESULT 41
US-08-630-915A-33/c
; Sequence 33, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: McCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; NUMBER OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
```

;  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,915A  
; FILING DATE: 03-APR-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-174  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4091 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-630-915A-33

Query Match 29.2%; Score 14; DB 3; Length 4091;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGTTCTGAGGCT 21  
|||||  
Db 3288 CGGTTCTGAGGCT 3275

RESULT 42  
US-09-879-957-33/c  
; Sequence 33, Application US/09879957  
; Patent No. 6709821  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; HOFFMAN, No. 6709821h  
; KAY, Brian K.  
; FOWLKES, Dana M.  
; MCCONNELL, Stephen J.  
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
; USING SAME  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/879,957  
; FILING DATE: 13-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/630,915  
; FILING DATE: 03-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872

;  
; REFERENCE/DOCKET NUMBER: 1101-174  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4091 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-879-957-33

Query Match 29.2%; Score 14; DB 4; Length 4091;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGTTCTGAGGCT 21  
|||||  
Db 3288 CGGTTCTGAGGCT 3275

RESULT 43  
US-09-289-368-1/c  
; Sequence 1, Application US/09289368  
; Patent No. 5998148  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Elizabeth J. Ackermann  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROTUBULE-ASSOCIATED PROTEIN 4 EXPRESSION  
; FILE REFERENCE: RTS-0051  
; CURRENT APPLICATION NUMBER: US/09/289,368  
; CURRENT FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 87  
; SEQ ID NO 1  
; LENGTH: 5022  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: {91}..(3549)  
US-09-289-368-1

Query Match 29.2%; Score 14; DB 2; Length 5022;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TGAGGGCTTACATG 27  
|||||  
Db 4755 TGAGGGCTTACATG 4742

RESULT 44  
US-09-949-016-14973/c  
; Sequence 14973, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 14973
; LENGTH: 7620
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14973

Query Match      29.2%; Score 14; DB 4; Length 7620;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TTCTGAGGGCTTAC 24
Db      4816 TTCTGAGGGCTTAC 4803

RESULT 45
US-09-949-016-17224/c
; Sequence 17224, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17224
; LENGTH: 8580
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17224

Query Match      29.2%; Score 14; DB 4; Length 8580;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GGTTCGTGAGGGCTT 22
Db      7909 GGTTCGTGAGGGCTT 7896

RESULT 46
US-09-147-119-5
; Sequence 5, Application US/09147119
; Patent No. 6338844
; GENERAL INFORMATION:
; APPLICANT: KURTH, Ruth
; APPLICANT: BAIER, Michael
; APPLICANT: BANNERT, No. 6338844bert
; APPLICANT: METZNER, Karin
; APPLICANT: WERNER, Albrecht
; TITLE OF INVENTION: GENOMIC NUCLEIC ACIDS, CDNA AND mRNA WHICH
; CODE FOR POLYPEPTIDES WITH IL-16 ACTIVITY, PROCESS FOR THE
; PRODUCTION THEREOF AND THEIR USE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth St., NW
; CITY: Washington
; STATE: DC USA
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/147,119
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/01753
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 196 14 099.4
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wong, King L.
; REGISTRATION NUMBER: 37,500
; REFERENCE/DOCKET NUMBER: P1614-8068
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9096 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1..338
; FEATURE:
; NAME/KEY: intron
; LOCATION: 339..663
; FEATURE:
; NAME/KEY: exon
; LOCATION: 664..832
; FEATURE:
; NAME/KEY: intron
; LOCATION: 833..2870
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2871..2972
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2973..5224
; FEATURE:
; NAME/KEY: exon
; LOCATION: 5225..5483
; FEATURE:
; NAME/KEY: intron
; LOCATION: 5484..5737
; FEATURE:
; NAME/KEY: exon
; LOCATION: 5738..5863
; FEATURE:
; NAME/KEY: intron
; LOCATION: 5864..7926
; FEATURE:
; NAME/KEY: exon
; LOCATION: 7927..9096
; FEATURE:
; NAME/KEY: -
; LOCATION: 356
; OTHER INFORMATION: /product= "N means between 1 -
; OTHER INFORMATION: about 6 bp"
US-09-147-119-5

Query Match      29.2%; Score 14; DB 3; Length 9096;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TTCTGAGGGCTTAC 24
Db      5000 TTCTGAGGGCTTAC 5013
```



RESULT 47  
US-09-949-016-14295  
; Sequence 14295, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14295  
; LENGTH: 9261  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-14295

Query Match 29.2%; Score 14; DB 4; Length 9261;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 TTACATGGATCACT 34  
|||||  
DB 6815 TTACATGGATCACT 6828

RESULT 48  
US-09-949-016-13013  
; Sequence 13013, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
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; Sequence 1, Application US/09147119

; Patent No. 6338844  
; GENERAL INFORMATION:  
; APPLICANT: KURTH, Ruth  
; APPLICANT: BAIER, Michael  
; APPLICANT: BANNERT, No. 6338844bert  
; APPLICANT: METZNER, Karin  
; APPLICANT: WERNER, Albrecht  
; TITLE OF INVENTION: GENOMIC NUCLEIC ACIDS, CDNA AND mRNA WHICH  
; CODE FOR POLYPEPTIDES WITH IL-16 ACTIVITY, PROCESS FOR THE  
; TITLE OF INVENTION: PRODUCTION THEREOF AND THEIR USE  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nikaïdo, Marmelstein, Murray & Oram LLP  
; STREET: 655 Fifteenth St., NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-5701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/147,119  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP97/01753  
; FILING DATE: 10-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 196 14 099.4  
; FILING DATE: 10-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wong, King L.  
; REGISTRATION NUMBER: 37,500  
; REFERENCE/DOCKET NUMBER: P1614-8068  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 638-5000  
; TELEFAX: (202) 638-4810  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
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; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
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; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
;           Gil H. Choi
;           Patrick S. Dillon
;           Craig A. Rosen
;           Steven C. Barash
;           Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: MSDOS version 6.2
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17310 base pairs
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| 16 | 33.3 | 1168  | 9  | US-09-770-445-56     | Sequence 56, Appl  |
| 16 | 33.3 | 1233  | 17 | US-10-425-114-31937  | Sequence 31937, A  |
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| 16 | 33.3 | 2401  | 17 | US-10-425-114-1427   | Sequence 1427, Ap  |
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| 118 | 15 | 31.2 | 5285    | 17 | US-10-379-632-79     | Sequence 79, Appl  | 191   | 14 | 29.2 | 765  | 18 | US-10-663-561-539    | Sequence 539, App  |
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| 121 | 15 | 31.2 | 5319    | 11 | US-09-968-007A-360   | Sequence 360, App  | c 194 | 14 | 29.2 | 913  | 17 | US-10-424-599-14560  | Sequence 14560, A  |
| 122 | 15 | 31.2 | 5319    | 17 | US-10-912-434-7      | Sequence 7, Appl   | 195   | 14 | 29.2 | 936  | 17 | US-10-240-240A-129   | Sequence 129, App  |
| 123 | 15 | 31.2 | 5339    | 17 | US-10-379-632-27     | Sequence 27, Appl  | 196   | 14 | 29.2 | 936  | 17 | US-10-774-355A-1118  | Sequence 1118, App |
| 124 | 15 | 31.2 | 5339    | 14 | US-10-197-666A-139   | Sequence 139, App  | c 198 | 14 | 29.2 | 981  | 17 | US-09-815-342-4682   | Sequence 4682, App |
| 125 | 15 | 31.2 | 5351    | 17 | US-10-379-632-76     | Sequence 76, Appl  | c 199 | 14 | 29.2 | 992  | 17 | US-10-282-122A-8172  | Sequence 8172, App |
| 126 | 15 | 31.2 | 5366    | 17 | US-10-379-632-46     | Sequence 46, Appl  | 200   | 14 | 29.2 | 992  | 17 | US-10-424-599-22495  | Sequence 22495, A  |
| 127 | 15 | 31.2 | 5368    | 17 | US-10-379-632-23     | Sequence 23, Appl  | c 202 | 14 | 29.2 | 1049 | 17 | US-10-282-122A-36482 | Sequence 36482, A  |
| 128 | 15 | 31.2 | 5382    | 17 | US-10-379-632-73     | Sequence 73, Appl  | c 203 | 14 | 29.2 | 1105 | 18 | US-10-425-115-96273  | Sequence 96273, A  |
| 129 | 15 | 31.2 | 5390    | 18 | US-10-684-432-241    | Sequence 241, App  | c 204 | 14 | 29.2 | 1140 | 17 | US-10-424-599-93384  | Sequence 93384, A  |
| 130 | 15 | 31.2 | 5434    | 17 | US-10-379-632-31     | Sequence 31, App   | c 205 | 14 | 29.2 | 1209 | 17 | US-10-282-122A-28025 | Sequence 28025, A  |
| 131 | 15 | 31.2 | 5436    | 17 | US-10-379-632-26     | Sequence 26, Appl  | c 206 | 14 | 29.2 | 1216 | 18 | US-10-437-963-85297  | Sequence 85297, A  |
| 132 | 15 | 31.2 | 5463    | 17 | US-10-379-632-48     | Sequence 48, Appl  | c 208 | 14 | 29.2 | 1242 | 9  | US-09-815-424-9900   | Sequence 9900, App |
| 133 | 15 | 31.2 | 5531    | 17 | US-10-379-632-20     | Sequence 20, Appl  | c 209 | 14 | 29.2 | 1242 | 17 | US-10-282-122A-39677 | Sequence 39677, A  |
| 134 | 15 | 31.2 | 5584    | 17 | US-10-379-632-45     | Sequence 45, Appl  | c 210 | 14 | 29.2 | 1458 | 17 | US-10-114-270-95     | Sequence 95, Appl  |
| 135 | 15 | 31.2 | 2940917 | 13 | US-10-027-632-174763 | Sequence 174763, A | c 211 | 14 | 29.2 | 1492 | 14 | US-10-062-548-23     | Sequence 23, Appl  |
| 136 | 15 | 31.2 | 2940917 | 17 | US-10-027-632-174763 | Sequence 174763, A | c 212 | 14 | 29.2 | 1492 | 19 | US-10-918-446-23     | Sequence 23, Appl  |
| 137 | 14 | 29.2 | 25      | 19 | US-10-719-900-531296 | Sequence 531296, A | c 213 | 14 | 29.2 | 1508 | 17 | US-10-108-260A-967   | Sequence 967, App  |
| 138 | 14 | 29.2 | 92      | 9  | US-09-969-373-344    | Sequence 314, App  | c 214 | 14 | 29.2 | 1512 | 18 | US-10-437-963-84929  | Sequence 84929, A  |
| 139 | 14 | 29.2 | 169     | 10 | US-09-754-853A-266   | Sequence 266, App  | c 215 | 14 | 29.2 | 1584 | 17 | US-10-369-493-45771  | Sequence 45771, A  |
| 140 | 14 | 29.2 | 193     | 11 | US-09-732-627A-2107  | Sequence 2107, App | c 216 | 14 | 29.2 | 1590 | 18 | US-10-739-930-4996   | Sequence 4996, App |
| 141 | 14 | 29.2 | 195     | 17 | US-10-424-599-134380 | Sequence 134380, A | c 217 | 14 | 29.2 | 1619 | 18 | US-09-873-367C-329   | Sequence 329, App  |
| 142 | 14 | 29.2 | 201     | 18 | US-10-719-993-17506  | Sequence 17506, A  | c 218 | 14 | 29.2 | 1662 | 17 | US-10-282-122A-23249 | Sequence 23249, A  |
| 143 | 14 | 29.2 | 216     | 18 | US-10-425-115-33137  | Sequence 33137, A  | c 219 | 14 | 29.2 | 1736 | 17 | US-10-104-047-1196   | Sequence 1196, App |
| 144 | 14 | 29.2 | 218     | 18 | US-10-425-115-176163 | Sequence 176163, A | c 220 | 14 | 29.2 | 1759 | 9  | US-09-938-842A-5326  | Sequence 5326, App |
| 145 | 14 | 29.2 | 251     | 18 | US-10-425-115-129138 | Sequence 129138, A | c 221 | 14 | 29.2 | 2000 | 11 | US-09-938-842A-5326  | Sequence 5326, App |
| 146 | 14 | 29.2 | 253     | 11 | US-09-732-627A-4567  | Sequence 4567, App | c 222 | 14 | 29.2 | 2165 | 13 | US-10-194-163-885    | Sequence 885, App  |
| 147 | 14 | 29.2 | 255     | 17 | US-10-305-720-461    | Sequence 461, App  | c 223 | 14 | 29.2 | 2174 | 13 | US-10-027-632-103226 | Sequence 103226, A |
| 148 | 14 | 29.2 | 259     | 18 | US-10-425-115-51406  | Sequence 51406, A  | c 224 | 14 | 29.2 | 2174 | 17 | US-10-027-632-103226 | Sequence 103226, A |
| 149 | 14 | 29.2 | 259     | 18 | US-10-425-115-91447  | Sequence 91447, A  | c 225 | 14 | 29.2 | 2218 | 18 | US-10-437-963-65487  | Sequence 65487, A  |
| 150 | 14 | 29.2 | 265     | 11 | US-09-987-899-5328   | Sequence 5328, App | c 226 | 14 | 29.2 | 2633 | 9  | US-09-864-864-314    | Sequence 314, App  |
| 151 | 14 | 29.2 | 272     | 11 | US-09-987-899-5328   | Sequence 5329, App | c 227 | 14 | 29.2 | 2638 | 17 | US-10-369-493-27088  | Sequence 27088, A  |
| 152 | 14 | 29.2 | 306     | 18 | US-10-437-963-89883  | Sequence 89883, A  | c 228 | 14 | 29.2 | 2859 | 9  | US-09-923-684-2      | Sequence 2, Appl   |
| 153 | 14 | 29.2 | 336     | 17 | US-10-424-599-68672  | Sequence 68672, A  | c 229 | 14 | 29.2 | 3130 | 9  | US-09-969-708-566    | Sequence 566, App  |
| 154 | 14 | 29.2 | 344     | 9  | US-09-878-134-220    | Sequence 220, App  | c 230 | 14 | 29.2 | 3130 | 9  | US-09-962-832-161    | Sequence 161, App  |
| 155 | 14 | 29.2 | 362     | 18 | US-10-674-124A-14201 | Sequence 14201, A  |       |    |      |      |    |                      |                    |
| 156 | 14 | 29.2 | 362     | 17 | US-10-424-599-87605  | Sequence 87605, A  |       |    |      |      |    |                      |                    |
| 157 | 14 | 29.2 | 384     | 17 | US-10-424-599-97319  | Sequence 97319, A  |       |    |      |      |    |                      |                    |

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|-------|----|------|--------|----|---------------------|--------------------|-------|----|------|---------|----|-----------------------|--------------------|
| c 231 | 14 | 29.2 | 3138   | 18 | US-10-741-601-265   | Sequence 265, App  | c 304 | 14 | 29.2 | 513509  | 10 | US-09-754-853A-4      | Sequence 4, Appli  |
| c 232 | 14 | 29.2 | 3179   | 17 | US-10-425-114-29880 | Sequence 29880, A  | c 305 | 14 | 29.2 | 1230025 | 17 | US-10-289-762-1       | Sequence 1, Appli  |
| c 233 | 14 | 29.2 | 3207   | 18 | US-10-741-601-268   | Sequence 268, App  | c 306 | 14 | 29.2 | 3186778 | 13 | US-10-027-632-174961  | Sequence 174961,   |
| c 234 | 14 | 29.2 | 3210   | 18 | US-10-478-914-4     | Sequence 4, Appli  | c 307 | 14 | 29.2 | 3186778 | 17 | US-10-027-632-174961  | Sequence 174961,   |
| c 235 | 14 | 29.2 | 3258   | 18 | US-10-437-963-49102 | Sequence 49102, A  | c 308 | 14 | 29.2 | 9025608 | 15 | US-10-356-761-1       | Sequence 1, Appli  |
| c 236 | 14 | 29.2 | 3285   | 17 | US-10-425-114-11232 | Sequence 11232, A  | c 309 | 13 | 27.1 | 20      | 8  | US-08-734-011-1       | Sequence 1, Appli  |
| c 237 | 14 | 29.2 | 3303   | 18 | US-10-741-601-266   | Sequence 266, App  | c 310 | 13 | 27.1 | 20      | 9  | US-09-863-806-9       | Sequence 9, Appli  |
| c 238 | 14 | 29.2 | 3373   | 18 | US-10-741-601-264   | Sequence 264, App  | c 311 | 13 | 27.1 | 20      | 9  | US-09-863-806-9       | Sequence 9, Appli  |
| c 239 | 14 | 29.2 | 3405   | 17 | US-10-150-559-1     | Sequence 1, Appli  | c 312 | 13 | 27.1 | 20      | 10 | US-09-948-909-9       | Sequence 9, Appli  |
| c 240 | 14 | 29.2 | 3405   | 17 | US-10-440-352-1     | Sequence 1, Appli  | c 313 | 13 | 27.1 | 20      | 10 | US-09-948-909-9       | Sequence 9, Appli  |
| c 241 | 14 | 29.2 | 3442   | 18 | US-10-741-601-263   | Sequence 263, App  | c 314 | 13 | 27.1 | 20      | 15 | US-10-290-473-9       | Sequence 9, Appli  |
| c 242 | 14 | 29.2 | 3442   | 18 | US-10-741-601-263   | Sequence 263, App  | c 315 | 13 | 27.1 | 20      | 15 | US-10-290-473-9       | Sequence 9, Appli  |
| c 243 | 14 | 29.2 | 3542   | 17 | US-10-424-599-96841 | Sequence 96841, A  | c 316 | 13 | 27.1 | 20      | 15 | US-10-290-473-9       | Sequence 9, Appli  |
| c 244 | 14 | 29.2 | 3548   | 18 | US-10-437-963-70323 | Sequence 70323, A  | c 317 | 13 | 27.1 | 20      | 19 | US-10-754-478-41      | Sequence 41, Appli |
| c 245 | 14 | 29.2 | 3560   | 17 | US-10-108-260A-1595 | Sequence 1595, Ap  | c 318 | 13 | 27.1 | 25      | 15 | US-10-098-263B-112700 | Sequence 112700,   |
| c 246 | 14 | 29.2 | 3621   | 14 | US-10-198-846-10650 | Sequence 10650, A  | c 319 | 13 | 27.1 | 25      | 19 | US-10-719-900-51194   | Sequence 51194, A  |
| c 247 | 14 | 29.2 | 3772   | 18 | US-10-437-963-14013 | Sequence 14013, A  | c 320 | 13 | 27.1 | 25      | 19 | US-10-719-900-87159   | Sequence 87159, A  |
| c 248 | 14 | 29.2 | 3828   | 18 | US-10-723-860-5337  | Sequence 5337, Ap  | c 321 | 13 | 27.1 | 25      | 19 | US-10-719-900-87159   | Sequence 87159, A  |
| c 249 | 14 | 29.2 | 3920   | 9  | US-09-923-684-1     | Sequence 1, Appli  | c 322 | 13 | 27.1 | 25      | 19 | US-10-719-900-126888  | Sequence 126888,   |
| c 250 | 14 | 29.2 | 3921   | 19 | US-10-852-943-94    | Sequence 94, Appli | c 323 | 13 | 27.1 | 25      | 19 | US-10-719-900-181503  | Sequence 181503,   |
| c 251 | 14 | 29.2 | 4073   | 17 | US-10-115-831-81    | Sequence 81, Appli | c 324 | 13 | 27.1 | 25      | 19 | US-10-719-900-261017  | Sequence 261017,   |
| c 252 | 14 | 29.2 | 4091   | 9  | US-09-879-957-33    | Sequence 33, Appli | c 325 | 13 | 27.1 | 25      | 19 | US-10-719-900-296870  | Sequence 296870,   |
| c 253 | 14 | 29.2 | 4091   | 18 | US-10-807-856-33    | Sequence 33, Appli | c 326 | 13 | 27.1 | 25      | 19 | US-10-719-900-317666  | Sequence 317666,   |
| c 254 | 14 | 29.2 | 4355   | 18 | US-10-437-963-28926 | Sequence 28926, A  | c 327 | 13 | 27.1 | 25      | 19 | US-10-719-900-344032  | Sequence 344032,   |
| c 255 | 14 | 29.2 | 5022   | 15 | US-10-171-581-157   | Sequence 157, App  | c 328 | 13 | 27.1 | 25      | 19 | US-10-719-900-408932  | Sequence 408932,   |
| c 256 | 14 | 29.2 | 5181   | 18 | US-10-437-963-12010 | Sequence 12010, A  | c 329 | 13 | 27.1 | 25      | 19 | US-10-719-900-419283  | Sequence 419283,   |
| c 257 | 14 | 29.2 | 5243   | 16 | US-10-252-157-193   | Sequence 193, App  | c 330 | 13 | 27.1 | 25      | 19 | US-10-719-900-481999  | Sequence 481999,   |
| c 258 | 14 | 29.2 | 5987   | 14 | US-10-198-846-10188 | Sequence 10188, A  | c 331 | 13 | 27.1 | 25      | 19 | US-10-719-900-822909  | Sequence 822909,   |
| c 259 | 14 | 29.2 | 15392  | 18 | US-10-719-993-93933 | Sequence 9393, Ap  | c 332 | 13 | 27.1 | 25      | 19 | US-10-719-900-895818  | Sequence 895818,   |
| c 260 | 14 | 29.2 | 17310  | 8  | US-08-781-986A-23   | Sequence 23, Appli | c 333 | 13 | 27.1 | 25      | 19 | US-10-719-900-899317  | Sequence 899317,   |
| c 261 | 14 | 29.2 | 17310  | 17 | US-10-329-624-23    | Sequence 23, Appli | c 334 | 13 | 27.1 | 25      | 19 | US-10-719-900-913162  | Sequence 913162,   |
| c 262 | 14 | 29.2 | 19832  | 19 | US-10-741-600-17778 | Sequence 17778, A  | c 335 | 13 | 27.1 | 25      | 19 | US-10-719-900-952127  | Sequence 952127,   |
| c 263 | 14 | 29.2 | 21045  | 9  | US-09-764-864-1695  | Sequence 1695, Ap  | c 336 | 13 | 27.1 | 64      | 18 | US-10-654-898A-1      | Sequence 1, Appli  |
| c 264 | 14 | 29.2 | 23307  | 10 | US-09-764-864-15530 | Sequence 5530, Ap  | c 337 | 13 | 27.1 | 65      | 10 | US-09-908-975-24314   | Sequence 24314, A  |
| c 265 | 14 | 29.2 | 23307  | 10 | US-09-764-864-15530 | Sequence 5530, Ap  | c 338 | 13 | 27.1 | 100     | 17 | US-10-242-535A-12091  | Sequence 12091, A  |
| c 266 | 14 | 29.2 | 23594  | 13 | US-10-087-192-1936  | Sequence 1936, Ap  | c 339 | 13 | 27.1 | 151     | 17 | US-10-085-783A-12091  | Sequence 12091, A  |
| c 267 | 14 | 29.2 | 27240  | 18 | US-10-741-601-5777  | Sequence 5777, Ap  | c 340 | 13 | 27.1 | 151     | 9  | US-09-783-590-3299    | Sequence 3299, Ap  |
| c 268 | 14 | 29.2 | 33488  | 17 | US-10-085-117-235   | Sequence 235, App  | c 341 | 13 | 27.1 | 192     | 17 | US-10-425-115-122490  | Sequence 122490,   |
| c 269 | 14 | 29.2 | 37004  | 18 | US-10-322-281-442   | Sequence 442, App  | c 342 | 13 | 27.1 | 192     | 17 | US-10-424-599-122004  | Sequence 122004,   |
| c 270 | 14 | 29.2 | 47322  | 18 | US-10-322-281-507   | Sequence 507, App  | c 343 | 13 | 27.1 | 201     | 9  | US-09-864-761-23759   | Sequence 23759, A  |
| c 271 | 14 | 29.2 | 49726  | 18 | US-10-719-993-7050  | Sequence 7050, Ap  | c 344 | 13 | 27.1 | 201     | 18 | US-10-741-601-5198    | Sequence 5198, Ap  |
| c 272 | 14 | 29.2 | 51256  | 17 | US-10-359-077-3     | Sequence 3, Appli  | c 345 | 13 | 27.1 | 201     | 18 | US-10-741-601-5206    | Sequence 5206, Ap  |
| c 273 | 14 | 29.2 | 51719  | 9  | US-09-918-686-2     | Sequence 2, Appli  | c 346 | 13 | 27.1 | 201     | 18 | US-10-741-601-5221    | Sequence 5221, Ap  |
| c 274 | 14 | 29.2 | 51719  | 16 | US-10-353-150-2     | Sequence 2, Appli  | c 347 | 13 | 27.1 | 201     | 18 | US-10-741-601-5227    | Sequence 5227, Ap  |
| c 275 | 14 | 29.2 | 52520  | 17 | US-10-741-601-5700  | Sequence 5700, Ap  | c 348 | 13 | 27.1 | 201     | 18 | US-10-741-601-5243    | Sequence 5243, Ap  |
| c 276 | 14 | 29.2 | 58822  | 17 | US-10-052-482-46    | Sequence 46, Appli | c 349 | 13 | 27.1 | 201     | 18 | US-10-741-601-5251    | Sequence 5251, Ap  |
| c 277 | 14 | 29.2 | 59065  | 16 | US-10-135-686-3     | Sequence 3, Appli  | c 350 | 13 | 27.1 | 201     | 18 | US-10-741-601-5267    | Sequence 5267, Ap  |
| c 278 | 14 | 29.2 | 59065  | 18 | US-10-820-230-3     | Sequence 3, Appli  | c 351 | 13 | 27.1 | 201     | 18 | US-10-741-601-5275    | Sequence 5275, Ap  |
| c 279 | 14 | 29.2 | 92139  | 9  | US-09-918-686-1     | Sequence 1, Appli  | c 352 | 13 | 27.1 | 201     | 18 | US-10-741-601-20130   | Sequence 20130, A  |
| c 280 | 14 | 29.2 | 92139  | 16 | US-10-353-150-1     | Sequence 1, Appli  | c 353 | 13 | 27.1 | 201     | 18 | US-10-719-993-14238   | Sequence 14238, A  |
| c 281 | 14 | 29.2 | 95108  | 18 | US-10-719-993-6807  | Sequence 6807, Ap  | c 354 | 13 | 27.1 | 201     | 18 | US-10-719-993-14238   | Sequence 14238, A  |
| c 282 | 14 | 29.2 | 96587  | 11 | US-09-997-722-250   | Sequence 250, App  | c 355 | 13 | 27.1 | 201     | 18 | US-10-719-993-49296   | Sequence 49296, A  |
| c 283 | 14 | 29.2 | 99357  | 11 | US-09-997-722-298   | Sequence 298, App  | c 356 | 13 | 27.1 | 201     | 19 | US-10-741-600-16083   | Sequence 16083, A  |
| c 284 | 14 | 29.2 | 105184 | 10 | US-09-847-513A-1    | Sequence 1, Appli  | c 357 | 13 | 27.1 | 201     | 19 | US-10-741-600-16089   | Sequence 16089, A  |
| c 285 | 14 | 29.2 | 118951 | 13 | US-10-161-572-11    | Sequence 11, Appli | c 358 | 13 | 27.1 | 201     | 19 | US-10-741-600-16105   | Sequence 16105, A  |
| c 286 | 14 | 29.2 | 123920 | 14 | US-10-087-192-1453  | Sequence 1453, Ap  | c 359 | 13 | 27.1 | 201     | 19 | US-10-741-600-16113   | Sequence 16113, A  |
| c 287 | 14 | 29.2 | 128978 | 18 | US-10-087-192-1453  | Sequence 1453, Ap  | c 360 | 13 | 27.1 | 201     | 19 | US-10-741-600-16128   | Sequence 16128, A  |
| c 288 | 14 | 29.2 | 130320 | 17 | US-10-775-169-345   | Sequence 345, App  | c 361 | 13 | 27.1 | 201     | 19 | US-10-741-600-16136   | Sequence 16136, A  |
| c 289 | 14 | 29.2 | 133893 | 13 | US-10-408-168-1     | Sequence 1, Appli  | c 362 | 13 | 27.1 | 201     | 19 | US-10-741-600-16132   | Sequence 16132, A  |
| c 290 | 14 | 29.2 | 153995 | 18 | US-10-322-281-721   | Sequence 721, App  | c 363 | 13 | 27.1 | 201     | 19 | US-10-741-600-16160   | Sequence 16160, A  |
| c 291 | 14 | 29.2 | 185458 | 18 | US-10-719-993-6864  | Sequence 6864, Ap  | c 364 | 13 | 27.1 | 201     | 19 | US-10-741-600-28282   | Sequence 28282, A  |
| c 292 | 14 | 29.2 | 185695 | 14 | US-10-020-141-11    | Sequence 11, Appli | c 365 | 13 | 27.1 | 201     | 19 | US-10-741-600-53564   | Sequence 53564, A  |
| c 293 | 14 | 29.2 | 185695 | 14 | US-10-017-721-1     | Sequence 1, Appli  | c 366 | 13 | 27.1 | 201     | 19 | US-10-741-600-54878   | Sequence 54878, A  |
| c 294 | 14 | 29.2 | 200000 | 18 | US-10-672-764A-30   | Sequence 30, Appli | c 367 | 13 | 27.1 | 201     | 19 | US-10-741-600-54879   | Sequence 54879, A  |
| c 295 | 14 | 29.2 | 210828 | 13 | US-10-087-192-1369  | Sequence 289, App  | c 368 | 13 | 27.1 | 201     | 19 | US-10-741-600-54880   | Sequence 54880, A  |
| c 296 | 14 | 29.2 | 215221 | 13 | US-10-087-192-1360  | Sequence 1360, App | c 369 | 13 | 27.1 | 201     | 19 | US-10-741-600-55168   | Sequence 55168, A  |
| c 297 | 14 | 29.2 | 230093 | 18 | US-10-719-993-6861  | Sequence 6861, Ap  | c 370 | 13 | 27.1 | 201     | 19 | US-10-741-600-55174   | Sequence 55174, A  |
| c 298 | 14 | 29.2 | 256157 | 13 | US-10-087-192-1204  | Sequence 1204, Ap  | c 371 | 13 | 27.1 | 201     | 19 | US-10-741-600-55556   | Sequence 55556, A  |
| c 299 | 14 | 29.2 | 256157 | 18 | US-10-322-281-776   | Sequence 776, App  | c 372 | 13 | 27.1 | 201     | 19 | US-10-741-600-57637   | Sequence 57637, A  |
| c 300 | 14 | 29.2 | 256190 | 18 | US-10-322-281-320   | Sequence 320, App  | c 373 | 13 | 27.1 | 201     | 19 | US-10-741-600-62526   | Sequence 62526, A  |
| c 301 | 14 | 29.2 | 302603 | 17 | US-10-271-416-8     | Sequence 8, Appli  | c 374 | 13 | 27.1 | 201     | 19 | US-10-741-600-69232   | Sequence 69232, A  |
| c 302 | 14 | 29.2 | 337022 | 18 | US-10-322-696-52    | Sequence 52, Appli | c 375 | 13 | 27.1 | 201     | 19 | US-10-741-600-69235   | Sequence 69235, A  |
| c 303 | 14 | 29.2 | 347001 | 18 | US-10-319-908-16    | Sequence 16, Appli | c 376 | 13 | 27.1 | 201     | 19 | US-10-741-600-69237   | Sequence 69237, A  |

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| C 377 | 13 | 27.1 | 201 | 19 | US-10-741-600-69239  | Sequence 69239, A  | C 450 | 13 | 27.1 | 341 | 9  | US-09-960-352-2808   | Sequence 2808, Ap  |
| C 378 | 13 | 27.1 | 201 | 19 | US-10-741-600-69241  | Sequence 69241, A  | C 451 | 13 | 27.1 | 344 | 18 | US-10-437-963-100958 | Sequence 100958, A |
| C 379 | 13 | 27.1 | 201 | 19 | US-10-741-600-69243  | Sequence 69243, A  | C 452 | 13 | 27.1 | 345 | 9  | US-09-974-300-6045   | Sequence 6045, Ap  |
| C 380 | 13 | 27.1 | 201 | 19 | US-10-741-600-69244  | Sequence 69244, A  | C 453 | 13 | 27.1 | 345 | 17 | US-10-282-122A-23111 | Sequence 23111, A  |
| C 381 | 13 | 27.1 | 201 | 19 | US-10-741-600-69246  | Sequence 69246, A  | C 454 | 13 | 27.1 | 348 | 18 | US-10-425-115-171870 | Sequence 171870, A |
| C 382 | 13 | 27.1 | 201 | 19 | US-10-741-600-69247  | Sequence 69247, A  | C 455 | 13 | 27.1 | 349 | 18 | US-10-674-124A-7294  | Sequence 7294, Ap  |
| C 383 | 13 | 27.1 | 201 | 19 | US-10-741-600-69248  | Sequence 69248, A  | C 456 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 384 | 13 | 27.1 | 201 | 19 | US-10-741-600-69262  | Sequence 69262, A  | C 457 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 385 | 13 | 27.1 | 201 | 19 | US-10-741-600-69265  | Sequence 69265, A  | C 458 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 386 | 13 | 27.1 | 201 | 19 | US-10-741-600-69265  | Sequence 69265, A  | C 459 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 387 | 13 | 27.1 | 201 | 19 | US-10-282-122A-3204  | Sequence 3204, Ap  | C 460 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 388 | 13 | 27.1 | 201 | 19 | US-10-242-535A-57526 | Sequence 57526, A  | C 461 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 389 | 13 | 27.1 | 201 | 19 | US-10-085-783A-57526 | Sequence 57526, A  | C 462 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 390 | 13 | 27.1 | 201 | 19 | US-10-282-122A-3132  | Sequence 3132, Ap  | C 463 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 391 | 13 | 27.1 | 201 | 19 | US-10-282-122A-3180  | Sequence 3180, Ap  | C 464 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 392 | 13 | 27.1 | 201 | 19 | US-10-424-599-92424  | Sequence 92424, A  | C 465 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 393 | 13 | 27.1 | 201 | 19 | US-09-923-876-742    | Sequence 742, App  | C 466 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 394 | 13 | 27.1 | 201 | 19 | US-09-923-876-742    | Sequence 742, App  | C 467 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 395 | 13 | 27.1 | 201 | 19 | US-10-282-122A-2361  | Sequence 2361, Ap  | C 468 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 396 | 13 | 27.1 | 201 | 19 | US-10-357-930-60687  | Sequence 60687, A  | C 469 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 397 | 13 | 27.1 | 201 | 19 | US-10-282-122A-1906  | Sequence 1906, Ap  | C 470 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 398 | 13 | 27.1 | 201 | 19 | US-09-895-828-98     | Sequence 98, Appl  | C 471 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 399 | 13 | 27.1 | 201 | 19 | US-10-114-666-98     | Sequence 98, Appl  | C 472 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 400 | 13 | 27.1 | 201 | 19 | US-10-357-930-60498  | Sequence 60498, A  | C 473 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 401 | 13 | 27.1 | 201 | 19 | US-10-357-930-60455  | Sequence 60455, A  | C 474 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 402 | 13 | 27.1 | 201 | 19 | US-10-357-930-60637  | Sequence 60637, A  | C 475 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 403 | 13 | 27.1 | 201 | 19 | US-10-357-930-60414  | Sequence 60414, A  | C 476 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 404 | 13 | 27.1 | 201 | 19 | US-10-357-930-60499  | Sequence 60499, A  | C 477 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 405 | 13 | 27.1 | 201 | 19 | US-10-357-930-60585  | Sequence 60585, A  | C 478 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 406 | 13 | 27.1 | 201 | 19 | US-10-357-930-60551  | Sequence 60551, A  | C 479 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 407 | 13 | 27.1 | 201 | 19 | US-10-357-930-60382  | Sequence 60382, A  | C 480 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 408 | 13 | 27.1 | 201 | 19 | US-10-430-201-167    | Sequence 167, App  | C 481 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 409 | 13 | 27.1 | 201 | 19 | US-10-430-201-167    | Sequence 167, App  | C 482 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 410 | 13 | 27.1 | 201 | 19 | US-10-357-930-60690  | Sequence 60690, A  | C 483 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 411 | 13 | 27.1 | 201 | 19 | US-10-424-599-128296 | Sequence 128296, A | C 484 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 412 | 13 | 27.1 | 201 | 19 | US-10-357-930-60444  | Sequence 60444, A  | C 485 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 413 | 13 | 27.1 | 201 | 19 | US-10-357-930-60635  | Sequence 60635, A  | C 486 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 414 | 13 | 27.1 | 201 | 19 | US-10-282-122A-2305  | Sequence 2305, Ap  | C 487 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 415 | 13 | 27.1 | 201 | 19 | US-10-357-930-60537  | Sequence 60537, A  | C 488 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 416 | 13 | 27.1 | 201 | 19 | US-10-357-930-60601  | Sequence 60601, A  | C 489 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 417 | 13 | 27.1 | 201 | 19 | US-10-424-599-108494 | Sequence 108494, A | C 490 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 418 | 13 | 27.1 | 201 | 19 | US-10-357-930-60576  | Sequence 60576, A  | C 491 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 419 | 13 | 27.1 | 201 | 19 | US-10-242-535A-19210 | Sequence 19210, A  | C 492 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 420 | 13 | 27.1 | 201 | 19 | US-10-085-783A-19210 | Sequence 19210, A  | C 493 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 421 | 13 | 27.1 | 201 | 19 | US-10-357-930-60532  | Sequence 60532, A  | C 494 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 422 | 13 | 27.1 | 201 | 19 | US-10-357-930-60400  | Sequence 60400, A  | C 495 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 423 | 13 | 27.1 | 201 | 19 | US-10-357-930-60634  | Sequence 60634, A  | C 496 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 424 | 13 | 27.1 | 201 | 19 | US-10-282-122A-3360  | Sequence 3360, Ap  | C 497 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 425 | 13 | 27.1 | 201 | 19 | US-10-357-930-60493  | Sequence 60493, A  | C 498 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 426 | 13 | 27.1 | 201 | 19 | US-10-357-930-60436  | Sequence 60436, A  | C 499 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 427 | 13 | 27.1 | 201 | 19 | US-10-357-930-60617  | Sequence 60617, A  | C 500 | 13 | 27.1 | 353 | 10 | US-09-803-719-203    | Sequence 719, A    |
| C 428 | 13 | 27.1 | 201 | 19 | US-10-242-535A-47698 | Sequence 47698, A  |       |    |      |     |    |                      |                    |
| C 429 | 13 | 27.1 | 201 | 19 | US-10-085-783A-47698 | Sequence 47698, A  |       |    |      |     |    |                      |                    |
| C 430 | 13 | 27.1 | 201 | 19 | US-10-357-930-60456  | Sequence 60456, A  |       |    |      |     |    |                      |                    |
| C 431 | 13 | 27.1 | 201 | 19 | US-10-424-599-70508  | Sequence 70508, A  |       |    |      |     |    |                      |                    |
| C 432 | 13 | 27.1 | 201 | 19 | US-09-893-737-63     | Sequence 63, Appl  |       |    |      |     |    |                      |                    |
| C 433 | 13 | 27.1 | 201 | 19 | US-10-357-930-60482  | Sequence 60482, A  |       |    |      |     |    |                      |                    |
| C 434 | 13 | 27.1 | 201 | 19 | US-10-357-930-60652  | Sequence 60652, A  |       |    |      |     |    |                      |                    |
| C 435 | 13 | 27.1 | 201 | 19 | US-10-282-122A-2152  | Sequence 2152, Ap  |       |    |      |     |    |                      |                    |
| C 436 | 13 | 27.1 | 201 | 19 | US-10-282-122A-2177  | Sequence 2177, Ap  |       |    |      |     |    |                      |                    |
| C 437 | 13 | 27.1 | 201 | 19 | US-10-021-323-1943   | Sequence 1943, Ap  |       |    |      |     |    |                      |                    |
| C 438 | 13 | 27.1 | 201 | 19 | US-10-424-599-110582 | Sequence 110582, A |       |    |      |     |    |                      |                    |
| C 439 | 13 | 27.1 | 201 | 19 | US-10-357-930-60543  | Sequence 60543, A  |       |    |      |     |    |                      |                    |
| C 440 | 13 | 27.1 | 201 | 19 | US-10-357-930-60604  | Sequence 60604, A  |       |    |      |     |    |                      |                    |
| C 441 | 13 | 27.1 | 201 | 19 | US-10-282-122A-21245 | Sequence 21245, A  |       |    |      |     |    |                      |                    |
| C 442 | 13 | 27.1 | 201 | 19 | US-09-814-353-3891   | Sequence 3891, Ap  |       |    |      |     |    |                      |                    |
| C 443 | 13 | 27.1 | 201 | 19 | US-09-814-353-10159  | Sequence 10159, A  |       |    |      |     |    |                      |                    |
| C 444 | 13 | 27.1 | 201 | 19 | US-10-674-124A-21341 | Sequence 21341, A  |       |    |      |     |    |                      |                    |
| C 445 | 13 | 27.1 | 201 | 19 | US-09-974-300-3609   | Sequence 3609, Ap  |       |    |      |     |    |                      |                    |
| C 446 | 13 | 27.1 | 201 | 19 | US-10-424-599-132445 | Sequence 132445, A |       |    |      |     |    |                      |                    |
| C 447 | 13 | 27.1 | 201 | 19 | US-10-425-115-64762  | Sequence 64762, A  |       |    |      |     |    |                      |                    |
| C 448 | 13 | 27.1 | 201 | 19 | US-10-425-115-1482   | Sequence 1482, Ap  |       |    |      |     |    |                      |                    |
| C 449 | 13 | 27.1 | 201 | 19 | US-09-783-590-10122  | Sequence 10122, A  |       |    |      |     |    |                      |                    |
|       |    |      |     |    | Sequence 78272, A    |                    |       |    |      |     |    |                      |                    |

## ALIGNMENTS

## RESULT 1

US-10-688-489-73  
; Sequence 73, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GP140-04.UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; PRIOR FILING DATE: 2003-10-16  
; PRIOR FILING DATE: 2002-10-16

; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 73  
; LENGTH: 48  
; TYPE: DNA  
; ORGANISM: West Nile Virus  
US-10-688-489-73

Query Match 100.0%; Score 48; DB 18; Length 48;  
Best Local Similarity 100.0%; Pred. No. 5.3e-19;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTACATGGATCACTTCGACGCTTTGTC 48  
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Db 1 TCCGAGACGGTCTGAGGGCTTACATGGATCACTTCGACGCTTTGTC 48

## RESULT 2

US-10-688-489-72  
; Sequence 72, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; TITLE OF INVENTION: West Nile Virus  
; FILE REFERENCE: GP140-04.UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; PRIOR FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 72  
; LENGTH: 70  
; TYPE: DNA  
; ORGANISM: West Nile Virus  
US-10-688-489-72

Query Match 100.0%; Score 48; DB 18; Length 70;  
Best Local Similarity 100.0%; Pred. No. 5.2e-19;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTACATGGATCACTTCGACGCTTTGTC 48  
|||||  
Db 1 TCCGAGACGGTCTGAGGGCTTACATGGATCACTTCGACGCTTTGTC 48

## RESULT 3

US-10-815-480-71/c  
; Sequence 71, Application US/10815480  
; Publication No. US20040229261A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Karen K. Y.  
; APPLICANT: Roche Molecular Systems, Inc.  
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain  
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese  
; TITLE OF INVENTION: Encephalitis Virus Serogroup  
; FILE REFERENCE: 022101-000230US  
; CURRENT APPLICATION NUMBER: US/10/815,480  
; CURRENT FILING DATE: 2004-03-31  
; PRIOR APPLICATION NUMBER: US 60/459,491

; PRIOR FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/552,454  
; PRIOR FILING DATE: 2004-03-12  
; PRIOR APPLICATION NUMBER: US 60/555,530  
; PRIOR FILING DATE: 2004-03-22  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 71  
; LENGTH: 98  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: region of  
; OTHER INFORMATION: conserved sequence in 3' untranslated region of  
; OTHER INFORMATION: the genome of flavivirus AF196835  
US-10-815-480-71

Query Match 79.2%; Score 38; DB 18; Length 98;  
Best Local Similarity 100.0%; Pred. No. 6.1e-13;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTACATGGATCACTTCGC 38  
|||||  
Db 68 TCCGAGACGGTCTGAGGGCTTACATGGATCACTTCGC 31

## RESULT 4

US-10-361-002-5/c  
; Sequence 5, Application US/10361002  
; Publication No. US20040170954A1  
; GENERAL INFORMATION:  
; APPLICANT: Clearant, Inc.  
; APPLICANT: McKenney, Keith  
; APPLICANT: Gillmeister, Lidja  
; APPLICANT: Marlowe, Kristina  
; APPLICANT: Armistead, David  
; TITLE OF INVENTION: Pathogen Inactivation Assay  
; FILE REFERENCE: CI-0043  
; CURRENT APPLICATION NUMBER: US/10/361,002  
; CURRENT FILING DATE: 2003-02-10  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 10945  
; TYPE: DNA  
; ORGANISM: West Nile virus  
US-10-361-002-5

Query Match 79.2%; Score 38; DB 18; Length 10945;  
Best Local Similarity 100.0%; Pred. No. 5.1e-13;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTACATGGATCACTTCGC 38  
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Db 10587 TCCGAGACGGTCTGAGGGCTTACATGGATCACTTCGC 10550

## RESULT 5

US-10-361-004-5/c  
; Sequence 5, Application US/10361004  
; Publication No. US20040170981A1  
; GENERAL INFORMATION:  
; APPLICANT: Clearant, Inc.  
; APPLICANT: McKenney, Keith  
; APPLICANT: Gillmeister, Lidja  
; APPLICANT: Marlowe, Kristina  
; APPLICANT: Armistead, David  
; TITLE OF INVENTION: Real-time Polymerase Chain Reaction Using Large Target Amplicons  
; FILE REFERENCE: CI-0042  
; CURRENT APPLICATION NUMBER: US/10/361,004  
; CURRENT FILING DATE: 2003-02-10  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn version 3.2

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; SEQ ID NO 5
; LENGTH: 10945
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-361-004-5

Query Match          79.2%; Score 38; DB 18; Length 10945;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGCTTACATGGATCACTTCGC 38
    |||||||
Db 10587 TCCGAGACGGTCTGAGGCTTACATGGATCACTTCGC 10550

RESULT 6
US-10-699-550-1/c
; Sequence 1, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 10975
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-699-550-1

Query Match          79.2%; Score 38; DB 18; Length 10975;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGCTTACATGGATCACTTCGC 38
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Db 10611 TCCGAGACGGTCTGAGGCTTACATGGATCACTTCGC 10574

RESULT 7
US-10-699-550-2/c
; Sequence 2, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
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; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-699-550-2

Query Match          79.2%; Score 38; DB 18; Length 11029;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGCTTACATGGATCACTTCGC 38
    |||||||
Db 10629 TCCGAGACGGTCTGAGGCTTACATGGATCACTTCGC 10592

RESULT 8
US-10-679-520A-66/c
; Sequence 66, Application US/10679520A
; Publication No. US20050031641A1
; GENERAL INFORMATION:
; APPLICANT: LOOSMORE, SHEENA MAY
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE FRANCIS
; APPLICANT: MINKE, JULES MAARTEN
; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
; FILE REFERENCE: 574313-3161.4
; CURRENT APPLICATION NUMBER: US/10/679,520A
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: 10/374,953
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 10/116,298
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,923
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: PCT/FR02/01200
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: FR 01/04737
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 66
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)..(10395)
US-10-679-520A-66

Query Match          79.2%; Score 38; DB 19; Length 11029;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGCTTACATGGATCACTTCGC 38
    |||||||
Db 10629 TCCGAGACGGTCTGAGGCTTACATGGATCACTTCGC 10592

RESULT 9
US-10-706-892-1/c
; Sequence 1, Application US/10706892
; Publication No. US20050058987A1
; GENERAL INFORMATION:
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY
; FILE REFERENCE: 454311-2231.1
; CURRENT APPLICATION NUMBER: US/10/706,892
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; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/427,117
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: west Nile virus
US-10-706-892-1

Query Match      79.2%; Score 38; DB 19; Length 11029;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTTGAGGGCTTACATGATCACTTCGC 38
Db 10629 TCCGAGACGGTCTTGAGGGCTTACATGATCACTTCGC 10592

RESULT 10
US-10-688-489-101/c
; Sequence 101, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 101
; LENGTH: 87
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-101

Query Match      68.8%; Score 33; DB 18; Length 87;
Best Local Similarity 100.0%; Pred. No. 6.8e-10;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACGGTCTTGAGGGCTTACATGATCACTTCGC 38
Db 87 GACGGTCTTGAGGGCTTACATGATCACTTCGC 55

RESULT 11
US-10-688-489-74
; Sequence 74, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16

; CURRENT FILING DATE: 2003-11-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: west Nile virus
US-10-706-892-1

Query Match      79.2%; Score 38; DB 19; Length 11029;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTTGAGGGCTTACATGATCACTTCGC 38
Db 10629 TCCGAGACGGTCTTGAGGGCTTACATGATCACTTCGC 10592

RESULT 10
US-10-688-489-101/c
; Sequence 101, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 101
; LENGTH: 87
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-101

Query Match      68.8%; Score 33; DB 18; Length 87;
Best Local Similarity 100.0%; Pred. No. 6.8e-10;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACGGTCTTGAGGGCTTACATGATCACTTCGC 38
Db 87 GACGGTCTTGAGGGCTTACATGATCACTTCGC 55

RESULT 11
US-10-688-489-74
; Sequence 74, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16

; CURRENT FILING DATE: 2003-11-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: west Nile virus
US-10-706-892-1

Query Match      79.2%; Score 38; DB 19; Length 11029;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTTGAGGGCTTACATGATCACTTCGC 38
Db 10629 TCCGAGACGGTCTTGAGGGCTTACATGATCACTTCGC 10592

RESULT 10
US-10-688-489-101/c
; Sequence 101, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 75
; LENGTH: 24
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-75

Query Match      50.0%; Score 24; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTTGAGGGCTTAC 24
Db 1 TCCGAGACGGTCTTGAGGGCTTAC 24

RESULT 12
US-10-688-489-75
; Sequence 75, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 75
; LENGTH: 24
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-75

Query Match      50.0%; Score 24; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTTGAGGGCTTAC 24
Db 1 TCCGAGACGGTCTTGAGGGCTTAC 24

RESULT 13
US-10-815-480-1/c
; Sequence 1, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K. Y.
; APPLICANT: Roche Molecular Systems, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; TITLE OF INVENTION: Encephalitis Virus Serogroup
; FILE REFERENCE: 022101-000230US
; CURRENT APPLICATION NUMBER: US/10/815,480
```

; CURRENT FILING DATE: 2004-03-31  
; PRIOR APPLICATION NUMBER: US 60/459,491  
; PRIOR FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/552,454  
; PRIOR FILING DATE: 2004-03-12  
; PRIOR APPLICATION NUMBER: US 60/555,530  
; PRIOR FILING DATE: 2004-03-22  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:region of  
; OTHER INFORMATION: conserved sequence in 3' untranslated region of  
; OTHER INFORMATION: the genomes of flaviviruses  
US-10-815-480-1

Query Match 50.0%; Score 24; DB 18; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.00021;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCGAGGGCTTAC 24  
|||  
Db 24 TCCGAGACGGTTCGAGGGCTTAC 1

RESULT 14  
US-10-815-480-2  
; Sequence 2, Application US/10815480  
; Publication No. US20040229261A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Karen K. Y.  
; APPLICANT: Roche Molecular Systems, Inc.  
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain  
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese  
; TITLE OF INVENTION: Encephalitis Virus Serogroup  
; FILE REFERENCE: 022101-000230US  
; CURRENT APPLICATION NUMBER: US/10/815,480  
; CURRENT FILING DATE: 2004-03-31  
; PRIOR APPLICATION NUMBER: US 60/459,491  
; PRIOR FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/552,454  
; PRIOR FILING DATE: 2004-03-12  
; PRIOR APPLICATION NUMBER: US 60/555,530  
; PRIOR FILING DATE: 2004-03-22  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:complement to  
; OTHER INFORMATION: SEQ ID NO:1  
US-10-815-480-2

Query Match 50.0%; Score 24; DB 18; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.00021;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCGAGGGCTTAC 24  
|||  
Db 2 TCCGAGACGGTTCGAGGGCTTAC 25

RESULT 15  
US-10-815-480-7/c  
; Sequence 7, Application US/10815480  
; Publication No. US20040229261A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Karen K. Y.

; APPLICANT: Roche Molecular Systems, Inc.  
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain  
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese  
; TITLE OF INVENTION: Encephalitis Virus Serogroup  
; FILE REFERENCE: 022101-000230US  
; CURRENT APPLICATION NUMBER: US/10/815,480  
; CURRENT FILING DATE: 2004-03-31  
; PRIOR APPLICATION NUMBER: US 60/459,491  
; PRIOR FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/552,454  
; PRIOR FILING DATE: 2004-03-12  
; PRIOR APPLICATION NUMBER: US 60/555,530  
; PRIOR FILING DATE: 2004-03-22  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Koutango virus  
; OTHER INFORMATION: Primer 1  
US-10-815-480-7

Query Match 50.0%; Score 24; DB 18; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.00021;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCGAGGGCTTAC 24  
|||  
Db 24 TCCGAGACGGTTCGAGGGCTTAC 1

RESULT 16  
US-10-815-480-8/c  
; Sequence 8, Application US/10815480  
; Publication No. US20040229261A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Karen K. Y.  
; APPLICANT: Roche Molecular Systems, Inc.  
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain  
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese  
; TITLE OF INVENTION: Encephalitis Virus Serogroup  
; FILE REFERENCE: 022101-000230US  
; CURRENT APPLICATION NUMBER: US/10/815,480  
; CURRENT FILING DATE: 2004-03-31  
; PRIOR APPLICATION NUMBER: US 60/459,491  
; PRIOR FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/552,454  
; PRIOR FILING DATE: 2004-03-12  
; PRIOR APPLICATION NUMBER: US 60/555,530  
; PRIOR FILING DATE: 2004-03-22  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Example Primer  
; OTHER INFORMATION: 1  
US-10-815-480-8

Query Match 50.0%; Score 24; DB 18; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.00021;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCGAGGGCTTAC 24  
|||  
Db 24 TCCGAGACGGTTCGAGGGCTTAC 1

RESULT 17

US-10-688-489-84  
; Sequence 84, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GP140-04 UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 84  
; LENGTH: 51  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(27)  
; OTHER INFORMATION: T7 promoter sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (28)...(51)  
; OTHER INFORMATION: WNV-complementary sequence  
US-10-688-489-84

Query Match 50.0%; Score 24; DB 18; Length 51;  
Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGCTTAC 24  
DB 28 TCCGAGACGGTCTGAGGCTTAC 51

RESULT 18  
US-10-688-489-76  
; Sequence 76, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GP140-04 UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 76  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: West Nile Virus  
US-10-688-489-76

Query Match 47.9%; Score 23; DB 18; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.00086;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGCTTA 23  
DB 1 TCCGAGACGGTCTGAGGCTTA 23

RESULT 19  
US-10-688-489-149  
; Sequence 149, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GP140-04 UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 149  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: West Nile Virus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(23)  
; OTHER INFORMATION: 2'-OME nucleotide analogs  
US-10-688-489-149

Query Match 47.9%; Score 23; DB 18; Length 23;  
Best Local Similarity 73.9%; Pred. No. 0.00086;  
Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTCTGAGGCTTACAT 26  
DB 1 GAGACGGTCTGAGGCTTACAU 23

RESULT 20  
US-10-688-489-85  
; Sequence 85, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GP140-04 UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
US-10-688-489-85

```
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(27)
; OTHER INFORMATION: T7 promoter sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28)..(50)
; OTHER INFORMATION: WNV-complementary sequence
US-10-688-489-85

Query Match      47.9%; Score 23; DB 18; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00083;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGCTTA 23
   |||||
Db 28 TCCGAGACGGTCTCGAGGCTTA 50

RESULT 21
US-10-688-489-77
; Sequence 77, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT FILING DATE: 2003-10-16
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 22
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-77

Query Match      45.8%; Score 22; DB 18; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGCTT 22
   |||||
Db 1 TCCGAGACGGTCTCGAGGCTT 22

RESULT 22
US-10-688-489-86
; Sequence 86, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT FILING DATE: 2003-10-16
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 36
; TYPE: RNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(36)
; OTHER INFORMATION: 2'-OME nucleotide analogs
US-10-688-489-195

Query Match      43.8%; Score 21; DB 18; Length 36;
Best Local Similarity 61.9%; Pred. No. 0.014;
Matches 13; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
```

```
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(27)
; OTHER INFORMATION: T7 promoter sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28)..(49)
; OTHER INFORMATION: WNV-complementary sequence
US-10-688-489-86
```

```
Query Match      45.8%; Score 22; DB 18; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGCTT 22
   |||||
Db 28 TCCGAGACGGTCTCGAGGCTT 49
```

```
RESULT 23
US-10-688-489-195
; Sequence 195, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 195
; LENGTH: 36
; TYPE: RNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(36)
; OTHER INFORMATION: 2'-OME nucleotide analogs
US-10-688-489-195
```

```
Query Match      43.8%; Score 21; DB 18; Length 36;
Best Local Similarity 61.9%; Pred. No. 0.014;
Matches 13; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
```

QY 28 GATCACTTCGACGCTTTGTC 48  
||:||||:||||:||||:||||:  
Db 1 GAUCACUUGCGAGCUUUGUC 21

RESULT 24  
US-10-706-892-2/c  
; Sequence 2, Application US/10706892  
; Publication No. US20050058987A1  
; GENERAL INFORMATION:  
; APPLICANT: SHI, PEI-YONG  
; TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY  
; FILE REFERENCE: 454311-2231.1  
; CURRENT APPLICATION NUMBER: US/10/706,892  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/427,117  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patentin Ver. 3.2  
; SEQ ID NO 2  
; LENGTH: 11029  
; TYPE: DNA  
; ORGANISM: West Nile virus  
US-10-706-892-2

Query Match 43.8%; Score 21; DB 19; Length 11029;  
Best Local Similarity 100.0%; Pred. No. 0.011; 0; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 0; Gaps 0;

QY 18 GCCTTACATGGATCACTTCGC 38  
|||||  
Db 10612 GCCTTACATGGATCACTTCGC 10592

RESULT 25  
US-10-688-489-116/c  
; Sequence 116, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Wu, Wen  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GP140-04.UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 116  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: West Nile Virus  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)-(19)  
; OTHER INFORMATION: 2'-OME nucleotide analogs  
US-10-688-489-116

Query Match 39.6%; Score 19; DB 18; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.23; 0; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 0; Gaps 0;

QY 6 GACGGTTCTGAGGGCTTAC 24  
|||||

Db 19 GACGGTTCTGAGGGCTTAC 1

RESULT 26  
US-10-688-489-114/c  
; Sequence 114, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GP140-04.UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 114  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: West Nile Virus  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)-(20)  
; OTHER INFORMATION: 2'-OME nucleotide analogs  
US-10-688-489-114

Query Match 37.5%; Score 18; DB 18; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.94; 0; Indels 0; Gaps 0;  
Matches 18; Conservative 0; Mismatches 0; Gaps 0;

QY 31 CACTTCGACGCTTTGTC 48  
|||||  
Db 20 CACTTCGACGCTTTGTC 3

RESULT 27  
US-10-688-489-196  
; Sequence 196, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GP140-04.UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 196  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: West Nile Virus  
; FEATURE:

; NAME/KEY: misc feature  
; LOCATION: (1)\_.(23)  
; OTHER INFORMATION: 2'-OME nucleotide analogs  
US-10-688-489-196

Query Match 33.3%; Score 16; DB 18; Length 23;  
Best Local Similarity 75.0%; Pred. No. 15;  
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 23 ACATGGATCACTTCGC 38  
|||:|:|:|:|:|:|  
Db 1 ACAUGGAUCAUCUUGC 16

## RESULT 28

US-09-987-899-5166  
; Sequence 5166, Application US/09987899  
; Publication No. US20040116682A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; FILE REFERENCE: 16517.258  
; CURRENT APPLICATION NUMBER: US/09/987,899  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 5166  
; LENGTH: 160  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700265822H1  
US-09-987-899-5166

Query Match 33.3%; Score 16; DB 11; Length 160;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37  
|||||:|:|:|:|:|:|  
Db 65 TACATGGATCACTTCG 80

## RESULT 29

US-09-987-899-5163  
; Sequence 5163, Application US/09987899  
; Publication No. US20040116682A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; FILE REFERENCE: 16517.258  
; CURRENT APPLICATION NUMBER: US/09/987,899  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 5163  
; LENGTH: 240  
; TYPE: DNA  
; ORGANISM: Zea mays

; FEATURE:  
; OTHER INFORMATION: Clone ID: 700167824H1  
US-09-987-899-5163

Query Match 33.3%; Score 16; DB 11; Length 240;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37  
|||||:|:|:|:|:|:|  
Db 43 TACATGGATCACTTCG 58

## RESULT 30

US-09-987-899-5161  
; Sequence 5161, Application US/09987899  
; Publication No. US20040116682A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; FILE REFERENCE: 16517.258  
; CURRENT APPLICATION NUMBER: US/09/987,899  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 5161  
; LENGTH: 256  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700029043H1  
US-09-987-899-5161

Query Match 33.3%; Score 16; DB 11; Length 256;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37  
|||||:|:|:|:|:|:|  
Db 8 TACATGGATCACTTCG 23

## RESULT 31

US-09-987-899-5159  
; Sequence 5159, Application US/09987899  
; Publication No. US20040116682A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; FILE REFERENCE: 16517.258  
; CURRENT APPLICATION NUMBER: US/09/987,899  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 5159  
; LENGTH: 274  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:

OTHER INFORMATION: Clone ID: 700574357H2  
US-09-987-899-5159

Query Match 33.3%; Score 16; DB 11; Length 274;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37  
|||||  
DB 95 TACATGGATCACTTCG 110  
|||||

## RESULT 32

US-09-987-899-5162  
; Sequence 5162, Application US/09987899  
; Publication No. US20040116682A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; TITLE OF INVENTION: With the Carbon Assimilation Pathway  
; FILE REFERENCE: 16517.258  
; CURRENT APPLICATION NUMBER: US/09/987,899  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 5162  
; LENGTH: 279  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700553323H1  
US-09-987-899-5162

Query Match 33.3%; Score 16; DB 11; Length 279;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37  
|||||  
DB 56 TACATGGATCACTTCG 71  
|||||

## RESULT 33

US-09-987-899-5157  
; Sequence 5157, Application US/09987899  
; Publication No. US20040116682A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; TITLE OF INVENTION: With the Carbon Assimilation Pathway  
; FILE REFERENCE: 16517.258  
; CURRENT APPLICATION NUMBER: US/09/987,899  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 5157  
; LENGTH: 313  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700077313H1

US-09-987-899-5157

Query Match 33.3%; Score 16; DB 11; Length 313;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37  
|||||  
DB 134 TACATGGATCACTTCG 149  
|||||

## RESULT 34

US-09-770-445-56  
; Sequence 56, Application US/09770445  
; Patent No. US20020023281A1  
; GENERAL INFORMATION:  
; APPLICANT: Goriach, Jorn  
; APPLICANT: An, Yong-Qiang  
; APPLICANT: Hamilton, Carol M.  
; APPLICANT: Price, Jennifer L.  
; APPLICANT: Raines, Tracy M.  
; APPLICANT: Yu, Yang  
; APPLICANT: Rameaka, Joshua G.  
; APPLICANT: Page, Amy  
; APPLICANT: Matthew, Abraham V.  
; APPLICANT: Ledford, Brooke L.  
; APPLICANT: Woessner, Jeffrey P.  
; APPLICANT: Haas, William David  
; APPLICANT: Garcia, Carlos A.  
; APPLICANT: Krickler, Maja  
; APPLICANT: Slader, Ted  
; APPLICANT: Davis, Keith R.  
; APPLICANT: Allen, Keith  
; APPLICANT: Hoffman, Neil  
; APPLICANT: Hurban, Patrick  
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
; TITLE OF INVENTION: thaliana  
; FILE REFERENCE: 2023US (PARA-012PRV)  
; CURRENT APPLICATION NUMBER: US/09/770,445  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/178,472  
; PRIOR FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 999  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 56  
; LENGTH: 1168  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(1168)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-770-445-56

Query Match 33.3%; Score 16; DB 9; Length 1168;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GCTTACATGGATCACT 34  
|||||  
DB 248 GCTTACATGGATCACT 263  
|||||

## RESULT 35

US-10-425-114-31937  
; Sequence 31937, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E

```
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 114
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 31937
; LENGTH: 1233
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73237H05_FLI
US-10-425-114-31937

Query Match      33.3%; Score 16; DB 17; Length 1233;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 TACATGGATCACTTCG 37
Db 58 TACATGGATCACTTCG 73

RESULT 36
US-10-024-130A-1/c
; Sequence 1, Application US/100241130A
; Publication No. US20030157583A1
; GENERAL INFORMATION:
; APPLICANT: Stevens, Donna
; APPLICANT: Wang, Michelle
; APPLICANT: Rice, John
; APPLICANT: Lanning, Beth
; APPLICANT: Broadwell, David
; APPLICANT: Glasbrook, No. US20030157583A1man
; APPLICANT: Sevala, Veeresh
; APPLICANT: Crawford, John
; APPLICANT: Stewart, Sandy
; TITLE OF INVENTION: METHODS FOR DETERMINING SQUALENE
; TITLE OF INVENTION: SYNTHASE ACTIVITY
; FILE REFERENCE: 2148US
; CURRENT APPLICATION NUMBER: US/10/024,130A
; CURRENT FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-024-130A-1

Query Match      33.3%; Score 16; DB 16; Length 1599;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GCTTACATGGATCACT 34
Db 1361 GCTTACATGGATCACT 1346

RESULT 37
US-10-425-114-33763
; Sequence 33763, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
```

```
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 33763
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLM017168D04_FLI
US-10-425-114-33763

Query Match      33.3%; Score 16; DB 17; Length 2000;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 TACATGGATCACTTCG 37
Db 834 TACATGGATCACTTCG 849

RESULT 38
US-10-425-114-1427
; Sequence 1427, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 1427
; LENGTH: 2401
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700152625_FLI
US-10-425-114-1427

Query Match      33.3%; Score 16; DB 17; Length 2401;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 TACATGGATCACTTCG 37
Db 1226 TACATGGATCACTTCG 1241

RESULT 39
US-10-437-963-42274
; Sequence 42274, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Li, Ping
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
```



; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 42274  
; LENGTH: 2973  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_45542C.1  
US-10-437-963-42274

Query Match 33.3%; Score 16; DB 18; Length 2973;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37  
|||  
DB 2051 TACATGGATCACTTCG 2066

RESULT 40  
US-10-425-114-4145  
; Sequence 4145, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 4145  
; LENGTH: 2989  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700349524\_FLI  
US-10-425-114-4145

Query Match 33.3%; Score 16; DB 17; Length 2989;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37  
|||  
DB 1850 TACATGGATCACTTCG 1865

RESULT 41  
US-10-425-114-1470  
; Sequence 1470, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 1470  
; LENGTH: 3244  
; TYPE: DNA  
; ORGANISM: Zea mays

; FEATURE:  
; OTHER INFORMATION: Clone ID: 700154435\_FLI  
US-10-425-114-1470

Query Match 33.3%; Score 16; DB 17; Length 3244;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37  
|||  
DB 2109 TACATGGATCACTTCG 2124

RESULT 42  
US-10-425-115-182436  
; Sequence 182436, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 182436  
; LENGTH: 3563  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)...(3563)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_97964C.1  
US-10-425-115-182436

Query Match 33.3%; Score 16; DB 18; Length 3563;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37  
|||  
DB 2146 TACATGGATCACTTCG 2161

RESULT 43  
US-10-437-963-42273  
; Sequence 42273, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 42273  
; LENGTH: 3858  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_45541C.1  
US-10-437-963-42273

Query Match 33.3%; Score 16; DB 18; Length 3858;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37  
|||||  
Db 2145 TACATGGATCACTTCG 2160

RESULT 44  
US-10-087-192-1129/c  
; Sequence 1129, Application US/10087192  
; Publication No. US20020182586A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
; TITLE OF INVENTION: CANCER  
; FILE REFERENCE: 529452000122  
; CURRENT APPLICATION NUMBER: US/10/087,192  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 2059  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1129  
; LENGTH: 57561  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(57561)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-087-192-1129

Query Match 33.3%; Score 16; DB 13; Length 57561;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CTATCATGGATCACTT 35  
|||||  
Db 258 CTATCATGGATCACTT 243

RESULT 45  
US-10-388-838-55  
; Sequence 55, Application US/10388838  
; Publication No. US20040180344A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc Malandro  
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer  
; FILE REFERENCE: 529452001600  
; CURRENT APPLICATION NUMBER: US/10/388,838  
; CURRENT FILING DATE: 2003-03-14  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 55  
; LENGTH: 94781  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(94781)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-388-838-55

Query Match 33.3%; Score 16; DB 18; Length 94781;

Best Local Similarity 100.0%; Pred. No. 11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GCGTTACATGGATCAC 33  
|||||  
Db 72560 GCGTTACATGGATCAC 72575

RESULT 46  
US-10-688-489-115/c  
; Sequence 115, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; TITLE OF INVENTION: West Nile Virus  
; FILE REFERENCE: GP140-04.0T  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 115  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: West Nile Virus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(20)  
; OTHER INFORMATION: 2'-OME nucleotide analogs  
US-10-688-489-115

Query Match 31.2%; Score 15; DB 18; Length 20;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 CATGGATCACTTCGC 38  
|||||  
Db 20 CATGGATCACTTCGC 6

RESULT 47  
US-10-688-489-103/c  
; Sequence 103, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; TITLE OF INVENTION: West Nile Virus  
; FILE REFERENCE: GP140-04.UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
US-10-688-489-103/c

; SEQ ID NO 103  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: West Nile Virus  
US-10-688-489-103

Query Match 31.2%; Score 15; DB 18; Length 52;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 CATGGATCACTTCGC 38  
|||  
DB 52 CATGGATCACTTCGC 38

RESULT 48

US-10-688-489-102/c  
; Sequence 102, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; TITLE OF INVENTION: West Nile Virus  
; FILE REFERENCE: GP140-04.UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 102  
; LENGTH: 69  
; TYPE: DNA  
; ORGANISM: West Nile Virus  
US-10-688-489-102

Query Match 31.2%; Score 15; DB 18; Length 69;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 CATGGATCACTTCGC 38  
|||  
DB 69 CATGGATCACTTCGC 55

RESULT 49

US-09-987-899-5802/c  
; Sequence 5802, Application US/09987899  
; Publication No. US20040116682A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; TITLE OF INVENTION: With the Carbon Assimilation Pathway  
; FILE REFERENCE: 16517.258  
; CURRENT APPLICATION NUMBER: US/09/987,899  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 5802

; LENGTH: 297  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700100107H1  
US-09-987-899-5802

Query Match 31.2%; Score 15; DB 11; Length 297;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 GGATCACTTCGCAGC 41  
|||  
DB 57 GGATCACTTCGCAGC 43

RESULT 50

US-09-987-899-5820/c  
; Sequence 5820, Application US/09987899  
; Publication No. US20040116682A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; TITLE OF INVENTION: With the Carbon Assimilation Pathway  
; FILE REFERENCE: 16517.258  
; CURRENT APPLICATION NUMBER: US/09/987,899  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 5820  
; LENGTH: 306  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700100451H1  
US-09-987-899-5820

Query Match 31.2%; Score 15; DB 11; Length 306;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 GGATCACTTCGCAGC 41  
|||  
DB 104 GGATCACTTCGCAGC 90

Search completed: March 25, 2005, 11:08:02  
Job time : 329.291 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 07:23:09 ; Search time 610.582 Seconds  
(without alignments)  
2460.130 Million cell updates/sec

Title: US-10-688-489-59  
Perfect score: 31  
Sequence: 1 tcgcgcacggaagttgagtagacggtgctg 31

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0  
Searched: 4708233 seqs, 24227607955 residues  
Word size : 0  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Listing first 500 summaries

## Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hgt:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sta:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 31    | 100.0       | 458    | 14 | AF458356 Kunjin vi |
| 2          | 31    | 100.0       | 462    | 14 | AF458350 West Nile |
| 3          | 31    | 100.0       | 463    | 14 | AF458343 West Nile |
| 4          | 31    | 100.0       | 463    | 14 | AF458344 West Nile |
| 5          | 31    | 100.0       | 463    | 14 | AF458347 West Nile |
| 6          | 31    | 100.0       | 463    | 14 | AF458348 West Nile |
| 7          | 31    | 100.0       | 463    | 14 | AF458355 West Nile |
| 8          | 31    | 100.0       | 545    | 14 | AF297850 Kunjin vi |
| 9          | 31    | 100.0       | 585    | 14 | AF297840 Kunjin vi |
| 10         | 31    | 100.0       | 593    | 14 | AF297847 Kunjin vi |
| 11         | 31    | 100.0       | 593    | 14 | AF297852 Kunjin vi |
| 12         | 31    | 100.0       | 594    | 14 | AF297853 Kunjin vi |
| 13         | 31    | 100.0       | 600    | 14 | AF297846 Kunjin vi |
| 14         | 31    | 100.0       | 616    | 14 | AF297845 Kunjin vi |
| 15         | 31    | 100.0       | 644    | 14 | AF297848 Kunjin vi |
| 16         | 31    | 100.0       | 657    | 14 | AF297849 Kunjin vi |
| 17         | 31    | 100.0       | 659    | 14 | AF196536 West Nile |
| 18         | 31    | 100.0       | 669    | 14 | AF196541 West Nile |
| 19         | 31    | 100.0       | 670    | 14 | AF196542 West Nile |

|    |    |       |       |    |                    |
|----|----|-------|-------|----|--------------------|
| 20 | 31 | 100.0 | 1524  | 14 | AF017254           |
| 21 | 31 | 100.0 | 10842 | 14 | AY278442 West Nile |
| 22 | 31 | 100.0 | 10845 | 14 | AY277252 West Nile |
| 23 | 31 | 100.0 | 10972 | 14 | AF317203 West Nile |
| 24 | 31 | 100.0 | 10984 | 14 | AY262283 West Nile |
| 25 | 31 | 100.0 | 10989 | 14 | AY268132 West Nile |
| 26 | 31 | 100.0 | 11029 | 14 | AF260968 West Nile |
| 27 | 31 | 100.0 | 11029 | 14 | AF260969 West Nile |
| 28 | 31 | 100.0 | 11029 | 14 | AF404757 West Nile |
| 29 | 30 | 96.8  | 456   | 14 | AF458351 Kunjin vi |
| 30 | 30 | 96.8  | 463   | 14 | AF458360 West Nile |
| 31 | 30 | 96.8  | 463   | 14 | AF458361 West Nile |
| 32 | 30 | 96.8  | 542   | 14 | AF297854 Kunjin vi |
| 33 | 30 | 96.8  | 587   | 14 | KUNNSGAB           |
| 34 | 30 | 96.8  | 587   | 14 | KUNNSGAB           |
| 35 | 30 | 96.8  | 601   | 14 | AF297844 Kunjin vi |
| 36 | 30 | 96.8  | 607   | 14 | AF297841 Kunjin vi |
| 37 | 30 | 96.8  | 609   | 14 | AF297856 Kunjin vi |
| 38 | 30 | 96.8  | 620   | 14 | AF297859 Kunjin vi |
| 39 | 30 | 96.8  | 622   | 14 | AF297842 Kunjin vi |
| 40 | 30 | 96.8  | 623   | 14 | AF297843 Kunjin vi |
| 41 | 30 | 96.8  | 627   | 14 | KUNNONCDB          |
| 42 | 30 | 96.8  | 633   | 14 | AF297858 Kunjin vi |
| 43 | 30 | 96.8  | 645   | 14 | AY187012 West Nile |
| 44 | 30 | 96.8  | 645   | 14 | AY187013 West Nile |
| 45 | 30 | 96.8  | 645   | 14 | AY187014 West Nile |
| 46 | 30 | 96.8  | 645   | 14 | AY187015 West Nile |
| 47 | 30 | 96.8  | 652   | 14 | AF297855 Kunjin vi |
| 48 | 30 | 96.8  | 10945 | 14 | AF202541 West Nile |
| 49 | 30 | 96.8  | 10975 | 14 | AF208518 West Nile |
| 50 | 30 | 96.8  | 10989 | 14 | AY268133 West Nile |
| 51 | 30 | 96.8  | 10998 | 14 | AY278441 West Nile |
| 52 | 30 | 96.8  | 11022 | 14 | AY274504 Kunjin vi |
| 53 | 30 | 96.8  | 11022 | 14 | AY274505 Kunjin vi |
| 54 | 30 | 96.8  | 11029 | 6  | AX576542 Sequence  |
| 55 | 30 | 96.8  | 11029 | 6  | AX577796 Sequence  |
| 56 | 30 | 96.8  | 11029 | 14 | AB185914 West Nile |
| 57 | 30 | 96.8  | 11029 | 14 | AB185915 West Nile |
| 58 | 30 | 96.8  | 11029 | 14 | AB185916 West Nile |
| 59 | 30 | 96.8  | 11029 | 14 | AB185917 West Nile |
| 60 | 30 | 96.8  | 11029 | 14 | AF196835 West Nile |
| 61 | 30 | 96.8  | 11029 | 14 | AF260967 West Nile |
| 62 | 30 | 96.8  | 11029 | 14 | AF404753 West Nile |
| 63 | 30 | 96.8  | 11029 | 14 | AF404754 West Nile |
| 64 | 30 | 96.8  | 11029 | 14 | AF404755 West Nile |
| 65 | 30 | 96.8  | 11029 | 14 | AF404756 West Nile |
| 66 | 30 | 96.8  | 11029 | 14 | AF481864 West Nile |
| 67 | 30 | 96.8  | 11029 | 14 | AF533540 West Nile |
| 68 | 30 | 96.8  | 11029 | 14 | AY289214 West Nile |
| 69 | 29 | 93.5  | 464   | 14 | AY590190 West Nile |
| 70 | 29 | 93.5  | 464   | 14 | AY590191 West Nile |
| 71 | 29 | 93.5  | 464   | 14 | AY590192 West Nile |
| 72 | 29 | 93.5  | 464   | 14 | AY590193 West Nile |
| 73 | 29 | 93.5  | 464   | 14 | AY590194 West Nile |
| 74 | 29 | 93.5  | 464   | 14 | AY590195 West Nile |
| 75 | 29 | 93.5  | 464   | 14 | AY590196 West Nile |
| 76 | 29 | 93.5  | 464   | 14 | AY590197 West Nile |
| 77 | 29 | 93.5  | 464   | 14 | AY590198 West Nile |
| 78 | 29 | 93.5  | 464   | 14 | AY590199 West Nile |
| 79 | 29 | 93.5  | 464   | 14 | AY590200 West Nile |
| 80 | 29 | 93.5  | 464   | 14 | AY590201 West Nile |
| 81 | 29 | 93.5  | 464   | 14 | AY590202 West Nile |
| 82 | 29 | 93.5  | 464   | 14 | AY590203 West Nile |
| 83 | 29 | 93.5  | 464   | 14 | AY590204 West Nile |
| 84 | 29 | 93.5  | 464   | 14 | AY590205 West Nile |
| 85 | 29 | 93.5  | 464   | 14 | AY590206 West Nile |
| 86 | 29 | 93.5  | 464   | 14 | AY590207 West Nile |
| 87 | 29 | 93.5  | 464   | 14 | AY590208 West Nile |
| 88 | 29 | 93.5  | 464   | 14 | AY590209 West Nile |
| 89 | 28 | 90.3  | 395   | 14 | AF458358 West Nile |
| 90 | 28 | 90.3  | 481   | 14 | AF458359 West Nile |
| 91 | 28 | 90.3  | 483   | 14 | AF458345 West Nile |
| 92 | 28 | 90.3  | 483   | 14 | AF458357 West Nile |

|     |    |      |        |    |          |                    |     |    |      |        |    |           |                     |
|-----|----|------|--------|----|----------|--------------------|-----|----|------|--------|----|-----------|---------------------|
| 93  | 28 | 90.3 | 484    | 14 | AF458354 | AF458354 West Nile | 166 | 15 | 48.4 | 3528   | 10 | MUSJAK3A  | L40172 Mus musculus |
| 94  | 28 | 90.3 | 497    | 14 | AF458346 | AF458346 West Nile | 167 | 15 | 48.4 | 3723   | 10 | MUSJAK3A  | L32955 Mouse prote  |
| 95  | 28 | 90.3 | 591    | 14 | AF196543 | AF196543 West Nile | 168 | 15 | 48.4 | 4016   | 10 | MUSJAK3H  | L33768 Mus musculus |
| 96  | 28 | 90.3 | 593    | 14 | AF196535 | L48977 West Nile v | 169 | 15 | 48.4 | 4638   | 1  | AB011811  | AB011811 Chromatiu  |
| 97  | 28 | 90.3 | 677    | 14 | AF196535 | AF196535 West Nile | 170 | 15 | 48.4 | 6794   | 1  | AE005671  | AE005671 Escherich  |
| 98  | 28 | 90.3 | 687    | 14 | AF196539 | AF196539 West Nile | 171 | 15 | 48.4 | 6947   | 1  | AB003398  | AB003398 Shewanell  |
| 99  | 28 | 90.3 | 917    | 14 | AF208017 | AF208017 West Nile | 172 | 15 | 48.4 | 10129  | 1  | AE006751  | AE006751 Sulfolobu  |
| 100 | 28 | 90.3 | 10962  | 14 | WNFGC    | ML2294 West Nile v | 173 | 15 | 48.4 | 10863  | 1  | AE005678  | AE005678 Caulobact  |
| 101 | 28 | 90.3 | 11057  | 14 | AF688948 | AY688948 West Nile | 174 | 15 | 48.4 | 15829  | 10 | MMU71201  | U71201 Mus musculus |
| 102 | 28 | 90.3 | 11064  | 14 | AY453412 | AY453412 Usutu vir | 175 | 15 | 48.4 | 31414  | 3  | CBF13557  | U41557 Caenorhabdi  |
| 103 | 28 | 90.3 | 11066  | 14 | AY453411 | AY453411 Usutu vir | 176 | 15 | 48.4 | 32320  | 3  | U68748    | Z68748 Caenorhabdi  |
| 104 | 27 | 87.1 | 583    | 14 | AF297857 | AF297857 Kunjin vi | 177 | 15 | 48.4 | 39330  | 3  | AC137816  | AC137816 Homo sapi  |
| 105 | 20 | 64.5 | 11028  | 14 | AY490240 | AY490240 West Nile | 178 | 15 | 48.4 | 42095  | 3  | DMC103E12 | AL132651 Drosophil  |
| 106 | 18 | 58.1 | 451    | 14 | AF458352 | AF458352 West Nile | 179 | 15 | 48.4 | 57213  | 2  | AC104415  | AC104415 Mus muscu  |
| 107 | 18 | 58.1 | 481    | 14 | AF458349 | AF458349 West Nile | 180 | 15 | 48.4 | 76052  | 2  | AC151322  | AC151322 Xenopus t  |
| 108 | 18 | 58.1 | 604    | 14 | KUNNS    | L49311 Kunjin viru | 181 | 15 | 48.4 | 91654  | 9  | AL357118  | AL357118 Human DNA  |
| 109 | 18 | 58.1 | 644    | 14 | AF196538 | AF196538 West Nile | 182 | 15 | 48.4 | 92911  | 2  | AC020218  | AC020218 Drosophil  |
| 110 | 18 | 58.1 | 648    | 14 | AF196540 | AF196540 West Nile | 183 | 15 | 48.4 | 103061 | 2  | AC151680  | AC151680 Gallus ga  |
| 111 | 17 | 54.8 | 35652  | 2  | AC017428 | AC017428 Drosophil | 184 | 15 | 48.4 | 110000 | 2  | AC108998  | Continuation (3 of  |
| 112 | 17 | 54.8 | 52872  | 6  | CQ576911 | AC007532 Sequence  | 185 | 15 | 48.4 | 110000 | 2  | AP006499  | Continuation (7 of  |
| 113 | 17 | 54.8 | 171105 | 3  | AC007532 | AC007532 Drosophil | 186 | 15 | 48.4 | 110000 | 2  | EX927234  | Continuation (3 of  |
| 114 | 17 | 54.8 | 181009 | 3  | AC007535 | AC007535 Drosophil | 187 | 15 | 48.4 | 110000 | 8  | CR382137  | CR382137 Debaryomy  |
| 115 | 17 | 54.8 | 295289 | 3  | AE003603 | AE003603 Drosophil | 188 | 15 | 48.4 | 110000 | 8  | CR382138  | Continuation (2 of  |
| 116 | 16 | 51.6 | 463    | 14 | AY278556 | AY278556 Japanese  | 189 | 15 | 48.4 | 114946 | 2  | AC151691  | AC151691 Gallus ga  |
| 117 | 16 | 51.6 | 572    | 14 | AF306514 | AF306514 Japanese  | 190 | 15 | 48.4 | 115603 | 2  | AC069498  | AC069498 Mus muscu  |
| 118 | 16 | 51.6 | 1323   | 6  | AX663976 | AX663976 Sequence  | 191 | 15 | 48.4 | 128469 | 2  | AC020029  | AC020029 Drosophil  |
| 119 | 16 | 51.6 | 3691   | 10 | AB041543 | AB041543 Mus muscu | 192 | 15 | 48.4 | 134728 | 8  | AC090683  | AC090683 Oryza sat  |
| 120 | 16 | 51.6 | 3986   | 10 | BC066816 | BC066816 Mus muscu | 193 | 15 | 48.4 | 135825 | 10 | AL645760  | AL645760 Mouse DNA  |
| 121 | 16 | 51.6 | 4000   | 10 | AK128931 | AK128931 Mus muscu | 194 | 15 | 48.4 | 137081 | 8  | AP003866  | AP003866 Oryza sat  |
| 122 | 16 | 51.6 | 5753   | 10 | AK173281 | AK173281 Mus muscu | 195 | 15 | 48.4 | 137132 | 9  | AC136628  | AC136628 Homo sapi  |
| 123 | 16 | 51.6 | 10664  | 14 | KUNCG    | D00246 Kunjin viru | 196 | 15 | 48.4 | 139182 | 9  | AC109917  | AC109917 Bos tauru  |
| 124 | 16 | 51.6 | 10741  | 14 | AY277251 | AY277251 West Nile | 197 | 15 | 48.4 | 140306 | 9  | HS1068F16 | AL023913 Human DNA  |
| 125 | 16 | 51.6 | 10963  | 14 | AF045551 | AF045551 Japanese  | 198 | 15 | 48.4 | 145154 | 2  | AF004400  | AP004400 Oryza sat  |
| 126 | 16 | 51.6 | 10963  | 14 | AF316157 | AF316157 Japanese  | 199 | 15 | 48.4 | 147702 | 2  | AC109918  | AC109918 Bos tauru  |
| 127 | 16 | 51.6 | 10965  | 14 | AB051292 | AB051292 Japanese  | 200 | 15 | 48.4 | 148852 | 9  | AC005878  | AC005878 citb 255   |
| 128 | 16 | 51.6 | 18385  | 1  | MAD7PMMO | BX649604 Methyloxy | 201 | 15 | 48.4 | 149615 | 2  | CR388383  | CR388383 Danilo rer |
| 129 | 16 | 51.6 | 31068  | 6  | CQ612365 | CQ612365 Sequence  | 202 | 15 | 48.4 | 150313 | 9  | AC137672  | AC137672 Homo sapi  |
| 130 | 16 | 51.6 | 61969  | 2  | AC014103 | AC014103 Drosophil | 203 | 15 | 48.4 | 152383 | 9  | H5F18108  | AP006595 Homo sapi  |
| 131 | 16 | 51.6 | 63314  | 2  | AC017803 | AC017803 Drosophil | 204 | 15 | 48.4 | 153894 | 8  | AP005468  | AP005468 Oryza sat  |
| 132 | 16 | 51.6 | 110000 | 1  | AE000516 | Continuation (15 o | 205 | 15 | 48.4 | 158312 | 2  | AC083922  | AC083922 Homo sapi  |
| 133 | 16 | 51.6 | 110000 | 2  | CR762462 | Continuation (2 of | 206 | 15 | 48.4 | 160770 | 9  | AC010336  | AC010336 Homo sapi  |
| 134 | 16 | 51.6 | 124372 | 10 | AC012104 | AC012104 Mus muscu | 207 | 15 | 48.4 | 163998 | 9  | AC022166  | AC022166 Homo sapi  |
| 135 | 16 | 51.6 | 139885 | 5  | AC009232 | AC009232 Homo sapi | 208 | 15 | 48.4 | 165002 | 2  | AL355814  | AL355814 Homo sapi  |
| 136 | 16 | 51.6 | 150975 | 5  | BX088694 | BX088694 Zebrafish | 209 | 15 | 48.4 | 167065 | 2  | AC150567  | AC150567 Bos tauru  |
| 137 | 16 | 51.6 | 158646 | 9  | AC142307 | AC142307 Pan trogl | 210 | 15 | 48.4 | 168764 | 1  | AP002569  | AP002569 Escherich  |
| 138 | 16 | 51.6 | 163933 | 5  | AL929559 | AL929559 Zebrafish | 211 | 15 | 48.4 | 169557 | 3  | AC104287  | AC104287 Drosophil  |
| 139 | 16 | 51.6 | 163970 | 3  | AC010580 | AC010580 Drosophil | 212 | 15 | 48.4 | 169623 | 10 | AC131581  | AC131581 Mus muscu  |
| 140 | 16 | 51.6 | 169271 | 3  | AC009916 | AC009916 Drosophil | 213 | 15 | 48.4 | 172061 | 3  | AC009203  | AC009203 Drosophil  |
| 141 | 16 | 51.6 | 169902 | 3  | AC008209 | AC008209 Drosophil | 214 | 15 | 48.4 | 173603 | 10 | AC132222  | AC132222 Mus muscu  |
| 142 | 16 | 51.6 | 176317 | 2  | AL670857 | AL670857 Mus muscu | 215 | 15 | 48.4 | 176769 | 5  | BX539308  | BX539308 Zebrafish  |
| 143 | 16 | 51.6 | 186802 | 5  | BX908803 | BX908803 Zebrafish | 216 | 15 | 48.4 | 177622 | 2  | AC023559  | AC023559 Homo sapi  |
| 144 | 16 | 51.6 | 189862 | 2  | AC108317 | AC108317 Rattus no | 217 | 15 | 48.4 | 177641 | 10 | AC146296  | AC146296 Homo sapi  |
| 145 | 16 | 51.6 | 215711 | 3  | AC008205 | AC008205 Drosophil | 218 | 15 | 48.4 | 177862 | 9  | AC084782  | AC084782 Homo sapi  |
| 146 | 16 | 51.6 | 226793 | 3  | AE003753 | AE003753 Drosophil | 219 | 15 | 48.4 | 177911 | 1  | AB017206  | AB017206 Lactobaci  |
| 147 | 16 | 51.6 | 228433 | 3  | AE003749 | AE003749 Drosophil | 220 | 15 | 48.4 | 178501 | 2  | AL392165  | AL392165 Homo sapi  |
| 148 | 16 | 51.6 | 231807 | 5  | EX000529 | EX000529 Zebrafish | 221 | 15 | 48.4 | 180571 | 9  | AC113425  | AC113425 Homo sapi  |
| 149 | 16 | 51.6 | 233428 | 2  | AC011064 | AC011064 Drosophil | 222 | 15 | 48.4 | 183043 | 6  | AX926717  | AX926717 Sequence   |
| 150 | 16 | 51.6 | 237686 | 2  | AC129817 | AC129817 Rattus no | 223 | 15 | 48.4 | 183095 | 8  | AP005186  | AP005186 Oryza sat  |
| 151 | 16 | 51.6 | 269675 | 2  | AC094496 | AC094496 Rattus no | 224 | 15 | 48.4 | 185580 | 2  | AC123732  | AC123732 Mus muscu  |
| 152 | 16 | 51.6 | 299450 | 1  | BX248338 | BX248338 Mycobacte | 225 | 15 | 48.4 | 185867 | 10 | AL606744  | AL606744 Mouse DNA  |
| 153 | 16 | 51.6 | 307337 | 1  | BX842856 | BX842856 Bdellovib | 226 | 15 | 48.4 | 185953 | 2  | AC136593  | AC136593 Homo sapi  |
| 154 | 16 | 51.6 | 348264 | 1  | BR246572 | BR246572 Mycobacte | 227 | 15 | 48.4 | 189186 | 2  | AC115861  | AC115861 Mus muscu  |
| 155 | 15 | 48.4 | 436    | 6  | AR305566 | AR305566 Sequence  | 228 | 15 | 48.4 | 189308 | 9  | AC068726  | AC068726 Homo sapi  |
| 156 | 15 | 48.4 | 600    | 8  | BT008964 | BT008964 Tricicum  | 229 | 15 | 48.4 | 190628 | 2  | AC024700  | AC024700 Homo sapi  |
| 157 | 15 | 48.4 | 606    | 8  | AR305579 | AR305579 Sequence  | 230 | 15 | 48.4 | 192199 | 2  | AC139312  | AC139312 Bos tauru  |
| 158 | 15 | 48.4 | 616    | 6  | AR305576 | AR305576 Sequence  | 231 | 15 | 48.4 | 195966 | 10 | AC125058  | AC125058 Mus muscu  |
| 159 | 15 | 48.4 | 606    | 8  | BT008964 | BT008964 Tricicum  | 232 | 15 | 48.4 | 200393 | 2  | AC150994  | AC150994 Bos tauru  |
| 160 | 15 | 48.4 | 616    | 6  | AR305576 | AR305576 Sequence  | 233 | 15 | 48.4 | 201720 | 10 | AL670778  | AL670778 Mouse DNA  |
| 161 | 15 | 48.4 | 673    | 6  | AR305575 | AR305575 Sequence  | 234 | 15 | 48.4 | 204513 | 2  | AC150900  | AC150900 Mus muscu  |
| 162 | 15 | 48.4 | 780    | 8  | CNS01BVP | BD162638 Novel pol | 235 | 15 | 48.4 | 205725 | 10 | AC122928  | AC122928 Mus muscu  |
| 163 | 15 | 48.4 | 1863   | 6  | BD162638 | BD162638 Novel pol | 236 | 15 | 48.4 | 206167 | 2  | AC113586  | AC113586 Mus muscu  |
| 164 | 15 | 48.4 | 1969   | 6  | AX120521 | AX120521 Sequence  | 237 | 15 | 48.4 | 207298 | 2  | AC136631  | AC136631 Homo sapi  |
| 165 | 15 | 48.4 | 2399   | 8  | PHCHIA   | AX173825 Sequence  | 238 | 15 | 48.4 | 207890 | 2  | AC102521  | AC102521 Mus muscu  |
|     |    |      |        |    |          | XL4589 Petunia CHI |     |    |      |        |    |           |                     |

|       |    |      |        |    |           |                    |       |    |      |      |    |                              |
|-------|----|------|--------|----|-----------|--------------------|-------|----|------|------|----|------------------------------|
| C 239 | 15 | 48.4 | 214508 | 2  | AC103532  | AC103532 Rattus no | 312   | 14 | 45.2 | 522  | 12 | AY202600 Arabidops           |
| C 240 | 15 | 48.4 | 215391 | 2  | AC120168  | Mus muscu          | C 313 | 14 | 45.2 | 536  | 6  | AR426219 Sequence            |
| C 241 | 15 | 48.4 | 216912 | 2  | AC114349  | Rattus no          | C 314 | 14 | 45.2 | 536  | 6  | AX986913 Sequence            |
| C 242 | 15 | 48.4 | 217459 | 2  | AC138998  | Homo sapi          | C 315 | 14 | 45.2 | 536  | 6  | BD121772 EST and e           |
| C 243 | 15 | 48.4 | 217585 | 2  | AC123325  | Rattus no          | C 316 | 14 | 45.2 | 562  | 14 | L48980 Koutango vi           |
| C 244 | 15 | 48.4 | 218208 | 2  | AC073700  | Mus muscu          | C 317 | 14 | 45.2 | 564  | 6  | AX896241 Sequence            |
| C 245 | 15 | 48.4 | 220632 | 2  | AC136596  | Homo sapi          | C 318 | 14 | 45.2 | 564  | 6  | BD031774 Sequence            |
| C 246 | 15 | 48.4 | 223274 | 2  | AC112443  | Rattus no          | C 319 | 14 | 45.2 | 579  | 6  | AR414185 Sequence            |
| C 247 | 15 | 48.4 | 223374 | 2  | AC1073750 | Mus muscu          | C 320 | 14 | 45.2 | 579  | 6  | AX971019 Sequence            |
| C 248 | 15 | 48.4 | 224040 | 2  | AC107566  | Rattus no          | C 321 | 14 | 45.2 | 579  | 6  | BD109738 EST and e           |
| C 249 | 15 | 48.4 | 224499 | 14 | AF482758  | Compox vi          | C 322 | 14 | 45.2 | 696  | 11 | BV076460 S212P6548           |
| C 250 | 15 | 48.4 | 224721 | 2  | AC139632  | Bos tauru          | C 323 | 14 | 45.2 | 822  | 11 | BV016791 S212P6528           |
| C 251 | 15 | 48.4 | 224821 | 2  | AC096276  | Rattus no          | C 324 | 14 | 45.2 | 884  | 8  | AY202271 Arabidops           |
| C 252 | 15 | 48.4 | 224859 | 2  | AC073800  | Mus muscu          | C 325 | 14 | 45.2 | 941  | 6  | CQ818142 Sequence            |
| C 253 | 15 | 48.4 | 227299 | 10 | AC138722  | AC138722 Mus muscu | C 326 | 14 | 45.2 | 977  | 8  | BT014412 Lycopersi           |
| C 254 | 15 | 48.4 | 228851 | 10 | AC123616  | Mus muscu          | C 327 | 14 | 45.2 | 1047 | 5  | AY225729 Micropter           |
| C 255 | 15 | 48.4 | 230200 | 2  | AC129375  | Rattus no          | C 328 | 14 | 45.2 | 1047 | 5  | AY225730 Micropter           |
| C 256 | 15 | 48.4 | 230236 | 10 | AC093366  | Mus muscu          | C 329 | 14 | 45.2 | 1047 | 5  | AY225731 Micropter           |
| C 257 | 15 | 48.4 | 231096 | 2  | AC125549  | Rattus no          | C 330 | 14 | 45.2 | 1047 | 5  | AY225732 Micropter           |
| C 258 | 15 | 48.4 | 232737 | 3  | AE003660  | Drosophill         | C 331 | 14 | 45.2 | 1047 | 5  | AY225733 Micropter           |
| C 259 | 15 | 48.4 | 234160 | 2  | AC103270  | Rattus no          | C 332 | 14 | 45.2 | 1047 | 5  | AY225734 Micropter           |
| C 260 | 15 | 48.4 | 234598 | 2  | AC115507  | Rattus no          | C 333 | 14 | 45.2 | 1100 | 10 | AF290194 Rattus no           |
| C 261 | 15 | 48.4 | 237222 | 2  | AC121742  | Rattus no          | C 334 | 14 | 45.2 | 1138 | 8  | AK104811 Oryza sat           |
| C 262 | 15 | 48.4 | 247577 | 2  | AC106930  | Rattus no          | C 335 | 14 | 45.2 | 1144 | 8  | AK066070 Oryza sat           |
| C 263 | 15 | 48.4 | 248475 | 2  | AC094641  | Rattus no          | C 336 | 14 | 45.2 | 1162 | 8  | AK108584 Oryza sat           |
| C 264 | 15 | 48.4 | 253169 | 2  | AC094461  | Rattus no          | C 337 | 14 | 45.2 | 1225 | 9  | HS329217 Homo sapi           |
| C 265 | 15 | 48.4 | 269195 | 2  | AC111879  | Rattus no          | C 338 | 14 | 45.2 | 1257 | 5  | DREVK2 X99290 D.terio Evx    |
| C 266 | 15 | 48.4 | 277935 | 1  | AC132671  | Rattus no          | C 339 | 14 | 45.2 | 1278 | 5  | XLU10161 U10161 Xenopus lae  |
| C 267 | 15 | 48.4 | 300350 | 1  | AP006574  | Gloeobact          | C 340 | 14 | 45.2 | 1320 | 12 | AF265109 Synthetic           |
| C 268 | 15 | 48.4 | 306598 | 3  | AB003419  | Drosophill         | C 341 | 14 | 45.2 | 1330 | 5  | BC049528 Dancio rer          |
| C 269 | 15 | 48.4 | 318862 | 2  | AC109547  | Rattus no          | C 342 | 14 | 45.2 | 1360 | 12 | AF265113 Synthetic           |
| C 270 | 15 | 48.4 | 328050 | 1  | AP005275  | AP005275 Coryneb   | C 343 | 14 | 45.2 | 1362 | 12 | AF265114 Synthetic           |
| C 271 | 15 | 48.4 | 340000 | 9  | HS21C046  | AL163246 Homo sapi | C 344 | 14 | 45.2 | 1363 | 12 | AF265112 Synthetic           |
| C 272 | 15 | 48.4 | 349174 | 1  | AB063522  | Wiggleswo          | C 345 | 14 | 45.2 | 1377 | 8  | AK108672 Oryza sat           |
| C 273 | 15 | 48.4 | 349887 | 1  | BX927149  | Coryneb            | C 346 | 14 | 45.2 | 1451 | 1  | AY697896 Unculture           |
| C 274 | 15 | 48.4 | 349980 | 6  | AX127144  | Sequence           | C 347 | 14 | 45.2 | 1473 | 8  | AY692997 Saccharom           |
| C 275 | 14 | 45.2 | 127    | 6  | CQ430592  | Sequence           | C 348 | 14 | 45.2 | 1569 | 8  | AK106909 Oryza sat           |
| C 276 | 14 | 45.2 | 151    | 6  | AX245342  | Sequence           | C 349 | 14 | 45.2 | 1676 | 8  | AF445196 Musa acum           |
| C 277 | 14 | 45.2 | 220    | 6  | BD077014  | 5' EST of          | C 350 | 14 | 45.2 | 1738 | 9  | HS984G1A AL050346 Novel hum  |
| C 278 | 14 | 45.2 | 223    | 6  | AX426218  | Sequence           | C 351 | 14 | 45.2 | 1841 | 14 | AJ7811402 Cherry ch          |
| C 279 | 14 | 45.2 | 223    | 6  | AX986912  | Sequence           | C 352 | 14 | 45.2 | 1844 | 9  | HSCOMT1 Z26490 H.sapiens C   |
| C 280 | 14 | 45.2 | 223    | 6  | BD121771  | EST and e          | C 353 | 14 | 45.2 | 1854 | 6  | AX834969 Sequence            |
| C 281 | 14 | 45.2 | 231    | 6  | CQ421725  | Sequence           | C 354 | 14 | 45.2 | 1854 | 9  | AK097708 Homo sapi           |
| C 282 | 14 | 45.2 | 236    | 6  | BD204219  | 5' EST and         | C 355 | 14 | 45.2 | 1865 | 9  | HUMCOMT L43122 Homo sapien   |
| C 283 | 14 | 45.2 | 348    | 14 | HCU56588  | U56588 Hepatitis C | C 356 | 14 | 45.2 | 1931 | 8  | AB019694 Homo sapi           |
| C 284 | 14 | 45.2 | 348    | 14 | HCU56589  | Hepatitis C        | C 357 | 14 | 45.2 | 1938 | 8  | AK109643 Oryza sat           |
| C 285 | 14 | 45.2 | 348    | 14 | HCU56590  | Hepatitis C        | C 358 | 14 | 45.2 | 1944 | 10 | WINKERA V00830 Mouse mRNA    |
| C 286 | 14 | 45.2 | 348    | 14 | HCU56594  | Hepatitis C        | C 359 | 14 | 45.2 | 1950 | 9  | AF171054 Homo sapi           |
| C 287 | 14 | 45.2 | 348    | 14 | HCU56595  | Hepatitis C        | C 360 | 14 | 45.2 | 1955 | 6  | AX195192 Sequence            |
| C 288 | 14 | 45.2 | 348    | 14 | HCU56601  | Hepatitis C        | C 361 | 14 | 45.2 | 1960 | 9  | AF044212 Homo sapi           |
| C 289 | 14 | 45.2 | 370    | 6  | CQ477062  | Sequence           | C 362 | 14 | 45.2 | 2010 | 6  | CQ602835 Sequence            |
| C 290 | 14 | 45.2 | 390    | 6  | CQ709746  | Sequence           | C 363 | 14 | 45.2 | 2084 | 11 | BV177077 sqm92606            |
| C 291 | 14 | 45.2 | 400    | 6  | BD076285  | 5' EST of          | C 364 | 14 | 45.2 | 2084 | 11 | BV177509 sqm95100            |
| C 292 | 14 | 45.2 | 406    | 9  | AF086763  | Homo sapi          | C 365 | 14 | 45.2 | 2084 | 11 | BV179316 sqmml0484           |
| C 293 | 14 | 45.2 | 409    | 6  | CQ729638  | Sequence           | C 366 | 14 | 45.2 | 2099 | 1  | PAFGK979 X98465 Pseudomonas  |
| C 294 | 14 | 45.2 | 419    | 6  | AR177398  | Sequence           | C 367 | 14 | 45.2 | 2113 | 6  | CQ716679 Sequence            |
| C 295 | 14 | 45.2 | 419    | 6  | BD132537  | Secreted           | C 368 | 14 | 45.2 | 2165 | 3  | AF145658 Drosophill          |
| C 296 | 14 | 45.2 | 419    | 6  | BD131472  | CDNA enco          | C 369 | 14 | 45.2 | 2180 | 9  | AF106697 Homo sapi           |
| C 297 | 14 | 45.2 | 425    | 6  | AR177379  | Sequence           | C 370 | 14 | 45.2 | 2184 | 9  | BC035394 Homo sapi           |
| C 298 | 14 | 45.2 | 425    | 6  | BD131453  | CDNA enco          | C 371 | 14 | 45.2 | 2187 | 6  | AR207293 Sequence            |
| C 299 | 14 | 45.2 | 427    | 6  | CQ506978  | Sequence           | C 372 | 14 | 45.2 | 2194 | 8  | SPIC70A L26343 Spiniacia ol  |
| C 300 | 14 | 45.2 | 440    | 6  | AR426220  | Sequence           | C 373 | 14 | 45.2 | 2262 | 1  | AF276976 Pseudom             |
| C 301 | 14 | 45.2 | 440    | 6  | AX986914  | Sequence           | C 374 | 14 | 45.2 | 2391 | 8  | AK073061 Oryza sat           |
| C 302 | 14 | 45.2 | 440    | 6  | BD121773  | EST and e          | C 375 | 14 | 45.2 | 2498 | 8  | AK109111 Oryza sat           |
| C 303 | 14 | 45.2 | 440    | 9  | BC015968  | Homo sapi          | C 376 | 14 | 45.2 | 2535 | 8  | SOSCE70 X61491 S.oleracea    |
| C 304 | 14 | 45.2 | 443    | 6  | AR509523  | Sequence           | C 377 | 14 | 45.2 | 2561 | 8  | SCYBR283C Z36152 S.cerevisia |
| C 305 | 14 | 45.2 | 446    | 14 | AY514902  | Fowl aden          | C 378 | 14 | 45.2 | 2571 | 3  | AY051852 Drosophill          |
| C 306 | 14 | 45.2 | 468    | 6  | AR425864  | Sequence           | C 379 | 14 | 45.2 | 2573 | 3  | DMU36584 U36584 Drosophila   |
| C 307 | 14 | 45.2 | 468    | 6  | AX986558  | Sequence           | C 380 | 14 | 45.2 | 2699 | 8  | SCU05336 U05336 Saccharomyc  |
| C 308 | 14 | 45.2 | 468    | 6  | BD121417  | EST and e          | C 381 | 14 | 45.2 | 2761 | 14 | AB028604 Tobacco 1           |
| C 309 | 14 | 45.2 | 495    | 14 | MVENS5GAD | L48975 Murray Vall | C 382 | 14 | 45.2 | 2761 | 14 | AB079689 Tobacco 1           |
| C 310 | 14 | 45.2 | 501    | 14 | MVENS5GAC | L48974 Murray Vall | C 383 | 14 | 45.2 | 2764 | 14 | AB055008 Tobacco 1           |
| C 311 | 14 | 45.2 | 504    | 9  | AY393090  | Homo sapi          | C 384 | 14 | 45.2 | 2816 | 6  | CQ590013 Sequence            |

|       |    |      |       |    |           |                    |       |    |      |       |    |          |                    |
|-------|----|------|-------|----|-----------|--------------------|-------|----|------|-------|----|----------|--------------------|
| C 385 | 14 | 45.2 | 2871  | 3  | BT011174  | BT011174 Drosophil | 458   | 14 | 45.2 | 58298 | 2  | AC149212 | AC149212 Medicago  |
| 386   | 14 | 45.2 | 2916  | 14 | FAD459805 | AJ459805 Fowl aden | 459   | 14 | 45.2 | 58976 | 9  | AL513243 | AL513243 Human DNA |
| 387   | 14 | 45.2 | 2922  | 8  | PSBLP     | X05979 Pea ELIP ge | C 460 | 14 | 45.2 | 63658 | 2  | AC018188 | AC018188 Drosophil |
| 388   | 14 | 45.2 | 2929  | 14 | FAD554049 | AJ554049 Fowl aden | C 461 | 14 | 45.2 | 64382 | 2  | AC100251 | AC100251 Mus muscu |
| 389   | 14 | 45.2 | 2952  | 3  | AK027212  | AK027212 Homo sapi | C 462 | 14 | 45.2 | 64827 | 8  | AB016873 | AB016873 Arabidops |
| 390   | 14 | 45.2 | 3071  | 3  | DRODERA   | L47260 Drosophila  | C 463 | 14 | 45.2 | 65608 | 2  | AC132197 | AC132197 Homo sapi |
| 391   | 14 | 45.2 | 3085  | 6  | CQ594678  | CQ594678 Sequence  | C 464 | 14 | 45.2 | 66188 | 9  | AL391136 | AL391136 Human DNA |
| C 392 | 14 | 45.2 | 3130  | 9  | AF201385  | AF201385 Homo sapi | C 465 | 14 | 45.2 | 67498 | 2  | AC012648 | AC012648 Drosophil |
| 393   | 14 | 45.2 | 3300  | 14 | FAD431719 | AJ431719 Fowl aden | C 466 | 14 | 45.2 | 68362 | 9  | AC096720 | AC096720 Homo sapi |
| 394   | 14 | 45.2 | 3315  | 14 | FAU26221  | U26221 Fowl adenov | C 467 | 14 | 45.2 | 70475 | 8  | AB018112 | AB018112 Arabidops |
| 395   | 14 | 45.2 | 3334  | 5  | BC057443  | BC057443 Danio rer | C 468 | 14 | 45.2 | 73294 | 2  | AC027231 | AC027231 Homo sapi |
| C 396 | 14 | 45.2 | 3358  | 6  | CQ590225  | CQ590225 Sequence  | C 469 | 14 | 45.2 | 74301 | 2  | AC137736 | AC137736 Homo sapi |
| C 397 | 14 | 45.2 | 4349  | 8  | AF034618  | AF034618 Spinacia  | C 470 | 14 | 45.2 | 74723 | 8  | EX842633 | EX842633 Neurospor |
| C 398 | 14 | 45.2 | 4384  | 3  | EMU548427 | AJ548427 Echinococ | C 471 | 14 | 45.2 | 75326 | 2  | AC026999 | AC026999 Homo sapi |
| 399   | 14 | 45.2 | 4477  | 3  | DROTPM    | M27659 D. melanog  | C 472 | 14 | 45.2 | 76410 | 10 | AL596180 | AL596180 Mouse DNA |
| 400   | 14 | 45.2 | 4488  | 6  | CQ595125  | CQ595125 Sequence  | C 473 | 14 | 45.2 | 76485 | 3  | AC024211 | AC024211 Caenorhab |
| 401   | 14 | 45.2 | 4618  | 6  | CQ602834  | CQ602834 Sequence  | C 474 | 14 | 45.2 | 76485 | 3  | AC024872 | AC024872 Caenorhab |
| 402   | 14 | 45.2 | 4720  | 8  | AF515628  | AF515628 Emericell | C 475 | 14 | 45.2 | 77858 | 2  | AC135758 | AC135758 Rattus no |
| C 403 | 14 | 45.2 | 5177  | 3  | BT001531  | BT001531 Drosophil | C 476 | 14 | 45.2 | 78419 | 3  | AC004639 | AC004639 Drosophil |
| C 404 | 14 | 45.2 | 5186  | 6  | CQ590012  | CQ590012 Sequence  | C 477 | 14 | 45.2 | 80141 | 9  | HSEWSGAR | Y07848 Homo sapien |
| 405   | 14 | 45.2 | 5523  | 14 | AEEHEXEND | L80007 Equine aden | C 478 | 14 | 45.2 | 80959 | 2  | AC010752 | AC010752 Drosophil |
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| 407   | 14 | 45.2 | 6361  | 10 | AY014962  | AY014962 Mus muscu | C 480 | 14 | 45.2 | 81347 | 8  | AB015478 | AB015478 Arabidops |
| 408   | 14 | 45.2 | 6536  | 9  | AF523117  | AF523117 Homo sapi | C 481 | 14 | 45.2 | 81901 | 2  | AC014473 | AC014473 Drosophil |
| 409   | 14 | 45.2 | 6898  | 6  | AX344815  | AX344815 Sequence  | C 482 | 14 | 45.2 | 82381 | 8  | ATF27619 | AL078467 Arabidops |
| C 410 | 14 | 45.2 | 7701  | 1  | AF051690  | AF051690 Pseudomon | C 483 | 14 | 45.2 | 82411 | 8  | AC068809 | AC068809 Genomic S |
| C 411 | 14 | 45.2 | 8046  | 6  | CQ595124  | CQ595124 Sequence  | C 484 | 14 | 45.2 | 82964 | 9  | AL604028 | AL604028 Human DNA |
| C 412 | 14 | 45.2 | 10091 | 1  | AF135398  | AF135398 Thermus b | C 485 | 14 | 45.2 | 83078 | 8  | AF072897 | AF072897 Arabidops |
| C 413 | 14 | 45.2 | 10413 | 1  | AE004865  | AE004865 Pseudomon | C 486 | 14 | 45.2 | 83373 | 8  | AB017064 | AB017064 Arabidops |
| C 414 | 14 | 45.2 | 11404 | 1  | AE003934  | AE003934 Xylella f | C 487 | 14 | 45.2 | 84761 | 9  | AC093648 | AC093648 Homo sapi |
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| C 417 | 14 | 45.2 | 12305 | 1  | AE008023  | AE008023 Agrobacte | C 490 | 14 | 45.2 | 84761 | 9  | AC093648 | AC093648 Homo sapi |
| C 418 | 14 | 45.2 | 13356 | 1  | AE011418  | AE011418 Leptospi  | C 491 | 14 | 45.2 | 84761 | 9  | AC093648 | AC093648 Homo sapi |
| 419   | 14 | 45.2 | 13373 | 10 | AB191468  | AB191468 Mus muscu | C 492 | 14 | 45.2 | 84761 | 9  | AC093648 | AC093648 Homo sapi |
| C 420 | 14 | 45.2 | 15666 | 1  | AF057695  | AF057695 Haemophil | C 493 | 14 | 45.2 | 84761 | 9  | AC093648 | AC093648 Homo sapi |
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| 425   | 14 | 45.2 | 23738 | 3  | CEP08H9   | Z77657 Caenorhabdi | C 498 | 14 | 45.2 | 84761 | 9  | AC093648 | AC093648 Homo sapi |
| 426   | 14 | 45.2 | 24595 | 1  | ATACH5    | X00493 Agrobacteri | C 499 | 14 | 45.2 | 84761 | 9  | AC093648 | AC093648 Homo sapi |
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| 430   | 14 | 45.2 | 24595 | 6  | BD016312  | BD016312 Method of |       |    |      |       |    |          |                    |
| C 431 | 14 | 45.2 | 24965 | 2  | AC014507  | AC014507 Drosophil |       |    |      |       |    |          |                    |
| C 432 | 14 | 45.2 | 26356 | 3  | AF077538  | AF077538 Caenorhab |       |    |      |       |    |          |                    |
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| 434   | 14 | 45.2 | 30328 | 9  | AY341246  | AY341246 Homo sapi |       |    |      |       |    |          |                    |
| C 435 | 14 | 45.2 | 32421 | 8  | SCDPB3    | X76053 S.cerevisia |       |    |      |       |    |          |                    |
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| C 437 | 14 | 45.2 | 32668 | 9  | MPU575934 | AJ575934 Micromono |       |    |      |       |    |          |                    |
| C 438 | 14 | 45.2 | 33473 | 9  | AL603751  | AL603751 Human DNA |       |    |      |       |    |          |                    |
| 439   | 14 | 45.2 | 34150 | 9  | AC068789  | AC068789 Homo sapi |       |    |      |       |    |          |                    |
| C 440 | 14 | 45.2 | 35468 | 3  | AF098500  | AF098500 Caenorhab |       |    |      |       |    |          |                    |
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| 442   | 14 | 45.2 | 38146 | 1  | AY524043  | AY524043 Micromono |       |    |      |       |    |          |                    |
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| C 449 | 14 | 45.2 | 43712 | 9  | HS984G1   | AL031186 Human DNA |       |    |      |       |    |          |                    |
| 450   | 14 | 45.2 | 44090 | 9  | AC000080  | AC000080 Homo sapi |       |    |      |       |    |          |                    |
| C 451 | 14 | 45.2 | 44872 | 5  | AC091773  | AC091773 Takifugu  |       |    |      |       |    |          |                    |
| C 452 | 14 | 45.2 | 45205 | 3  | U41014    | U41014 Caenorhabdi |       |    |      |       |    |          |                    |
| 453   | 14 | 45.2 | 45256 | 9  | AC000090  | AC000090 Homo sapi |       |    |      |       |    |          |                    |
| C 454 | 14 | 45.2 | 47319 | 6  | AC059533  | AC059533 Sequence  |       |    |      |       |    |          |                    |
| C 455 | 14 | 45.2 | 47425 | 2  | AC009934  | AC009934 Homo sapi |       |    |      |       |    |          |                    |
| C 456 | 14 | 45.2 | 51531 | 2  | AC017444  | AC017444 Drosophil |       |    |      |       |    |          |                    |
| C 457 | 14 | 45.2 | 57050 | 7  | AY129333  | AY129333 Mycobacte |       |    |      |       |    |          |                    |

## ALIGNMENTS

|            |            |   |        |     |        |                 |
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| RESULT 1   | AP458356   | Kunjin virus strain K6453 nonstructural protein 5 gene, partial | 458 bp | RNA | linear | VRL 18-JUN-2003 |
| LOCUS      | AP458356   |   |        |     |        |                 |
| DEFINITION | AP458356   | Kunjin virus strain K6453 nonstructural protein 5 gene, partial |        |     |        |                 |
| ACCESSION  | AP458356   |   |        |     |        |                 |
| VERSION    | AP458356.1 | GI:21636491   |        |     |        |                 |
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| SOURCE     |            |   |        |     |        |                 |
| ORGANISM   |            |   |        |     |        |                 |
| REFERENCE  |            |   |        |     |        |                 |
| AUTHORS    |            |   |        |     |        |                 |
| TITLE      |            |   |        |     |        |                 |
| JOURNAL    |            |   |        |     |        |                 |
| MEDLINE    |            |   |        |     |        |                 |
| PUBMED     |            |   |        |     |        |                 |
| REFERENCE  |            |   |        |     |        |                 |
| AUTHORS    |            |   |        |     |        |                 |
| TITLE      |            |   |        |     |        |                 |
| JOURNAL    |            |   |        |     |        |                 |

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.  
1 (bases 1 to 458)  
Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.  
Mouse neuroinvasive phenotype of West Nile virus strains varies depending upon virus genotype  
Virology 296 (1), 17-23 (2002)  
22033887  
12036314  
2 (bases 1 to 458)  
Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.  
Direct Submission  
Submitted (14-DEC-2001) Department of Pathology and WHO  
Collaborating Center for Tropical Diseases, The University of Texas  
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA



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AF458350      462 bp RNA linear VRL 18-JUN-2003
LOCUS      West Nile virus strain And-27875 nonstructural protein 5 gene,
DEFINITION partial cds.
ACCESSION AF458350
VERSION AF458350.1 GI:21636479
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
VIRUSES; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 462)
AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE    Mouse neuroinvasive phenotype of West Nile virus strains varies
          depending upon virus genotype
JOURNAL  Virology 296 (1), 17-23 (2002)
MEDLINE  22033887
PUBMED   12036314
REFERENCE 2 (bases 1 to 462)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE    Direct Submission
JOURNAL  Submitted (14-DEC-2001) Department of Pathology and WHO
          Collaborating Center for Tropical Diseases, The University of Texas
          Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA

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LOCUS      West Nile virus strain 68856 nonstructural protein 5 gene, partial
DEFINITION cds.
ACCESSION AF458344
VERSION AF458344.1 GI:21636467
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
VIRUSES; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 463)
AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE    Mouse neuroinvasive phenotype of West Nile virus strains varies
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depending upon virus genotype  
 Virology 296 (1), 17-23 (2002)  
 MEDLINE 22033887  
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 REFERENCE 2 (bases 1 to 463)  
 AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO  
 Collaborating Center for Tropical Diseases, The University of Texas  
 Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA  
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 KEYWORDS  
 SOURCE West Nile virus (WNV)  
 ORGANISM West Nile virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Flavivirus; Japanese encephalitis virus group.  
 REFERENCE 1 (bases 1 to 463)  
 AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.  
 TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies  
 depending upon virus genotype  
 JOURNAL Virology 296 (1), 17-23 (2002)  
 MEDLINE 22033887  
 PUBMED 12036314  
 REFERENCE 2 (bases 1 to 463)  
 AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO  
 Collaborating Center for Tropical Diseases, The University of Texas  
 Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA  
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 DEFINITION partial cds.  
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 VERSION AF458348.1 GI:21636475  
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 SOURCE West Nile virus (WNV)  
 ORGANISM West Nile virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Flavivirus; Japanese encephalitis virus group.  
 REFERENCE 1 (bases 1 to 463)  
 AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.  
 TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies  
 depending upon virus genotype  
 JOURNAL Virology 296 (1), 17-23 (2002)  
 MEDLINE 22033887  
 PUBMED 12036314  
 REFERENCE 2 (bases 1 to 463)  
 AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO  
 Collaborating Center for Tropical Diseases, The University of Texas  
 Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA  
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SOURCE West Nile virus (WNV)
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 463)
AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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1 (bases 1 to 545)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 545)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 585)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
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AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
FEATURES
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Db 324 TCGCCACCGGAAGTTGAGTAGACGCTGCTG 354
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AF297840
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DEFINITION
ACCESSION AF297840
VERSION AF297840.1 GI:11991970
KEYWORDS
SOURCE Kunjin virus
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 585)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 585)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 585)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
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Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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and Hall,R.A.
Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
JOURNAL
REFERENCE 3 (bases 1 to 594)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
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DEFINITION
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VERSION AF297846.1 GI:11991982
KEYWORDS Kunjin virus
ORGANISM Kunjin virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 600)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469815
PUBMED 11585535
REFERENCE 2 (bases 1 to 600)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 616)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
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DB 355 TCGCCACCGGAGTTGAGTAGACGGTGCTG 385

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LOCUS Kunjin virus isolate CX255 nonstructural protein 5 gene, partial
DEFINITION
ACCESSION AF297845
VERSION AF297845.1 GI:11991980
KEYWORDS Kunjin virus
ORGANISM Kunjin virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 616)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 616)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 616)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
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ACCESSION
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VERSION
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  Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
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REFERENCE
  1 (bases 1 to 644)
  Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
  Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
  The relationships between West Nile and Kunjin viruses
  Emerging Infect. Dis. 7 (4), 697-705 (2001)
TITLE
  Kunjin virus
JOURNAL
  MEDLINE
  21469816
PUBMED
  11585535
REFERENCE
  Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
  and Hall,R.A.
  Definitive studies of the relationships between West Nile and
  Kunjin viruses
  Unpublished
  3 (bases 1 to 657)
  Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
  and Hall,R.A.
  Direct Submission
  Submitted (22-AUG-2000) Microbiology and Parasitology, University
  of Queensland, St Lucia, QLD 4072, Australia
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  1..657
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    cds.
  ACCESSION
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  VERSION
    AF297849.1 GI:11991988
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    Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
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    Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
    Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
    The relationships between West Nile and Kunjin viruses
    Emerging Infect. Dis. 7 (4), 697-705 (2001)
  TITLE
    Kunjin virus
  JOURNAL
    MEDLINE
    21469816
  PUBMED
    11585535
  REFERENCE
    Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
    and Hall,R.A.
    Definitive studies of the relationships between West Nile and
    Kunjin viruses
    Unpublished
    3 (bases 1 to 659)
    Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
    and Hall,R.A.
    Direct Submission
    Submitted (20-OCT-1999) Department of Microbiology and
    Parasitology, University of Queensland, St. Lucia, Brisbane, QLD
    4072, Australia
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JOURNAL
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  Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
  and Hall,R.A.
  Definitive studies of the relationships between West Nile and
  Kunjin viruses
  Unpublished
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  Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
  and Hall,R.A.
  Direct Submission
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  DEFINITION
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    West Nile virus isolate Araldj polyprotein gene, partial cds.
  ACCESSION
    AF196536
  VERSION
    AF196536.1 GI:15865586
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    West Nile virus
  SOURCE
    West Nile virus
  ORGANISM
    Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
    Flavivirus; Japanese encephalitis virus group.
  REFERENCE
    1 (bases 1 to 659)
    Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
    Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
    The relationships between West Nile and Kunjin viruses
    Emerging Infect. Dis. 7 (4), 697-705 (2001)
  TITLE
    Kunjin viruses
  JOURNAL
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    Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
    and Hall,R.A.
    Definitive studies of the relationships between West Nile and
    Kunjin viruses
    Unpublished
    3 (bases 1 to 659)
    Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
    and Hall,R.A.
    Direct Submission
    Submitted (20-OCT-1999) Department of Microbiology and
    Parasitology, University of Queensland, St. Lucia, Brisbane, QLD
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Db 391 TCGCCACCGGAAGTTGAGTAGACGCTGCTG 421
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LOCUS AF196541 669 bp RNA linear VRL 05-MAR-2002
DEFINITION West Nile virus isolate ArTB3573 polyprotein gene, partial cds.
ACCESSION AF196541
VERSION AF196541.1 GI:15865591
KEYWORDS
SOURCE West Nile virus
ORGANISM
REFERENCE
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL Unpublished
REFERENCE
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (20-OCT-1999) Department of Microbiology and
Parasitology, University of Queensland, St. Lucia, Brisbane, QLD
4072, Australia
FEATURES
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Db 391 TCGCCACCGGAAGTTGAGTAGACGCTGCTG 421
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DEFINITION West Nile virus isolate HB6343 polyprotein gene, partial cds.
ACCESSION AF196542
VERSION AF196542.1 GI:15865593
KEYWORDS
SOURCE West Nile virus
ORGANISM
REFERENCE
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL Unpublished
REFERENCE
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (20-OCT-1999) Department of Microbiology and
Parasitology, University of Queensland, St. Lucia, Brisbane, QLD
4072, Australia
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LOCUS AF017254 1524 bp RNA linear VRL 01-DEC-2000
DEFINITION West Nile virus nonstructural protein NS5 (NS5) gene, partial cds.
ACCESSION AF017254
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Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 22

AY277252 10845 bp RNA linear VRL 03-MAY-2003  
West Nile virus isolate LEIV-Vlg99-27889, complete genome.

AY277252

AY277252.1 GI:30349727

West Nile virus (WNV)

West Nile virus

Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Flavivirus; Japanese encephalitis virus group.

1 (bases 1 to 10845)

Prilipov, A.G., Kinney, R.M., Samokhvalov, E.I., Savage, H.M.,

Alkhovsky, S.V., Tseychia, R., Gromashevsky, V.L., Sadykova, G.K.,

Shatalov, A.G., Usachev, E.V., Mokhonov, V.V., Voronina, A.G.,

Butenko, A.M., Larichev, V.F., Gubler, D.J. and Lvov, D.K.

Analysis of a new variants of West Nile virus

Unpublished

2 (bases 1 to 10845)

Prilipov, A.G., Kinney, R.M., Samokhvalov, E.I., Savage, H.M.,

Alkhovsky, S.V., Tseychia, R., Gromashevsky, V.L., Sadykova, G.K.,

Shatalov, A.G., Usachev, E.V., Mokhonov, V.V., Voronina, A.G.,

Butenko, A.M., Larichev, V.F., Gubler, D.J. and Lvov, D.K.

Direct Submission

Submitted (15-APR-2003) Molecular Genetic, Ivanovsky Virology

Institute, Gamalei 16, Moscow 123098, Russia

Location/Qualifiers

1. 10845

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/country="Russia; Volgograd, low Volga"

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## ORIGIN

Query Match 100.0%; Score 31; DB 14; Length 10845;  
Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31

Db 10522 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552

## RESULT 23

AF317203

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

West Nile virus

West Nile virus

Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Japanese encephalitis virus group.

1 (bases 1 to 10972)

Platonov, A.E., Karan, L., Yazishina, S., Obukhov, I.L., Shipulina, O.

and Shipulin, G.A.

Genetic similarity of West Nile viruses caused epidemics in

Volgograd 1999 and Romania 1996

Unpublished

REFERENCE 2 (bases 1 to 10972)

AF317203 10972 bp RNA linear VRL 11-FEB-2001  
West Nile virus VLG-4 polyprotein precursor, gene, complete cds.

AF317203.1 GI:12744408

## AUTHORS

Karan,L., Yazishina,S., Obukhov,I.L., Shipulina,O., Shipulin,G.A.  
and Platonov,A.E.  
Direct Submission  
Submitted (26-Oct-2000) Central Research Institute of Epidemiology,  
Novogireevskaya Str. 3A, Moscow 111123, Russia

## JOURNAL

## FEATURES

source

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## ORIGIN

Query Match 100.0%; Score 31; DB 14; Length 10972;

Best Local Similarity 100.0%; Pred. No. 2.1e-07;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31

DB 10490 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 10520

## RESULT 24

## AY262283

LOCUS AY262283 10984 bp RNA linear VRL 29-OCT-2003

DEFINITION West Nile virus isolate KN3829 polyprotein gene, complete cds.

ACCESSION AY262283

VERSION AY262283.1 GI:30230630

## KEYWORDS

## SOURCE

West Nile virus (WNV)  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Flavivirus; Japanese encephalitis virus group.

## REFERENCE

## AUTHORS

1 (bases 1 to 10984)  
Charrel,R.N., Braut,A.C., Gallian,P., Lemasson,J.-J., Murgue,B.,  
Murri,S., Pastorino,B., Zeller,H., de Chesse,R., de Micco,P. and de  
Lamballerie,X.

## TITLE

Evolutionary relationship between Old World West Nile virus  
strains. Evidence for viral gene flow between africa, the middle  
east, and europe

JOURNAL Virology 315 (2), 381-388 (2003)

## MEDLINE

22949215

## PUBMED

14585341

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## source

## 1. .10984

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/mol\_type="genomic RNA"

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ORIGIN
Query Match 100.0%; Score 31; DB 14; Length 10984;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCCACCGAAGTTGAGTAGACGCTGCTG 31
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Db 10485 TCCGCCACCGAAGTTGAGTAGACGCTGCTG 10515
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AY268132 10989 bp RNA linear VRL 03-NOV-2003
LOCUS West Nile virus strain PaAn001 polyprotein (pol) gene, complete
DEFINITION
ACCESSION AY268132
VERSION AY268132.1 GI:33242574
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus
VIRUSES: sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 10989)
AUTHORS Charrel,R.N., Brault,A.C., Gallian,P., Lemasson,J.-J., Murgue,B.,
Murri,S., Pascorino,B., Zeller,H., de chesse,R., de Micco,P. and de
Lamballerie,X.
TITLE Evolutionary relationship between Old World West Nile virus
strains. Evidence for viral gene flow between africa, the middle
east, and europe
JOURNAL Virology 315 (2), 381-388 (2003)
MEDLINE 22949215
PUBMED 14585341
REFERENCE 2 (bases 1 to 10989)
AUTHORS de Lamballerie,X., Brault,A.C., Gallian,P., Lemasson,J., Murgue,B.,
Murri,S., Pascorino,B., Zeller,H., Dechesse,R., de Micco,P. and
Charrel,R.N.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2003) Virology, Medical University, 27 bd Jean
Moulin, Marseille 13005, France
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| SOURCE    | West Nile virus   |            |            |
| ORGANISM  | Viruses; aeRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.  |            |            |
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| AUTHORS   | Bowen, M., Meyer, R.F., McKinney, N., Morrill, W. and Lanciotti, R.   |            |            |
| TITLE     | Complete genomic sequence of West Nile virus strain Eg101   |            |            |
| JOURNAL   | Unpublished   |            |            |
| REFERENCE | 2 (bases 1 to 11029)  |            |            |
| AUTHORS   | Bowen, M., Meyer, R.F., McKinney, N., Morrill, W. and Lanciotti, R.   |            |            |
| TITLE     | Direct Submission   |            |            |
| JOURNAL   | Submitted (27-APR-2000) Arbovirus Diseases Branch, Centers for Disease Control & Prevention, Rampart Road, Fort Collins, CO 80521, USA  |            |            |
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West Nile virus strain R097-50, complete genome.
DEFINITION AF260969
ACCESSION AF260969.1 GI:9930137
VERSION AF260969.1
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Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 11029)
Savage,H.M., Ceianu,C., Nicolescu,G., Karabatsos,N., Lanciotti,R.,
Vladimirescu,A., Laviu,L., Ungureanu,A., Romanca,C. and Teai,T.F.
Entomologic and avian investigations of an epidemic of West Nile
fever in Romania in 1996, with serologic and molecular
Characterization of a virus isolate from mosquitoes
Am. J. Trop. Med. Hyg. 61 (4), 600-611 (1999)
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Bower,M., Meyer,R.F., McKinney,N., Morrill,W. and Lanciotti,R.
Direct Submission
Submitted (27-APR-2000) Arbovirus Diseases Branch, Centers for
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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

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ORGANISM

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TITLE

JOURNAL

MEDLINE

PUBMED

AUTHORS

TITLE

JOURNAL

FEATURES

source

CDS

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NTVKLTSGHLKCRVMEKQLQKGTGYGVSATANAKVLI ELEPFGTDSYIVVGRDEQ  
PKVP ISSVASLNDLTVPGLRVTVNPFVSVATANAKVLI ELEPFGTDSYIVVGRDEQ  
INHHWKGSSIGKAFATTLTGAQRALAGDTPANDFGSGGVFTSVGAHVQVGGAF  
ESLPGMSWITQGLLALLMNGINARDRSIALTELVGGVLLFLSVNVHADTGCAD  
ISRLQRCGSGFVINDVEAMDRYKYPETPQGLAKIIQAHKEGVCGLSRVSRLEH  
QMWESVDELNTLTKENGVDLSVVVEKQMGYKSAKPKRTATTKEKLEIHWKANGSIL  
FAPELANNTFVDPGETKCEPTONRANNSLEVDFGLTSTRFLKVRKSGNTTCELS  
KIIIGTAVKNNIAHSDLSYIESRLNDTWKLERAVLGKSCVTWPEHTLWGDGLIES  
DLIIPVTLNAGPSNHRNPQYKTONQGPWDEGRVEIDFYCPTTTLTSESGHGRPA  
TRTTTSCGLITDMCCSCTLPPLRYOTDSGWYGMETRPQRHDEKTLVQGVNAYNA  
DMIDFPQGLLVFLATQVEQLRKWTAKISNPAILLALLLVFGGITTIVDVRVTVLH  
GAFAESNSGDDVHLAMATFKIOPVFMVASFLKARNQENILLMLAAVFFQVMAH  
DAQILLWEIPDLNLSAAVMMILRAITFTTSTNVVPLLALLPGLRCLNDVRYIL  
LLMWIGISLIREKRSAAKKGASLLCLALASTGLTFNPMILAAGLIACDNRKGPWA  
TEVMTAGLSEFAIVGLAELDIDSMATPMTIAGLMAFAFVTSKSTDMWIERTADISW  
ESDAEITGSSERVDRLDDCNFOLMNDPGAPWKIMLRMACLAISATWPAHLPSTV  
GPMITLQYTKRGVNDTPSPKEYKGGDTTGVYRIMTRGLLGSYQAGAGVNVGSPFH  
TKNHTTGALMSGGRDIPYWSVKGEDRICYGGPKWLQHKWNGODEVQMIIVBPGKN  
LVNQVTPGVFKTPEGEGAVTLDPFTTSGSPIDVKNQDVGILYGVNGVIMPNSYS  
AIVQGERMDEIPAGPEPMLKKQITVLDLHPGAGKTRILPOIIEKAINRRLTAV  
LAPTRVAAEMAEALRGIPRYOTSAVTRHNGNEIVDMVCHATLTHRLMSPHRVNV  
NLVFMDEAHFTDPAIAARGYSTKVELGAAAIEMTATPGTSDTPESNPSIDLO  
TEIPDRANSGYEWITEYIGKTVFVSPKMGNEIALCLOKAGKVVQLARKSYETET  
PKCKNDWDFTITDISEMGANFKASVIDSRKSKYPTIITEGEGRVILGEPASVATA  
SAAQRKIRGNPSQGVDECYGHTNEDDSNFHWTAEARIMLNDINHPNGLIAOFYQ  
PERREKVTMDGEYRLBERNFLELTADLPVLAAYVVAANVSPKTRREAGLITIAAAY  
TNTLEDNEVEVITKGERKILRPWIDARVSDHQAALFAKFDQSGKSGQIGLIEV  
LGMPEHFMGTKEALDTPVAVTAEGRAHRAHMLBELPALQTIALLISVMTWG  
VFLLMQRKIGIKGLGVLVGATPFCMAEVPKTIAGMLLLSLLMLVLIPEPEK  
ORSTQDNLAVELICVLTLSAVANAEMHMDTKSDISSIFGQRIEVENKFNSEGEFL  
LDLRPATWSLYAVTAVTAPLKLITSDITNTSLTSINVQASALFTLARGPFPVDV  
GVSAALLAAGCWQGVTLVTATLFFCHYAVVWPGVQAEASRQRTAAGTAMKNA  
VVDGIVATDPELETPPIQKVGQIMLILVSLAAVVVNPVSKTRREAGLITIAAAY  
TLWENGASVYMNATTAIGLCHIRGWSLCSITWTLLIKMNDPKLKGKAGKRLVER  
VWKEKLNQTKBEFTRYRKEAIIEVDRSAAKHARKNGVNTGHPVSGTAKLRWLVER  
RFLPVPCKVIDLGGCGGCYMATOKRQVRYGTGKGGPCHPEPQLVYSYGNVITM  
KSGVDVYFRSECCDILLDIGHSSSSAEVEEHTIIRVLEWEDWLRHGPREFPCVKVL  
CPYMPKVIKMKELLQRRYGGVLRNPLSRNTHMYVWVSASGVNHSVNTSVDENH  
RMEKRTWKGSPQYEDVNLGSTRVAGKPLNSDTSKIKRIERLREYSSTTHDENH  
PYRTWNYGSDYDKVPTSGASLVNGLVLLSKPDWTITNTVTMTATDTPFGQORVFK  
EKVDTKAPEPEGVKVLNETTNWLAFLAREKPRMCSREEFTKYNKSNAAALGAMPE  
EKNQWSAREAVDPKPEWEDBEREHLGECHTCIYNMKGKREKVEGFKAGKGR  
AIFPMWLGARFLFEALGFLEHNLGRKNSGGVGLQKGLIILUREVTRPGGI  
IADDTAGWDTRIADLENEAKVLELLEDEHRRRLARAIILETVYRHKVYKVRPAADR  
TMDVTSRQDQSGSVYVALNTFTNLAVQLVRMMEGEVIGVDDVEKTLKPGKPV  
RTWLFENGEEBLRMAVGGDDCVVPLDLDRAFSLFNAMSKVKVQIDQKPGTGY  
DWQVPPCSNHFTELIMKQDRTLVPCRGODELVGRARI SPGAGWNRVDRCLAKSYA  
QMLLLYFHRDRDLMANAICSAVPVNVPTGRTTWSIHAGGEMTTEDMLEVNRVW  
IEENWMDKTPVEKSDVPVSGKREDIWCGLIGTRARATWENIQVAINQVRAIG  
DEKYVDYMSLSKRYEDTILVEDTVL"



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3'UTR
ORIGIN
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    Best Local Similarity 100.0%; Pred. No. 7e-07;
    Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
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Db 299 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 328

RESULT 32
AF297854
LOCUS
DEFINITION
    Kunjin virus isolate WK436 nonstructural protein 5 gene, partial
    cds.
ACCESSION
    AF297854
VERSION
    AF297854.1 GI:11991998
KEYWORDS
    Kunjin virus
SOURCE
    Kunjin virus
ORGANISM
    Kunjin virus
    Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
    Flavivirus; Japanese encephalitis virus group.
REFERENCE
    1 (bases 1 to 542)
AUTHORS
    Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
    Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE
    The relationships between West Nile and Kunjin viruses
JOURNAL
    Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE
    21469816
PUBMED
    11585535
REFERENCE
    2 (bases 1 to 542)
AUTHORS
    Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
    and Hall,R.A.
TITLE
    Definitive studies of the relationships between West Nile and
    Kunjin viruses
JOURNAL
    Unpublished
REFERENCE
    3 (bases 1 to 542)
AUTHORS
    Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
    and Hall,R.A.
TITLE
    Direct Submission
JOURNAL
    Submitted (22-AUG-2000) Microbiology and Parasitology, University
    of Queensland, St Lucia, QLD 4072, Australia
FEATURES
    source
    1..542
    /organism="Kunjin virus"
    /mol_type="genomic RNA"
    /isolate="WK436"
    /db_xref="taxon:11077"
    <1..243
    /notes="NS5"
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    /product="nonstructural protein 5"
    /protein_id="AA042392.1"
    /db_xref="GI:11991998"
    /translation="NEWMDKTPVEKMSDVPYSGKREDIWCGLIGTRARATWAENIQ
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ORIGIN
    Query Match      96.8%; Score 30; DB 14; Length 542;
    Best Local Similarity 100.0%; Pred. No. 7e-07;
    Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
    |||||
Db 363 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 392

RESULT 33
KUNNS5GAA
LOCUS
DEFINITION
    Kunjin virus nonstructural protein (NS5) gene, 3' end of cds.
ACCESSION
    L48978

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/product="nonstructural protein"  
/protein id="AAB02078.1"  
/db\_xref="GI:1066805"  
/translation="WMEDKTPVEKWSDPYSGKREDIWGSLIGTRARATWAENIQVA  
INQVRSIIIGDEKYVDYMSLSKRYEDTLVETVL"

## ORIGIN

Query Match 96.8%; Score 30; DB 14; Length 587;  
Best Local Similarity 100.0%; Pred. No. 7e-07;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGCCACCGGAAGTTGAGTAGACGGTGCTG 31  
|||||  
Db 355 CGCCACCGGAAGTTGAGTAGACGGTGCTG 384  
|||||

## RESULT 35

AF297844  
LOCUS  
DEFINITION  
Kunjin virus isolate CHI6549B nonstructural protein 5 gene, partial cds.

ACCESSION AF297844  
VERSION AF297844.1 GI:11991978

## KEYWORDS

SOURCE Kunjin virus

## ORGANISM

Kunjin virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Flavivirus; Japanese encephalitis virus group.

## REFERENCE

AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,

1 (bases 1 to 601)

Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.

The relationships between West Nile and Kunjin viruses

Emerging Infect. Dis. 7 (4), 697-705 (2001)

## MEDLINE

21469816

## PUBMED

11595535

## REFERENCE

2 (bases 1 to 601)

Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.

and Hall,R.A.

Definitive studies of the relationships between West Nile and

Kunjin viruses

Unpublished

3 (bases 1 to 601)

Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.

and Hall,R.A.

Direct Submission

Submitted (22-AUG-2000) Microbiology and Parasitology, University

of Queensland, St Lucia, QLD 4072, Australia

Location/Qualifiers

1. .601

/organism="Kunjin virus"

/mol\_type="genomic RNA"

/isolate="CHI6549B"

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<1. .242

/note="NS5"

/codon\_start=3

/product="nonstructural protein 5"

/protein id="AAG42382.1"

/db\_xref="GI:11991979"

/translation="EMWEDTTPVEKWSDPYSGKREDIWGSLIGTRARATWAENIQV

AINQVRSIIIGDEKYVDYMSLSKRYEDTLVETVL"

## ORIGIN

Query Match 96.8%; Score 30; DB 14; Length 601;

Best Local Similarity 100.0%; Pred. No. 7.1e-07;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGCCACCGGAAGTTGAGTAGACGGTGCTG 31  
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Db 362 CGCCACCGGAAGTTGAGTAGACGGTGCTG 391  
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## RESULT 36

## AF297841

## LOCUS

DEFINITION

Kunjin virus isolate CHI6465C nonstructural protein 5 gene, partial

cds.

ACCESSION AF297841

VERSION AF297841.1 GI:11991972

## KEYWORDS

SOURCE Kunjin virus

## ORGANISM

Kunjin virus

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Flavivirus; Japanese encephalitis virus group.

1 (bases 1 to 607)

Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,

Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.

The relationships between West Nile and Kunjin viruses

Emerging Infect. Dis. 7 (4), 697-705 (2001)

21469816

## PUBMED

11595535

## REFERENCE

2 (bases 1 to 607)

Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.

and Hall,R.A.

Definitive studies of the relationships between West Nile and

Kunjin viruses

Unpublished

3 (bases 1 to 607)

Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.

and Hall,R.A.

Direct Submission

Submitted (22-AUG-2000) Microbiology and Parasitology, University

of Queensland, St Lucia, QLD 4072, Australia

Location/Qualifiers

1. .607

/organism="Kunjin virus"

/mol\_type="genomic RNA"

/isolate="CHI6465C"

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<1. .255

/note="NS5"

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/translation="WIEENWMDKTPVEKWSDPYSGKREDIWGSLIGTRARATWA

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Best Local Similarity 100.0%; Pred. No. 7.1e-07;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGCCACCGGAAGTTGAGTAGACGGTGCTG 31  
|||||

Db 375 CGCCACCGGAAGTTGAGTAGACGGTGCTG 404  
|||||

## RESULT 37

AF297856

LOCUS

DEFINITION

Kunjin virus isolate P1553 nonstructural protein 5 gene, partial

cds.

ACCESSION AF297856

VERSION AF297856.1 GI:11992002

## KEYWORDS

SOURCE Kunjin virus

## ORGANISM

Kunjin virus

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Flavivirus; Japanese encephalitis virus group.

1 (bases 1 to 609)

Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,

Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.

The relationships between West Nile and Kunjin viruses

Emerging Infect. Dis. 7 (4), 697-705 (2001)

21469816

11585535  
2 (bases 1 to 609)  
Scherrret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.  
and Hall,R.A.  
Definitive studies of the relationships between West Nile and  
Kunjin viruses  
Unpublished  
JOURNAL  
REFERENCE  
AUTHORS  
3 (bases 1 to 609)  
Scherrret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.  
and Hall,R.A.  
Direct Submission  
Submitted (22-AUG-2000) Microbiology and Parasitology, University  
of Queensland, St Lucia, QLD 4072, Australia  
Location/Qualifiers  
1..609  
/organism="Kunjin virus"  
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/translation="WIDENEMWEDKTPVEKMSDVPYSGKREDIWCGLIGTRARATWA  
ENIQVAINQVRSIIIGDEKYVDYMSLSKRYEDTTLVEDTVL"  
ORIGIN  
Query Match 96.8%; Score 30; DB 14; Length 609;  
Best Local Similarity 100.0%; Pred. No. 7.1e-07;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31  
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Db 384 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 413  
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RESULT 38  
AF297859  
LOCUS  
DEFINITION  
Kunjin virus isolate MRM5373 nonstructural protein 5 gene, partial  
cds.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Kunjin virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Flavivirus; Japanese encephalitis virus group.  
1 (bases 1 to 620)  
Scherrret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,  
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.  
The relationships between West Nile and Kunjin viruses  
Emerging Infect. Dis. 7 (4), 697-705 (2001)  
JOURNAL  
MEDLINE  
PUBMED  
21469816  
11585535  
2 (bases 1 to 620)  
Scherrret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.  
and Hall,R.A.  
Definitive studies of the relationships between West Nile and  
Kunjin viruses  
Unpublished  
JOURNAL  
REFERENCE  
AUTHORS  
3 (bases 1 to 622)  
Scherrret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.  
and Hall,R.A.  
Direct Submission  
Submitted (22-AUG-2000) Microbiology and Parasitology, University  
of Queensland, St Lucia, QLD 4072, Australia  
Location/Qualifiers  
1..622  
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QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31

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/db\_xref="GI:11992009"  
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ORIGIN  
Query Match 96.8%; Score 30; DB 14; Length 620;  
Best Local Similarity 100.0%; Pred. No. 7.1e-07;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31  
|||||  
Db 371 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 400  
|||||  
RESULT 39  
AF297842  
LOCUS  
DEFINITION  
Kunjin virus isolate CH16514C nonstructural protein 5 gene, partial  
cds.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Kunjin virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Flavivirus; Japanese encephalitis virus group.  
1 (bases 1 to 622)  
Scherrret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,  
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.  
The relationships between West Nile and Kunjin viruses  
Emerging Infect. Dis. 7 (4), 697-705 (2001)  
JOURNAL  
MEDLINE  
PUBMED  
21469816  
11585535  
2 (bases 1 to 622)  
Scherrret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.  
and Hall,R.A.  
Definitive studies of the relationships between West Nile and  
Kunjin viruses  
Unpublished  
JOURNAL  
REFERENCE  
AUTHORS  
3 (bases 1 to 622)  
Scherrret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.  
and Hall,R.A.  
Direct Submission  
Submitted (22-AUG-2000) Microbiology and Parasitology, University  
of Queensland, St Lucia, QLD 4072, Australia  
Location/Qualifiers  
1..622  
/organism="Kunjin virus"  
/mol\_type="genomic RNA"  
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/db\_xref="taxon:11077"  
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/protein\_id="AAG42380.1"  
/db\_xref="GI:11991975"  
/translation="NEWEMDKTPVEKMSDVPYSGKREDIWCGLIGTRARATWAENIQ  
VAINQVRSIIIGDEKYVDYMSLSKRYEDTTLVEDTVL"  
ORIGIN  
Query Match 96.8%; Score 30; DB 14; Length 622;  
Best Local Similarity 100.0%; Pred. No. 7.1e-07;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31

|            |   |                                    |                    |           |             |  |  |  |  |  |
|------------|---|------------------------------------|--------------------|-----------|-------------|--|--|--|--|--|
| TITLE      | Nucleotide and complete amino acid sequences of Kunjin virus: definitive gene order and characteristics of the virus-specified proteins |                                    |                    |           |             |  |  |  |  |  |
| JOURNAL    | J. Gen. Virol. 69 (Pt 1), 1-21 (1988)   |                                    |                    |           |             |  |  |  |  |  |
| MEDLINE    | 88089524  |                                    |                    |           |             |  |  |  |  |  |
| PUBMED     | 2826659   |                                    |                    |           |             |  |  |  |  |  |
| REFERENCE  | 2 (bases 1 to 627)  |                                    |                    |           |             |  |  |  |  |  |
| AUTHORS    | Khromykh,A.A. and Westaway,E.G.   |                                    |                    |           |             |  |  |  |  |  |
| TITLE      | Completion of Kunjin virus RNA sequence and recovery of an infectious RNA transcribed from stably cloned full-length cDNA               |                                    |                    |           |             |  |  |  |  |  |
| JOURNAL    | J. Virol. 68 (7), 4580-4588 (1994)  |                                    |                    |           |             |  |  |  |  |  |
| MEDLINE    | 94267921  |                                    |                    |           |             |  |  |  |  |  |
| PUBMED     | 8207832   |                                    |                    |           |             |  |  |  |  |  |
| COMMENT    | Original source text: Kunjin virus (strain MRM 61C) mature RNA.   |                                    |                    |           |             |  |  |  |  |  |
| FEATURES   | Location/Qualifiers   |                                    |                    |           |             |  |  |  |  |  |
| source     | 1. .627   |                                    |                    |           |             |  |  |  |  |  |
|            | /organism="Kunjin virus"  |                                    |                    |           |             |  |  |  |  |  |
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|            | /strain="MRM 61C"   |                                    |                    |           |             |  |  |  |  |  |
|            | /db_xref="taxon:11077"  |                                    |                    |           |             |  |  |  |  |  |
|            | /dev_stage="mature"   |                                    |                    |           |             |  |  |  |  |  |
|            | 4. .627   |                                    |                    |           |             |  |  |  |  |  |
|            | /note="putative"  |                                    |                    |           |             |  |  |  |  |  |
|            | /citation={2}   |                                    |                    |           |             |  |  |  |  |  |
| 3' UTR     |   |                                    |                    |           |             |  |  |  |  |  |
| ORIGIN     |   |                                    |                    |           |             |  |  |  |  |  |
|            | Query Match   | 96.8%;                             | Score 30;          | DB 14;    | Length 627; |  |  |  |  |  |
|            | Best Local Similarity   | 100.0%;                            | Pred. No. 7,1e-07; |           |             |  |  |  |  |  |
|            | Matches 30;   | Conservative 0;                    | Mismatches 0;      | Indels 0; | Gaps 0;     |  |  |  |  |  |
| QY         | 2   | CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31  |                    |           |             |  |  |  |  |  |
|            |   |                                    |                    |           |             |  |  |  |  |  |
| Db         | 121   | CGGCCACCGGAAGTTGAGTAGACGGTGCTG 150 |                    |           |             |  |  |  |  |  |
| RESULT 42  |   |                                    |                    |           |             |  |  |  |  |  |
| AF297858   |   |                                    |                    |           |             |  |  |  |  |  |
| LOCUS      | Kunjin virus isolate OR205 nonstructural protein 5 gene, partial cds  |                                    |                    |           |             |  |  |  |  |  |
| DEFINITION | AF297858 633 bp RNA linear VRL 05-MAR-2002  |                                    |                    |           |             |  |  |  |  |  |
| ACCESSION  | AF297858  |                                    |                    |           |             |  |  |  |  |  |
| VERSION    | AF297858.1 GI:11992006  |                                    |                    |           |             |  |  |  |  |  |
| KEYWORDS   | Kunjin virus  |                                    |                    |           |             |  |  |  |  |  |
| SOURCE     | Kunjin virus  |                                    |                    |           |             |  |  |  |  |  |
| ORGANISM   | Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.                      |                                    |                    |           |             |  |  |  |  |  |
| REFERENCE  | 1 (bases 1 to 633)  |                                    |                    |           |             |  |  |  |  |  |
| AUTHORS    | Scherrert,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.                   |                                    |                    |           |             |  |  |  |  |  |
| TITLE      | The relationships between West Nile and Kunjin viruses  |                                    |                    |           |             |  |  |  |  |  |
| JOURNAL    | Emerging Infect. Dis. 7 (4), 697-705 (2001)   |                                    |                    |           |             |  |  |  |  |  |
| MEDLINE    | 21469816  |                                    |                    |           |             |  |  |  |  |  |
| PUBMED     | 11585535  |                                    |                    |           |             |  |  |  |  |  |
| REFERENCE  | 2 (bases 1 to 633)  |                                    |                    |           |             |  |  |  |  |  |
| AUTHORS    | Scherrert,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.   |                                    |                    |           |             |  |  |  |  |  |
| TITLE      | Definitive studies of the relationships between West Nile and Kunjin viruses  |                                    |                    |           |             |  |  |  |  |  |
| JOURNAL    | Unpublished   |                                    |                    |           |             |  |  |  |  |  |
| REFERENCE  | 3 (bases 1 to 633)  |                                    |                    |           |             |  |  |  |  |  |
| AUTHORS    | Scherrert,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.   |                                    |                    |           |             |  |  |  |  |  |
| TITLE      | Direct Submission   |                                    |                    |           |             |  |  |  |  |  |
| JOURNAL    | Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia                          |                                    |                    |           |             |  |  |  |  |  |
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**TITLE**  
**JOURNAL**

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Db 383 CGCCACCGGAAGTTGAGTAGACGGTGCTG 412

RESULT 47
AF297855
LOCUS
DEFINITION
Kunjin virus isolate OR354 nonstructural protein 5 gene, partial cds.
ACCESSION
AF297855
VERSION
AF297855.1 GI:11992000
KEYWORDS
Kunjin virus
SOURCE
Kunjin virus
ORGANISM
Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 652)
Scherreret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.L., Briese,T., Gould,E.A. and Hall,R.A.
The relationships between West Nile and Kunjin viruses
Emerging Infect. Dis. 7 (4), 697-705 (2001)
21469816
PUBMED
REFERENCE
2 (bases 1 to 652)
Scherreret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
3 (bases 1 to 652)
Scherreret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Direct Submission
Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
FEATURES
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Best Local Similarity 100.0%; Pred. No. 7.1e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGCCACCGGAAGTTGAGTAGACGGTGCTG 31
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Db 385 CGCCACCGGAAGTTGAGTAGACGGTGCTG 414

RESULT 48
AF202541
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DEFINITION
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NS2b, NS3, NS4a, NS4b, NS5) gene, complete cds.
ACCESSION
AF202541
VERSION
AF202541.1 GI:6581069
KEYWORDS
West Nile virus
SOURCE
West Nile virus
ORGANISM
West Nile virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 10945)
Jia,X.Y., Briese,T., Jordan,I., Rambaut,A., Chi,H.C.,

FEATURES
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Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 383 CGCCACCGGAAGTTGAGTAGACGGTGCTG 412

RESULT 46
AY187015
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DEFINITION
West Nile virus strain 123 NS5 gene, partial cds.
ACCESSION
AY187015
VERSION
AY187015.1 GI:30983584
KEYWORDS
West Nile virus (WNV)
SOURCE
West Nile virus
ORGANISM
West Nile virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 645)
Beasley,D.W.C., Davis,C.T., Guzman,H., Vanlandingham,D.L., Travassos
da Rosa,A.P., Parsons,R.E., Higgs,S., Tesh,R.B. and Barrett,A.D.
Limited evolution of West Nile virus has occurred during its
southwesterly spread in the United States
Virology 309 (2), 190-195 (2003)
22644768
PUBMED
REFERENCE
2 (bases 1 to 645)
Beasley,D.W.C., Davis,C.T., Guzman,H., Vanlandingham,D.L.,
Travassos da Rosa,A.P.A., Parsons,R.E., Higgs,S., Tesh,R.B. and
Barrett,A.D.T.
Direct Submission
Submitted (26-NOV-2002) Pathology, University of Texas Medical
Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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QY 2 CGCCACCGGAAGTTGAGTAGACGGTGCTG 31
|||||

```

Mackenzie, J.S., Hall, R.A., Scherret, J. and Lipkin, W.I.  
Genetic analysis of West Nile New York 1999 encephalitis virus  
Lancet 354 (9194), 1971-1972 (1999)  
20086017  
10622305  
2 (bases 1 to 10945)  
Jia, X.Y., Briese, T., Jordan, I. and Lipkin, W.I.  
Direct Submission  
Submitted (06-NOV-1999) Emerging Diseases Laboratory, Dept.  
Microbiology & Molecular Genetics and Neurology, University of  
California, Irvine, 3101 Gillespie Neuroscience Facility, Irvine,  
CA 92697-4292, USA

FEATURES

source

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RESULT 49

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DEFINITION Flavivirus; Japanese encephalitis virus group.  
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VERSION AF206518.2 GI:7717200  
KEYWORDS West Nile virus  
SOURCE West Nile virus  
ORGANISM West Nile virus

REFERENCE

1 (bases 1 to 10975)  
AUTHORS Anderson, J.F., Andreadis, T.G., Vosebrinck, C.R., Tirrell, S.,  
Wakem, B.M., French, R.A., Garmendia, A.E. and Van Kruiningen, H.J.  
TITLE Isolation of West Nile virus from mosquitoes, crows, and a Cooper's  
hawk in Connecticut

JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
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TITLE  
JOURNAL  
REFERENCE  
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TITLE  
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REFERENCE  
AUTHORS  
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COMMENT  
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source

Science 286 (5448), 2331-2333 (1999)  
20070287  
10600741  
2 (bases 1 to 10975)  
Vosebrinck, C.R., Anderson, J.F. and Andreadis, T.G.  
Genome Sequence of West Nile Virus from Culex pipiens isolate  
Unpublished  
3 (bases 1 to 10975)  
Anderson, J.F., Andreadis, T.G. and Vosebrinck, C.R.  
Direct Submission  
Submitted (18-NOV-1999) Soil and Water, Connecticut Agricultural  
Experiment Station, 123 Huntington Street, New Haven, CT 06511, USA  
4 (bases 1 to 10975)  
Anderson, J.F., Andreadis, T.G. and Vosebrinck, C.R.  
Direct Submission  
Submitted (08-MAY-2000) Soil and Water, Connecticut Agricultural  
Experiment Station, 123 Huntington Street, New Haven, CT 06511, USA  
Sequence update by submitter  
On May 8, 2000 this sequence version replaced gi:6636507.  
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ORIGIN

Query Match 96.8%; Score 30; DB 14; Length 10975;  
Best Local Similarity 100.0%; Fred. No. 8.3e-07;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 10505 CCGCACCGGAAAGTTGAGTAGACGGTGCTG 10534  
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RESULT 50  
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VERSION  
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AUTHORS  
TITLE  
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FEATURES  
source

AY268133 10989 bp RNA linear VRL 03-NOV-2003  
West Nile virus strain PAH001 polyprotein (pol) gene, complete cds.  
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West Nile virus (WNV)  
West Nile virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Flavivirus; Japanese encephalitis virus group.  
1 (bases 1 to 10989)  
Charrel, R.N., Brault, A.C., Gallian, P., Lemasson, J.-J., Murgue, B.,  
Murri, S., Pastorino, B., Zeller, H., de cheese, R., de Micco, P. and de  
Lamballerie, X.  
Evolutionary relationship between Old World West Nile virus  
strains. Evidence for viral gene flow between africa, the middle  
east, and europe  
Virology 315 (2), 381-388 (2003)  
22949215  
14585341  
2 (bases 1 to 10989)  
de Lamballerie, X., Brault, A.C., Gallian, P., Lemasson, J., Murgue, B.,  
Murri, S., Pastorino, B., Zeller, H., Decheese, R., de Micco, P. and  
Charrel, R.N.  
Direct Submission  
Submitted (03-APR-2003) Virology, Medical University, 27 bd Jean  
Moulin, Marseille 13005, France  
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## ORIGIN

Query Match 96.8%; Score 30; DB 14; Length 10989;

Query Match 98.6%; SCORE 30; DB 14;  
Best Local Similarity 100.0%; Pred. No. 8.3e-07;

Best local similarity 100.0%; Freq. NO: 8.3e-07;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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[illegible]

Search completed: March 25, 2005, 09:31:42  
Job time : 668.582 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 00:26:37 ; Search time 157.747 Seconds  
(without alignments)  
1163.332 Million cell updates/sec

Title: US-10-688-489-59

Perfect score: 31

Sequence: 1 tcgccaccggaagttagtagacggtgctg 31

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

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2: Geneseq1990s.\*

3: Geneseq2000s.\*

4: Geneseq2001s.\*

5: Geneseq2001bs.\*

6: Geneseq2002s.\*

7: Geneseq2002bs.\*

8: Geneseq2003s.\*

9: Geneseq2003bs.\*

10: Geneseq2003cs.\*

11: Geneseq2003ds.\*

12: Geneseq2004s.\*

13: Geneseq2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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| 1          | 31    | 100.0       | 31     | ADN36737  | Adn36737 West Nile  |
| 2          | 30    | 96.8        | 10945  | ADN32078  | Adn32078 Genomic D  |
| 3          | 30    | 96.8        | 10945  | ADN367768 | Adn367768 West Nile |
| 4          | 30    | 96.8        | 10975  | ADN98022  | Adn98022 West Nile  |
| 5          | 30    | 96.8        | 11029  | ABZ68481  | Abz68481 Nucleotid  |
| 6          | 30    | 96.8        | 11029  | ABV74821  | Abv74821 West Nile  |
| 7          | 30    | 96.8        | 11029  | ADN98023  | Adn98023 West Nile  |
| 8          | 28    | 90.3        | 10962  | ADK13681  | Adk13681 West Nile  |
| 9          | 22    | 71.0        | 22     | ADN36746  | Adn36746 West Nile  |
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| 11         | 21    | 67.7        | 21     | ADN36745  | Adn36745 West Nile  |
| 12         | 21    | 67.7        | 21     | ADN36748  | Adn36748 West Nile  |
| 13         | 20    | 64.5        | 20     | ADN36749  | Adn36749 West Nile  |
| 14         | 20    | 64.5        | 20     | ADN36740  | Adn36740 West Nile  |
| 15         | 20    | 64.5        | 20     | ADN36747  | Adn36747 West Nile  |
| 16         | 19    | 61.3        | 19     | ADN36744  | Adn36744 West Nile  |
| 17         | 19    | 61.3        | 19     | ADN36738  | Adn36738 West Nile  |
| 18         | 18    | 58.1        | 18     | ADN36742  | Adn36742 West Nile  |
| 19         | 18    | 58.1        | 19     | ADN36739  | Adn36739 West Nile  |
| 20         | 18    | 58.1        | 26     | ADN36825  | Adn36825 West Nile  |

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| 21 | 17 | 54.8 | 17     | 6  | ACN01373    | WNV Hamme           |
| 22 | 17 | 54.8 | 17     | 6  | ACN04650    | WNV Zinzy           |
| 23 | 17 | 54.8 | 17     | 6  | ACN07292    | WNV Amber           |
| 24 | 17 | 54.8 | 17     | 6  | ACN09625    | WNV minus           |
| 25 | 17 | 54.8 | 17     | 6  | ACN07461    | WNV minus           |
| 26 | 17 | 54.8 | 17     | 6  | ACN09628    | WNV minus           |
| 27 | 17 | 54.8 | 17     | 6  | ACN01372    | WNV Hamme           |
| 28 | 17 | 54.8 | 17     | 6  | ACN13635    | WNV minus           |
| 29 | 17 | 54.8 | 17     | 6  | ACN07462    | WNV minus           |
| 30 | 17 | 54.8 | 17     | 6  | ACN09624    | WNV minus           |
| 31 | 17 | 54.8 | 17     | 6  | ACN05425    | WNV DNazy           |
| 32 | 17 | 54.8 | 17     | 6  | ACN04649    | WNV Zinzy           |
| 33 | 17 | 54.8 | 17     | 6  | ACN09626    | WNV minus           |
| 34 | 17 | 54.8 | 17     | 6  | ACN07290    | WNV Amber           |
| 35 | 17 | 54.8 | 17     | 6  | ACN07291    | WNV Amber           |
| 36 | 17 | 54.8 | 17     | 6  | ACN07463    | WNV minus           |
| 37 | 17 | 54.8 | 17     | 6  | ACN07465    | WNV minus           |
| 38 | 17 | 54.8 | 17     | 6  | ACN09627    | WNV minus           |
| 39 | 17 | 54.8 | 17     | 6  | ACN07293    | WNV Amber           |
| 40 | 17 | 54.8 | 17     | 6  | ACN07464    | WNV minus           |
| 41 | 17 | 54.8 | 18     | 12 | ADN36743    | Adn36743 West Nile  |
| 42 | 17 | 54.8 | 53872  | 4  | ABL04952    | Abi04952 Drosophill |
| 43 | 16 | 51.6 | 17     | 6  | ACN14228    | WNV minus           |
| 44 | 16 | 51.6 | 17     | 6  | ACN12344    | WNV minus           |
| 45 | 16 | 51.6 | 17     | 6  | ACN03350    | WNV Inozy           |
| 46 | 16 | 51.6 | 628    | 3  | AAF08395    | Aaf08395 Fusarium   |
| 47 | 16 | 51.6 | 1323   | 10 | ABZ71129    | Abz71129 Mycobacte  |
| 48 | 16 | 51.6 | 1326   | 4  | AAH51995    | Aah51995 Mycobacte  |
| 49 | 16 | 51.6 | 31068  | 4  | ABL28588    | Abi28588 Drosophill |
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| 53 | 15 | 48.4 | 17     | 6  | ACN12345    | WNV minus           |
| 54 | 15 | 48.4 | 17     | 6  | ACN09623    | WNV minus           |
| 55 | 15 | 48.4 | 21     | 12 | ADN36782    | Adn36782 West Nile  |
| 56 | 15 | 48.4 | 22     | 12 | ADN36863    | Adn36863 West Nile  |
| 57 | 15 | 48.4 | 25     | 9  | ACI27596    | Act27596 Human mic  |
| 58 | 15 | 48.4 | 28     | 12 | ADN36864    | Adn36864 West Nile  |
| 59 | 15 | 48.4 | 69     | 12 | ADN36780    | Adn36780 West Nile  |
| 60 | 15 | 48.4 | 87     | 12 | ADN36779    | Adn36779 West Nile  |
| 61 | 15 | 48.4 | 214    | 10 | ABX83471    | Abx83471 Corn ear-  |
| 62 | 15 | 48.4 | 436    | 9  | ACH03748    | Acho3748 Wheat ste  |
| 63 | 15 | 48.4 | 551    | 10 | ADD34062    | Add34062 Mouse mit  |
| 64 | 15 | 48.4 | 600    | 9  | ACH03761    | Acho3761 Wheat ste  |
| 65 | 15 | 48.4 | 616    | 9  | ACH03758    | Acho3758 Corn ster  |
| 66 | 15 | 48.4 | 673    | 9  | ACH03757    | Acho3757 Corn ster  |
| 67 | 15 | 48.4 | 1795   | 6  | ABQ42685    | Abq42685 Oligonucl  |
| 68 | 15 | 48.4 | 1795   | 6  | ABQ42684    | Abq42684 Oligonucl  |
| 69 | 15 | 48.4 | 1863   | 5  | AAH65402    | Aah65402 C glutam   |
| 70 | 15 | 48.4 | 1969   | 11 | ADL65984    | Adl65984 C. glutam  |
| 71 | 15 | 48.4 | 2448   | 13 | ADR85016    | Adr85016 Aspergill  |
| 72 | 15 | 48.4 | 3246   | 8  | ACC57669    | Acc57669 Mouse pro  |
| 73 | 15 | 48.4 | 4016   | 2  | AAT11083    | Aat11083 Mouse JAK  |
| 74 | 15 | 48.4 | 8448   | 13 | ADR84429    | Adr84429 Aspergill  |
| 75 | 15 | 48.4 | 35998  | 12 | ADQ97983    | Adq97983 Mouse can  |
| 76 | 15 | 48.4 | 110000 | 10 | ADF77343_18 | Continuation (19 o  |
| 77 | 15 | 48.4 | 349980 | 5  | AAH68525    | Aah68525 C glutam   |
| 78 | 14 | 45.2 | 17     | 6  | ACN04651    | WNV Zinzy           |
| 79 | 14 | 45.2 | 17     | 6  | ACN03349    | WNV Inozy           |
| 80 | 14 | 45.2 | 103    | 3  | AAH53431    | Aah53431 Human thl  |
| 81 | 14 | 45.2 | 127    | 4  | AAI23156    | Aai23156 Human bre  |
| 82 | 14 | 45.2 | 151    | 4  | AAH37214    | Aah37214 Novel hum  |
| 83 | 14 | 45.2 | 220    | 2  | AAH40667    | Aah40667 Human sec  |
| 84 | 14 | 45.2 | 231    | 4  | AAI14294    | Aai14294 Human bre  |
| 85 | 14 | 45.2 | 236    | 3  | AAZ42671    | Aaz42671 Human 5'   |
| 86 | 14 | 45.2 | 370    | 5  | ABV08938    | Abv08938 Human pro  |
| 87 | 14 | 45.2 | 400    | 2  | AAH41295    | Aah41295 Human sec  |
| 88 | 14 | 45.2 | 408    | 12 | ADQ84440    | Adq84440 Human tum  |
| 89 | 14 | 45.2 | 408    | 12 | ADQ85224    | Adq85224 Human tum  |
| 90 | 14 | 45.2 | 408    | 13 | ADQ83268    | Adq83268 Human tum  |
| 91 | 14 | 45.2 | 419    | 2  | AAV33191    | Aav33191 Secreterd  |
| 92 | 14 | 45.2 | 419    | 2  | AAZ40834    | Aaz40834 Secreterd  |
| 93 | 14 | 45.2 | 419    | 11 | ADM77856    | Adm77856 Human CDN  |

|       |    |      |        |    |           |                              |       |    |      |        |    |           |                     |
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| C 94  | 14 | 45.2 | 419    | 12 | ADP19132  | Adp19132 Human sec           | C 167 | 14 | 45.2 | 185035 | 12 | ADQ20284  | Adq20284 Human sof  |
| C 95  | 14 | 45.2 | 425    | 5  | AAZ40815  | Aaz40815 Secreted            | C 168 | 13 | 41.9 | 13     | 5  | ABH13266  | Abh13266 Oligonucl  |
| C 96  | 14 | 45.2 | 425    | 5  | AAZ40815  | Aaz40815 Secreted            | C 169 | 13 | 41.9 | 13     | 5  | ABH13267  | Abh13267 Oligonucl  |
| C 97  | 14 | 45.2 | 425    | 11 | ADM7792   | Adm7792 Human cDN            | C 170 | 13 | 41.9 | 17     | 6  | ACN09622  | Acn09622 WNV minus  |
| C 98  | 14 | 45.2 | 425    | 12 | ADP19113  | Adp19113 Human sec           | C 171 | 13 | 41.9 | 17     | 6  | ACN03348  | Acn03348 WNV Inoxy  |
| C 99  | 14 | 45.2 | 427    | 5  | ABV38826  | Abv38826 Human pro           | C 172 | 13 | 41.9 | 17     | 6  | ACN14229  | Acn14229 WNV minus  |
| 100   | 14 | 45.2 | 456    | 9  | ACH39996  | Ach39996 Human foe           | C 173 | 13 | 41.9 | 18     | 2  | AAV44610  | Aav44610 Human unc  |
| 101   | 14 | 45.2 | 515    | 6  | ABV97326  | Abv97326 Human pan           | C 174 | 13 | 41.9 | 19     | 12 | ADN36783  | Adn36783 West Nile  |
| 102   | 14 | 45.2 | 516    | 6  | ABV96872  | Abv96872 Human pan           | C 175 | 13 | 41.9 | 40     | 3  | AAZ296102 | Aaz296102 Polyucl   |
| C 103 | 14 | 45.2 | 516    | 13 | ACN46696  | Acn46696 Cotton pr           | C 176 | 13 | 41.9 | 52     | 8  | ACA02212  | ACA02212 D. melano  |
| C 104 | 14 | 45.2 | 542    | 12 | ADJ10678  | Adj10678 Recombina           | C 177 | 13 | 41.9 | 52     | 8  | ACA02212  | ACA02212 D. melano  |
| C 105 | 14 | 45.2 | 564    | 3  | AAC08029  | Aac08029 Human sec           | C 178 | 13 | 41.9 | 59     | 4  | AAI14118  | Aai14118 Antibody   |
| C 106 | 14 | 45.2 | 574    | 13 | ADR65698  | Adr65698 Cotton CD           | C 179 | 13 | 41.9 | 87     | 2  | AAV08087  | Aav08087 Fragment   |
| C 107 | 14 | 45.2 | 576    | 13 | ACN51680  | Acn51680 Cotton an           | C 180 | 13 | 41.9 | 87     | 2  | AAZ06298  | Aaz06298 Synthetic  |
| C 108 | 14 | 45.2 | 654    | 4  | ABA09109  | Aba09109 Human HSP           | C 181 | 13 | 41.9 | 88     | 6  | AAI172469 | Aai172469 D. melano |
| C 109 | 14 | 45.2 | 659    | 13 | ADR63650  | Adr63650 Cotton CD           | C 182 | 13 | 41.9 | 88     | 6  | ACA02213  | ACA02213 D. melano  |
| C 110 | 14 | 45.2 | 668    | 5  | AAH64916  | Aah64916 Human sec           | C 183 | 13 | 41.9 | 100    | 8  | ACD69141  | AcD69141 E. coli K  |
| C 111 | 14 | 45.2 | 941    | 12 | ADO40822  | Ado40822 DNA encod           | C 184 | 13 | 41.9 | 216    | 11 | ABD15615  | Abd15615 Pseudomon  |
| C 112 | 14 | 45.2 | 1087   | 11 | ACN84344  | Acn84344 Breast ca           | C 185 | 13 | 41.9 | 300    | 6  | ABL73959  | AbL73959 Corn taas  |
| C 113 | 14 | 45.2 | 1100   | 2  | AAV18890  | Aav18890 Rat Hyper           | C 186 | 13 | 41.9 | 302    | 4  | AAZ59160  | Aaz59160 Human can  |
| C 114 | 14 | 45.2 | 1100   | 3  | AAZ75037  | Aaz75037 cDNA enco           | C 187 | 13 | 41.9 | 313    | 4  | AAH71336  | Aah71336 Human cer  |
| C 115 | 14 | 45.2 | 1100   | 10 | ADG32027  | Adg32027 Rat hyper           | C 188 | 13 | 41.9 | 313    | 4  | AAH71336  | Aah71336 Human cer  |
| C 116 | 14 | 45.2 | 1149   | 10 | ACF68233  | Acf68233 Photorhab           | C 189 | 13 | 41.9 | 334    | 3  | AAA31143  | Aaa31143 Plant mic  |
| C 117 | 14 | 45.2 | 1455   | 3  | AAF21889  | Aaf21889 Human bre           | C 190 | 13 | 41.9 | 343    | 6  | ABQ85935  | Abq85935 Arabidops  |
| C 118 | 14 | 45.2 | 1659   | 13 | ADS49819  | Ads49819 Bacterial           | C 191 | 13 | 41.9 | 358    | 6  | ABQ85702  | Abq85702 Arabidops  |
| 119   | 14 | 45.2 | 1738   | 9  | ADAL13428 | Adal13428 Human rho          | C 192 | 13 | 41.9 | 366    | 4  | ABQ85441  | Abq85441 DNA encod  |
| 120   | 14 | 45.2 | 1738   | 9  | ADAL13428 | Adal13428 Human rho          | C 193 | 13 | 41.9 | 368    | 9  | ACH46578  | Ach46578 Human inf  |
| 121   | 14 | 45.2 | 1738   | 10 | ADG47133  | Adg47133 Human rho           | C 194 | 13 | 41.9 | 375    | 13 | ACN50396  | Acn50396 Cotton ma  |
| 122   | 14 | 45.2 | 1738   | 10 | ADG47133  | Adg47133 Human rho           | C 195 | 13 | 41.9 | 390    | 2  | AAV08037  | Aav08037 Light cha  |
| 123   | 14 | 45.2 | 1738   | 12 | ADQ86031  | Adq86031 Human rho           | C 196 | 13 | 41.9 | 390    | 2  | AAZ06301  | Aaz06301 Human chi  |
| C 124 | 14 | 45.2 | 1845   | 5  | AAZ89517  | Aaz89517 Human tum           | C 197 | 13 | 41.9 | 413    | 8  | ABX44157  | Abx44157 Bovine ES  |
| C 125 | 14 | 45.2 | 1854   | 11 | ADM03408  | Adm03408 Human cDN           | C 198 | 13 | 41.9 | 424    | 6  | ABT06970  | Abt06970 Human ova  |
| C 126 | 14 | 45.2 | 1912   | 5  | AAZ84651  | Aaz84651 DNA encod           | C 199 | 13 | 41.9 | 424    | 6  | ABT06970  | Abt06970 Human ova  |
| C 127 | 14 | 45.2 | 1955   | 4  | AAZ09956  | Aaz09956 Human dru           | C 200 | 13 | 41.9 | 429    | 8  | ABX72848  | Abx72848 Human ova  |
| C 128 | 14 | 45.2 | 1959   | 3  | AAZ59835  | Aaz59835 Human SEC           | C 201 | 13 | 41.9 | 445    | 11 | ADM65226  | Adm65226 Bovine ES  |
| C 129 | 14 | 45.2 | 1959   | 3  | AAZ53429  | Aaz53429 Human thi           | C 202 | 13 | 41.9 | 445    | 11 | ADM65181  | Adm65181 Human Y C  |
| C 130 | 14 | 45.2 | 2010   | 4  | ABL22235  | AbL22235 Drosophil           | C 203 | 13 | 41.9 | 446    | 11 | ADM65178  | Adm65178 Human Y C  |
| C 131 | 14 | 45.2 | 2114   | 13 | ADQ85985  | Adq85985 Human tum           | C 204 | 13 | 41.9 | 454    | 3  | AAA31071  | Aaa31071 Plant mic  |
| C 132 | 14 | 45.2 | 2180   | 11 | ADN95847  | Adn95847 Human BEC           | C 205 | 13 | 41.9 | 458    | 6  | ABL93710  | AbL93710 Arabidops  |
| C 133 | 14 | 45.2 | 2180   | 13 | ACN40882  | Acn40882 Tumour-as           | C 206 | 13 | 41.9 | 462    | 5  | ABV49656  | Abv49656 Human pro  |
| C 134 | 14 | 45.2 | 2187   | 3  | AAZ92220  | Aaz92220 Human thi           | C 207 | 13 | 41.9 | 464    | 6  | ABN25122  | Abn25122 Human ORF  |
| C 135 | 14 | 45.2 | 2187   | 6  | AAI72961  | Aai72961 Human thi           | C 208 | 13 | 41.9 | 468    | 4  | ABA26645  | AbA26645 Probe #51  |
| C 136 | 14 | 45.2 | 2310   | 11 | ABD11602  | Abd11602 Pseudomon           | C 209 | 13 | 41.9 | 473    | 9  | ACH35927  | Ach35927 Human end  |
| C 137 | 14 | 45.2 | 2655   | 5  | AAZ89516  | Aaz89516 DNA encod           | C 210 | 13 | 41.9 | 474    | 3  | AAC42810  | Aac42810 Arabidops  |
| C 138 | 14 | 45.2 | 2816   | 4  | ABL13687  | AbL13687 Drosophil           | C 211 | 13 | 41.9 | 490    | 8  | ABZ55607  | Abz55607 Aspergill  |
| C 139 | 14 | 45.2 | 3085   | 4  | ABL16797  | AbL16797 Drosophil           | C 212 | 13 | 41.9 | 498    | 10 | ADE81712  | Ade81712 Arabidops  |
| 140   | 14 | 45.2 | 3562   | 5  | ABA16080  | AbA16080 Human ner           | C 213 | 13 | 41.9 | 499    | 2  | AAQ40729  | Aaq40729 Human eps  |
| 141   | 14 | 45.2 | 3564   | 5  | ABA16079  | AbA16079 Human ner           | C 214 | 13 | 41.9 | 500    | 13 | ACN45774  | Acn45774 Cotton pr  |
| 142   | 14 | 45.2 | 3564   | 5  | ABA16081  | AbA16081 Human ner           | C 215 | 13 | 41.9 | 501    | 6  | ABQ42601  | Abq42601 Oligonucl  |
| C 143 | 14 | 45.2 | 3858   | 4  | ABL13828  | AbL13828 Drosophil           | C 216 | 13 | 41.9 | 501    | 6  | ABQ42600  | Abq42600 Oligonucl  |
| 144   | 14 | 45.2 | 4488   | 4  | ABL17095  | AbL17095 Drosophil           | C 217 | 13 | 41.9 | 507    | 6  | ABN68232  | Abn68232 Streptoco  |
| 145   | 14 | 45.2 | 4618   | 4  | ABL22234  | AbL22234 Drosophil           | C 218 | 13 | 41.9 | 511    | 6  | ABQ21475  | Abq21475 Oligonucl  |
| C 146 | 14 | 45.2 | 4851   | 8  | ACN37619  | Acn37619 Prokaryot           | C 219 | 13 | 41.9 | 511    | 6  | ABQ21474  | Abq21474 Oligonucl  |
| C 147 | 14 | 45.2 | 5186   | 4  | ABL13686  | AbL13686 Drosophil           | C 220 | 13 | 41.9 | 514    | 13 | ACN45487  | Acn45487 Cotton pr  |
| C 148 | 14 | 45.2 | 6307   | 6  | ABL33341  | AbL33341 Human im            | C 221 | 13 | 41.9 | 519    | 10 | ADE59753  | Ade59753 Rat gene   |
| 149   | 14 | 45.2 | 6898   | 6  | ABN80223  | Abn80223 Human che           | C 222 | 13 | 41.9 | 528    | 6  | ABZ14654  | Abz14654 Arabidops  |
| C 150 | 14 | 45.2 | 6932   | 13 | ADR84543  | Adr84543 Aspergill           | C 223 | 13 | 41.9 | 528    | 13 | ACN60951  | Acn60951 Cotton gy  |
| C 151 | 14 | 45.2 | 8046   | 4  | ABL17094  | AbL17094 Drosophil           | C 224 | 13 | 41.9 | 529    | 5  | AAH87936  | Aah87936 Peppermin  |
| 152   | 14 | 45.2 | 10428  | 12 | ADJ81646  | Adj81646 Human tyr           | C 225 | 13 | 41.9 | 546    | 4  | ABL13169  | AbL13169 Drosophil  |
| C 153 | 14 | 45.2 | 18796  | 4  | AAZ59517  | Aaz59517 Propionib           | C 226 | 13 | 41.9 | 546    | 9  | ACH27564  | Ach27564 Human adu  |
| 154   | 14 | 45.2 | 18796  | 8  | ACF64446  | Acf64446 Propionib           | C 227 | 13 | 41.9 | 549    | 3  | AAC94357  | Aac94357 Cat flea   |
| C 155 | 14 | 45.2 | 20261  | 4  | ABL16796  | AbL16796 Drosophil           | C 228 | 13 | 41.9 | 559    | 6  | ABQ16264  | Abq16264 Oligonucl  |
| 156   | 14 | 45.2 | 24593  | 1  | AAZ50226  | Aaz50226 Sequence            | C 229 | 13 | 41.9 | 559    | 3  | ABQ16265  | Abq16265 Oligonucl  |
| C 157 | 14 | 45.2 | 24596  | 1  | AAZ50182  | Aaz50182 Complete            | C 230 | 13 | 41.9 | 566    | 3  | ABQ40030  | Abq40030 Arabidops  |
| C 158 | 14 | 45.2 | 34719  | 12 | ADP90617  | Adp90617 Micromono           | C 231 | 13 | 41.9 | 579    | 6  | ABK76120  | Abk76120 Bacillus   |
| C 159 | 14 | 45.2 | 3712   | 12 | ADQ18757  | Adq18757 Human sof           | C 232 | 13 | 41.9 | 580    | 4  | AAI193755 | Aai193755 Human pol |
| C 160 | 14 | 45.2 | 47318  | 11 | ACN44730  | Acn44730 Human gen           | C 233 | 13 | 41.9 | 583    | 6  | ABQ60208  | Abq60208 Human col  |
| C 161 | 14 | 45.2 | 66566  | 3  | AAZ53450  | Aaz53450 Human thi           | C 234 | 13 | 41.9 | 597    | 4  | ABL22817  | AbL22817 Drosophil  |
| C 162 | 14 | 45.2 | 110000 | 3  | AAF22303  | Aaf22303 Continuation (4 of  | C 235 | 13 | 41.9 | 600    | 6  | ABK48977  | Abk48977 Physice-b  |
| 163   | 14 | 45.2 | 110000 | 10 | ACF67367  | Acf67367 Continuation (10 of | C 236 | 13 | 41.9 | 602    | 6  | ABV96080  | Abv96080 Human pan  |
| 164   | 14 | 45.2 | 110000 | 3  | ACF65384  | Acf65384 Continuation (4 of  | C 237 | 13 | 41.9 | 603    | 10 | ADF00887  | Adf00887 Bacterial  |
| C 165 | 14 | 45.2 | 185035 | 6  | ABT10147  | Abt10147 Human bre           | C 238 | 13 | 41.9 | 612    | 13 | ACN46486  | Acn46486 Cotton pr  |
| C 166 | 14 | 45.2 | 185035 | 8  | ACA64951  | Aca64951 Human FEN           | C 239 | 13 | 41.9 | 624    | 11 | ABD03668  | Abd03668 Pseudomon  |
|       |    |      |        |    |           |                              | C 240 | 13 | 41.9 | 628    | 4  | AAK91018  | Aak91018 Human dig  |

|       |    |      |      |    |           |                     |       |    |      |      |    |           |                     |
|-------|----|------|------|----|-----------|---------------------|-------|----|------|------|----|-----------|---------------------|
| C 240 | 13 | 41.9 | 628  | 5  | AAS32053  | Aas32053 Human liv  | C 313 | 13 | 41.9 | 1320 | 10 | ADC61134  | Adc61134 Baeyer-Vi  |
| C 241 | 13 | 41.9 | 628  | 6  | ABN90408  | Abn90408 Human liv  | 314   | 13 | 41.9 | 1324 | 3  | AAC45583  | Aac45583 Arabidops  |
| C 242 | 13 | 41.9 | 628  | 11 | ADJ15321  | Adj15321 Human liv  | 315   | 13 | 41.9 | 1325 | 3  | AAC33679  | Aac33679 Arabidops  |
| C 243 | 13 | 41.9 | 630  | 4  | AAO08468  | Aao08468 Human sec  | C 316 | 13 | 41.9 | 1326 | 5  | AAH68314  | Aah68314 C glutami  |
| C 244 | 13 | 41.9 | 651  | 8  | ACA30042  | Aca30042 Prokaryot  | C 317 | 13 | 41.9 | 1332 | 13 | ADG61662  | Adg61662 Bacterial  |
| C 245 | 13 | 41.9 | 651  | 10 | ADH85534  | Adh85534 Enterococ  | C 318 | 13 | 41.9 | 1338 | 4  | ABL28569  | AbL28569 Drosophil  |
| C 246 | 13 | 41.9 | 651  | 11 | ABD15572  | Abd15572 Pseudomon  | C 319 | 13 | 41.9 | 1342 | 9  | ADL65332  | AdL65332 Arabidops  |
| C 247 | 13 | 41.9 | 654  | 10 | ADC93120  | Adc93120 E. faeciu  | C 320 | 13 | 41.9 | 1342 | 6  | ADL15462  | AdL15462 DNA encod  |
| C 248 | 13 | 41.9 | 657  | 10 | ADP00507  | Adp00507 Bacterial  | C 321 | 13 | 41.9 | 1342 | 10 | ADD30225  | Add30225 Plant yle  |
| C 249 | 13 | 41.9 | 660  | 4  | AAK66329  | Aak66329 Human imm  | C 322 | 13 | 41.9 | 1342 | 12 | ADJ43616  | Adj43616 Plant tra  |
| C 250 | 13 | 41.9 | 666  | 6  | ABQ22365  | Abq22365 Oligonuel  | C 323 | 13 | 41.9 | 1342 | 12 | ADQ02314  | AdQ02314 Thalecres  |
| C 251 | 13 | 41.9 | 666  | 6  | ABQ22364  | Abq22364 Oligonuel  | C 324 | 13 | 41.9 | 1342 | 12 | ADO03426  | Ado03426 Thalecres  |
| C 252 | 13 | 41.9 | 667  | 4  | AAF71326  | Aaf71326 Corynebac  | C 325 | 13 | 41.9 | 1342 | 12 | ADQ16261  | AdQ16261 Thalecres  |
| C 253 | 13 | 41.9 | 677  | 6  | ABQ65789  | Abq65789 Arabidops  | C 326 | 13 | 41.9 | 1345 | 6  | ABL60012  | AbL60012 Novel hum  |
| C 254 | 13 | 41.9 | 684  | 3  | AAZ36248  | Aaz36248 cDNA enco  | C 327 | 13 | 41.9 | 1353 | 6  | ABL01533  | AbL01533 Murine ap  |
| C 255 | 13 | 41.9 | 686  | 3  | AAF14763  | Aaf14763 Aspergill  | C 328 | 13 | 41.9 | 1359 | 11 | ABD13452  | Abd13452 Pseudomon  |
| C 256 | 13 | 41.9 | 717  | 2  | AAV44637  | Aav44637 Human unc  | C 329 | 13 | 41.9 | 1360 | 2  | AAV21282  | Aav21282 Mus muscu  |
| C 257 | 13 | 41.9 | 732  | 12 | ACH87446  | Ach87446 Human gen  | C 330 | 13 | 41.9 | 1376 | 12 | ADL90359  | AdL90359 Clostridi  |
| C 258 | 13 | 41.9 | 743  | 5  | AAAS91497 | Aaas91497 DNA encod | C 331 | 13 | 41.9 | 1376 | 12 | ADL90357  | AdL90357 Clostridi  |
| C 259 | 13 | 41.9 | 751  | 4  | AAAS23274 | Aaas23274 DNA encod | C 332 | 13 | 41.9 | 1376 | 12 | ADL90353  | AdL90353 Clostridi  |
| C 260 | 13 | 41.9 | 752  | 4  | AAH03559  | Aah03559 Human CDN  | C 333 | 13 | 41.9 | 1376 | 12 | ADL90355  | AdL90355 Clostridi  |
| C 261 | 13 | 41.9 | 753  | 10 | ADP81903  | Adp81903 Leukaemia  | C 334 | 13 | 41.9 | 1381 | 12 | ADN60478  | Adn60478 B. lichen  |
| C 262 | 13 | 41.9 | 761  | 6  | ABQ32387  | Abq32387 Oligonuel  | C 335 | 13 | 41.9 | 1385 | 12 | ADL90351  | AdL90351 Clostridi  |
| C 263 | 13 | 41.9 | 761  | 6  | ABQ32386  | Abq32386 Oligonuel  | C 336 | 13 | 41.9 | 1404 | 11 | ABD05514  | AbD05514 Pseudomon  |
| C 264 | 13 | 41.9 | 780  | 11 | ABD15488  | Abd15488 Pseudomon  | C 337 | 13 | 41.9 | 1405 | 12 | ADN60474  | Adn60474 B. lichen  |
| C 265 | 13 | 41.9 | 795  | 8  | ABZ51382  | Abz51382 Aspergill  | C 338 | 13 | 41.9 | 1411 | 3  | AAC46753  | Aac46753 Arabidops  |
| C 266 | 13 | 41.9 | 800  | 12 | ADL18154  | Adl18154 P. aerugi  | C 339 | 13 | 41.9 | 1431 | 3  | AAC46348  | Aac46348 Arabidops  |
| C 267 | 13 | 41.9 | 803  | 2  | AAZ24839  | Aaz24839 Human sec  | C 340 | 13 | 41.9 | 1433 | 3  | ABL08297  | AbL08297 Drosophil  |
| C 268 | 13 | 41.9 | 803  | 8  | ADA40091  | Ada40091 Human sec  | C 341 | 13 | 41.9 | 1435 | 3  | ABL040039 | AbL040039 Arabidops |
| C 269 | 13 | 41.9 | 803  | 10 | ADC73665  | Adc73665 Human sec  | C 342 | 13 | 41.9 | 1447 | 5  | AAAS65340 | Aaas65340 DNA encod |
| C 270 | 13 | 41.9 | 814  | 3  | AAF08534  | Aaf08534 Fusarium   | C 343 | 13 | 41.9 | 1462 | 4  | ABL09327  | AbL09327 Drosophil  |
| C 271 | 13 | 41.9 | 825  | 8  | ACA51699  | Aca51699 Prokaryot  | C 344 | 13 | 41.9 | 1464 | 4  | AAAS4301  | Aaas4301 Pseudomon  |
| C 272 | 13 | 41.9 | 831  | 5  | AAAS78026 | Aaas78026 DNA encod | C 345 | 13 | 41.9 | 1497 | 2  | AAQ03572  | Aaq03572 Sequence   |
| C 273 | 13 | 41.9 | 833  | 11 | ADP65885  | Adp65885 Mouse EST  | C 346 | 13 | 41.9 | 1497 | 2  | AAQ03571  | Aaq03571 Sequence   |
| C 274 | 13 | 41.9 | 849  | 11 | ABD13423  | Abd13423 Pseudomon  | C 347 | 13 | 41.9 | 1497 | 2  | AAQ03367  | Aaq03367 Phenol ox  |
| C 275 | 13 | 41.9 | 852  | 12 | ACH87068  | Ach87068 Human gen  | C 348 | 13 | 41.9 | 1525 | 3  | AAQ03358  | Aaq03358 Arabidops  |
| C 276 | 13 | 41.9 | 862  | 8  | ACA48745  | Aca48745 Prokaryot  | C 349 | 13 | 41.9 | 1530 | 2  | AAV21283  | Aav21283 Mus muscu  |
| C 277 | 13 | 41.9 | 879  | 12 | ADN72326  | Adn72326 Thale cre  | C 350 | 13 | 41.9 | 1548 | 13 | ADR85685  | Adr85685 Aspergill  |
| C 278 | 13 | 41.9 | 909  | 13 | ADS48012  | Ads48012 Bacterial  | C 351 | 13 | 41.9 | 1548 | 13 | ADR84911  | Adr84911 Aspergill  |
| C 279 | 13 | 41.9 | 936  | 10 | ADC23800  | Adc23800 DNA encod  | C 352 | 13 | 41.9 | 1548 | 13 | ADR85498  | Adr85498 Aspergill  |
| C 280 | 13 | 41.9 | 936  | 12 | ADH35901  | Adh35901 Chemical   | C 353 | 13 | 41.9 | 1548 | 13 | ADR85098  | Adr85098 Aspergill  |
| C 281 | 13 | 41.9 | 936  | 12 | ADG93602  | Adg93602 Nitrilase  | C 354 | 13 | 41.9 | 1558 | 8  | ABZ34834  | Abz34834 Coding se  |
| C 282 | 13 | 41.9 | 936  | 12 | ADG36362  | Adg36362 DNA encod  | C 355 | 13 | 41.9 | 1558 | 11 | ADN95492  | Adn95492 Human BEC  |
| C 283 | 13 | 41.9 | 936  | 12 | AD164320  | Ad164320 DNA encod  | C 356 | 13 | 41.9 | 1563 | 11 | ABD03962  | Abd03962 Pseudomon  |
| C 284 | 13 | 41.9 | 945  | 11 | ABD15527  | Abd15527 Pseudomon  | C 357 | 13 | 41.9 | 1596 | 3  | ADC61124  | Adc61124 Baeyer-Vi  |
| C 285 | 13 | 41.9 | 947  | 6  | ABL89703  | AbL89703 Human pol  | C 358 | 13 | 41.9 | 1605 | 3  | AAC42127  | Aac42127 Arabidops  |
| C 286 | 13 | 41.9 | 982  | 13 | ADG611352 | Adg611352 Bacterial | C 359 | 13 | 41.9 | 1671 | 4  | AAAS67852 | Aaas67852 Corynebac |
| C 287 | 13 | 41.9 | 990  | 3  | AAQ33134  | Aaq33134 Arabidops  | C 360 | 13 | 41.9 | 1671 | 11 | ABD03748  | AbD03748 Pseudomon  |
| C 288 | 13 | 41.9 | 1002 | 8  | ACF39335  | Acf39335 Mycobacte  | C 361 | 13 | 41.9 | 1680 | 11 | ABD05483  | AbD05483 Pseudomon  |
| C 289 | 13 | 41.9 | 1008 | 12 | ADQ07694  | Ado07694 Mouse pol  | C 362 | 13 | 41.9 | 1685 | 3  | AAC39029  | Aac39029 Arabidops  |
| C 290 | 13 | 41.9 | 1030 | 3  | AAQ45904  | Aac45904 Arabidops  | C 363 | 13 | 41.9 | 1695 | 12 | ADJ35101  | Adj35101 DNA encod  |
| C 291 | 13 | 41.9 | 1035 | 3  | AAQ47938  | Aac47938 Arabidops  | C 364 | 13 | 41.9 | 1730 | 5  | AAS88807  | Aas88807 DNA encod  |
| C 292 | 13 | 41.9 | 1045 | 6  | ABK35230  | Abk35230 Human CDN  | C 365 | 13 | 41.9 | 1753 | 10 | ADC30827  | Adc30827 Human nov  |
| C 293 | 13 | 41.9 | 1049 | 3  | AAQ35933  | Aac35933 Arabidops  | C 366 | 13 | 41.9 | 1754 | 12 | ADG32542  | Adg32542 DNA encod  |
| C 294 | 13 | 41.9 | 1058 | 3  | AAQ77714  | Aac77714 Human can  | C 367 | 13 | 41.9 | 1826 | 12 | AAQ90837  | Aaq90837 Maize his  |
| C 295 | 13 | 41.9 | 1065 | 13 | ADR47154  | Adr47154 Nocardiop  | C 368 | 13 | 41.9 | 1833 | 2  | AAQ03578  | Aaq03578 Synthetic  |
| C 296 | 13 | 41.9 | 1085 | 4  | ABA09563  | Aba09563 Human bk2  | C 369 | 13 | 41.9 | 1833 | 2  | AAT05738  | Aat05738 B. thurin  |
| C 297 | 13 | 41.9 | 1085 | 4  | AAK52774  | Aak52774 Human pol  | C 370 | 13 | 41.9 | 1833 | 2  | AAT40340  | Aat40340 Synthetic  |
| C 298 | 13 | 41.9 | 1089 | 2  | AAV21284  | Aav21284 Mus muscu  | C 371 | 13 | 41.9 | 1833 | 2  | ADG25143  | Adg25143 Codon opt  |
| C 299 | 13 | 41.9 | 1097 | 3  | AAQ42265  | Aac42265 Arabidops  | C 372 | 13 | 41.9 | 1833 | 3  | AAAS59994 | Aaz59994 Synthetic  |
| C 300 | 13 | 41.9 | 1098 | 6  | ABSG64870 | Absg64870 DNA encod | C 373 | 13 | 41.9 | 1833 | 11 | ACH95250  | Ach95250 Klebsiell  |
| C 301 | 13 | 41.9 | 1104 | 11 | ABD05533  | Abd05533 Pseudomon  | C 374 | 13 | 41.9 | 1834 | 13 | ADG61396  | Adg61396 Bacterial  |
| C 302 | 13 | 41.9 | 1116 | 6  | ABK75724  | Abk75724 Bacillus   | C 375 | 13 | 41.9 | 1860 | 8  | ACA30477  | Aca30477 Prokaryot  |
| C 303 | 13 | 41.9 | 1146 | 10 | ADG50518  | Aad50518 Mycobacte  | C 376 | 13 | 41.9 | 1995 | 11 | ABD07179  | Abd07179 Pseudomon  |
| C 304 | 13 | 41.9 | 1212 | 6  | ABZ13761  | Abz13761 Arabidops  | C 377 | 13 | 41.9 | 2000 | 10 | ACC60755  | Acc60755 Gene sequ  |
| C 305 | 13 | 41.9 | 1250 | 5  | AAAS78025 | Aaas78025 DNA encod | C 378 | 13 | 41.9 | 2000 | 10 | ADG61933  | Adg61933 Disease c  |
| C 306 | 13 | 41.9 | 1257 | 11 | ABD02288  | Abd02288 Pseudomon  | C 379 | 13 | 41.9 | 2009 | 3  | AAAN36211 | Aac36211 Arabidops  |
| C 307 | 13 | 41.9 | 1266 | 10 | ACF58067  | Acf58067 D. melano  | C 380 | 13 | 41.9 | 2017 | 1  | AAN91804  | Aan91804 Human pap  |
| C 308 | 13 | 41.9 | 1268 | 3  | AAQ36637  | Aac36637 Arabidops  | C 381 | 13 | 41.9 | 2024 | 12 | ADG98281  | Adg98281 Mouse ClG  |
| C 309 | 13 | 41.9 | 1278 | 11 | ABD03879  | Abd03879 Pseudomon  | C 382 | 13 | 41.9 | 2037 | 5  | AAG67460  | Aah67460 C glutami  |
| C 310 | 13 | 41.9 | 1287 | 6  | ABZ14624  | Abz14624 Arabidops  | C 383 | 13 | 41.9 | 2043 | 6  | ABZ13532  | Abz13532 Arabidops  |
| C 311 | 13 | 41.9 | 1288 | 6  | ABQ14513  | Abq14513 Oligonuel  | C 384 | 13 | 41.9 | 2043 | 2  | ABZ23149  | Abz23149 Environme  |
| C 312 | 13 | 41.9 | 1288 | 6  | ABQ14512  | Abq14512 Oligonuel  | C 385 | 13 | 41.9 | 2049 | 2  | AAQ03573  | Aaq03573 Phenol ox  |



XX (GENP-) GEN-PROBE INC.  
 XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;  
 XX WPI; 2004-389590/36.  
 DR  
 XX New hybridization assay probe comprising target-complementary sequence of  
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
 PT  
 XX Claim 18; SEQ ID NO 59; 135pp; English.  
 PS  
 XX This invention relates to a novel hybridisation assay probe, for  
 CC detecting a nucleic acid, which is a probe sequence that comprises a  
 CC target-complementary sequence of bases, and optionally one or more base  
 CC sequences that are not complementary to the nucleic acid that is to be  
 CC detected. The hybridisation assay probes and the kits are useful in  
 CC detecting and amplifying a target nucleic acid sequence, for example  
 CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC birds and culex mosquitoes, with humans and horses serving as incidental  
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
 CC invention may allow for accurate and efficient high throughput screening.  
 CC The present sequence is that of an oligonucleotide probe which is related  
 CC to the invention.  
 XX  
 XX Sequence 31 BP; 6 A; 8 C; 11 G; 6 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 31; DB 12; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-08;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGCCACCGGAAGTTGAGTAGACGCTGCTG 31  
 DB 1 TCCGCCACCGGAAGTTGAGTAGACGCTGCTG 31  
 RESULT 2  
 ADR32078  
 ID ADR32078 standard; DNA; 10945 BP.  
 AC ADR32078;  
 XX  
 XX 18-NOV-2004 (first entry)  
 DT  
 DE Genomic DNA of a West Nile virus.  
 XX  
 XX analysis; target; real time PCR; ds; genomic.  
 KW  
 XX West Nile virus.  
 OS  
 XX WO2004072230-A2.  
 PN  
 XX 26-AUG-2004.  
 PD  
 XX 10-FEB-2004; 2004WO-US0002012.  
 PF  
 XX 10-FEB-2003; 2003US-00361004.  
 PR  
 XX (CLEA-) CLEARANT INC.  
 PA  
 XX Mckenney K, Gillmeister L, Marlowe K, Armistead D;  
 PI  
 XX WPI; 2004-625843/60.  
 DR  
 XX Analyzing a target nucleic acid sequence in a biological material by real  
 PT time PCR using nucleic acid primers that are separated by at least 750  
 PT nucleic acid residues in the target sequence.  
 PT  
 XX Disclosure; SEQ ID NO 5; 96pp; English.  
 PS  
 XX The invention relates to a novel method for analysing a target nucleic  
 CC acid sequence in a biological material. The method comprises adding at

CC least two nucleic acid primers that hybridise under stringent conditions  
 CC to predetermined nucleic acid sequences of the target nucleic acid  
 CC sequence that are separated by at least 750 nucleic acid residues,  
 CC amplifying the target nucleic acid sequence by PCR, and detecting and  
 CC quantifying the target nucleic acid sequence. The methods and  
 CC compositions of the present invention are useful for analysing a target  
 CC nucleic acid sequence in a biological material by real time PCR using  
 CC nucleic acid primers that are separated by at least 750 nucleic acid  
 CC residues in the target sequence. This polynucleotide sequence represents  
 CC the genomic DNA of a West Nile virus used in the target analysis method  
 CC of the invention.  
 XX  
 XX Sequence 10945 BP; 2999 A; 2457 C; 3143 G; 2346 T; 0 U; 0 Other;  
 SQ  
 Query Match 96.8%; Score 30; DB 13; Length 10945;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 CCGCCACCGGAAGTTGAGTAGACGCTGCTG 31  
 DB 10481 CCGCCACCGGAAGTTGAGTAGACGCTGCTG 10510  
 RESULT 3  
 ADR67768  
 ID ADR67768 standard; DNA; 10945 BP.  
 XX  
 XX ADR67768;  
 AC  
 XX 18-NOV-2004 (first entry)  
 DT  
 DE West Nile virus DNA detected by novel detection method.  
 XX  
 XX ds; detection; pathogen.  
 KW  
 XX West Nile virus.  
 OS  
 XX WO2004072231-A2.  
 PN  
 XX 26-AUG-2004.  
 PD  
 XX 10-FEB-2004; 2004WO-US0002013.  
 PF  
 XX 10-FEB-2003; 2003US-00361002.  
 PR  
 XX (CLEA-) CLEARANT INC.  
 PA  
 XX Mckenney K, Gillmeister L, Marlowe K, Armistead D;  
 PI  
 XX WPI; 2004-625844/60.  
 DR  
 XX Determining level of potentially active biological pathogens in  
 PT biological material, by adding nucleic acid primer pairs to biological  
 PT material, amplifying target nucleic acid by PCR, detecting and  
 PT quantifying target nucleic acid.  
 XX  
 XX Disclosure; SEQ ID NO 5; 111pp; English.  
 PS  
 XX The invention relates to a method of determining (M1) level of  
 CC potentially active biological pathogens in biological material, involves  
 CC adding at least two nucleic acid primer pairs to biological material,  
 CC amplifying target nucleic acid sequences by PCR, and detecting and  
 CC quantifying target nucleic acid sequences, where quantity of the nucleic  
 CC acid sequences is proportional to number of biological pathogens in  
 CC biological material. (M1) is useful for determining level of potentially  
 CC active biological pathogens in a biological material such as cells,  
 CC tissues, blood or blood components, proteins, enzymes, immunoglobulins,  
 CC botanicals, food, ligaments, tendons, nerves, bone, teeth, skin grafts,  
 CC bone marrow, heart valves, cartilage, cornea, arteries, veins, organs,  
 CC lipids, carbohydrates, collagen, chitin and its derivatives, forensic  
 CC samples, mummified material, human or animal remains, stem cells, islet  
 CC of Langerhans cells, cells for transplantation, red blood cells, white  
 CC blood cells or platelets. The biological pathogen is chosen from

CC bacteria, viruses, fungi and single cell parasites. The biological  
 CC pathogen is chosen from Aspergillus, Candida, Histoplasma  
 CC Saccharomyces, Coccidioides, Cryptococcus, Escherichia, Bacillus,  
 CC Campylobacter, Helicobacter, Listeria, Clostridium, Streptococcus,  
 CC Enterococcus, Staphylococcus, Brucella, Haemophilus, Salmonella,  
 CC Yersinia, Pseudomonas, Serratia, Enterobacter, Klebsiella, Proteus,  
 CC Citrobacter, Corynebacterium, Propionibacterium and Coccidia. The  
 CC biological pathogen is chosen from Adeno-associated virus (AAV),  
 CC California encephalitis virus, Coronavirus, Coxsackievirus-A,  
 CC Coxsackievirus-B, Eastern equine encephalitis virus (EDEV), Echovirus,  
 CC Hantavirus, Hepatitis A virus (HAV), Hepatitis C virus (HCV), Hepatitis  
 CC Delta virus (HDV), Hepatitis E virus (HEV), Hepatitis G virus (HGV), HIV,  
 CC Human T-lymphotrophic virus (HTLV), Influenza virus (Flu virus), Measles  
 CC virus (Rubella), Mumps virus, Norwalk virus, Parainfluenza virus, Polio  
 CC virus, Rabies virus, Respiratory Syncytial virus, Rhinovirus, Rubella  
 CC virus, Saint Louis encephalitis virus, Western equine encephalitis virus  
 CC (WEEV), Yellow fever virus, Adenovirus, Cytomegalovirus (CMV), Epstein-  
 CC Barr virus (EBV), Hepatitis B virus (HBV), Herpes simplex virus 1, Herpes  
 CC simplex virus 2, Molluscum contagiosum, Papilloma virus (HPV), Smallpox  
 CC virus (Variola), Vaccinia virus, Venezuelan equine encephalitis virus  
 CC (VEEV), Ebola virus, West Nile virus, Human Parvovirus B19 and Rotavirus.  
 CC (M1) is useful for determining the effectiveness of a sterilization  
 CC process applied to a biological material. (M1) is useful in determining  
 CC whether the biological pathogen is inactive or active. (M1) enables  
 CC determination of whether the particular biological pathogen is present in  
 CC a biological material as shown by amplification of first target sequence  
 CC and whether the biological pathogen is inactive or active. (M1) enables  
 CC evaluation of the effectiveness of sterilization processes, and  
 CC determination of both the original level and the residual level of  
 CC potentially active biological pathogens. This sequence corresponds to a  
 CC West Nile virus DNA detected by the method of the invention.

XX SQ Sequence 10945 BP; 2999 A; 2457 C; 3143 G; 2346 T; 0 U; 0 Other;

Query Match 96.8%; Score 30; DB 13; Length 10945;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGCCACCGGAAGTTGAGTAGACGGTGCTG 31  
 DB 10481 CGCCACCGGAAGTTGAGTAGACGGTGCTG 10510

RESULT 4  
 ADN98022  
 ID ADN98022 standard; DNA; 10975 BP.

AC ADN98022;

DT 29-JUL-2004 (first entry)

DE West Nile Virus isolate 2741 complete genome sequence.

KW ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;  
 KW Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.

OS West Nile virus.

PN WO2004040263-A2.

PD 13-MAY-2004.

PF 31-OCT-2003; 2003WO-US034823.

XX 31-OCT-2002; 2002US-0422755P.

PR 06-JUN-2003; 2003US-0476513P.

XX (HEAL-) HEALTH RES INC.

PI Wong SJ, Pei-Yong S;

XX WPI; 2004-400223/37.

DR GENBANK; AF206518.

XX New diagnostic kit comprising West Nile Virus (WNV) envelope protein  
 PT reactive with antibody against WNV and cross-reactive with antibody  
 PT against a flavivirus, useful in diagnosing flavivirus infection caused by  
 PT DENV, WNV, JEV or SLEV.

XX Disclosure; Fig 37; 212pp; English.

XX The invention relates to a diagnostic kit comprising at least one  
 CC isolated and purified polypeptide comprising a West Nile Virus (WNV)  
 CC envelope (E) protein or its immunogenic fragment having a native  
 CC conformation or non-denatured structure and that is reactive with  
 CC antibodies against WNV and cross-reactive with antibodies against a  
 CC flavivirus. The diagnostic kit is useful in diagnosing flavivirus  
 CC infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to  
 CC the complete nucleotide sequence of the WNV isolate 2741.

XX SQ Sequence 10975 BP; 3007 A; 2460 C; 3149 G; 2359 T; 0 U; 0 Other;

Query Match 96.8%; Score 30; DB 12; Length 10975;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGCCACCGGAAGTTGAGTAGACGGTGCTG 31  
 DB 10505 CGCCACCGGAAGTTGAGTAGACGGTGCTG 10534

RESULT 5  
 ABZ68481  
 ID ABZ68481 standard; DNA; 11029 BP.

XX AC ABZ68481;

XX DT 22-APR-2003 (first entry)

XX DE Nucleotide sequence of the genome of West Nile virus IS-98-ST1.

XX KW WNV; IS-98-ST1; Flavivirus; infection; encephalitis; gene; ss.

XX OS West Nile virus.

PH Key Location/Qualifiers  
 FT CDS 97..10397  
 FT /\*tag= a  
 FT /product= "polyprotein"

XX WO200281511-A1.

XX 17-OCT-2002.

XX 04-APR-2002; 2002WO-FR001168.

XX 04-APR-2001; 2001FR-00004599.

XX 06-SEP-2001; 2001FR-00011525.

XX (INSP) INST PASTEUR.

XX (KIMR-) KIMRON VETERINARY INST.

XX Despres P, Deubel V, Guenet J, Drouet M, Malkinson M, Banet C;

XX Frenkiel M, Courageot M, Coulbaly F, Catteau A, Flamand M, Weber P;

XX Ceccaldi P;

XX WPI; 2003-058498/05.

XX P-PSDB; ABP70647.

XX New neurovirulent strain of West Nile virus, useful in diagnosis and

XX screening for antiviral agents, also related nucleic acids, proteins and

XX antibodies.

XX Claim 1; Page 34-49; 68pp; French.

XX The present sequence represents the genome of a strain of West Nile virus

CC (WNV), designated IS-98-ST1. This strain is a neuroinvasive and  
CC neurovirulent strain of WNV. Polynucleotides and polypeptides derived  
CC from the IS-98-ST1 genome are useful for diagnosis and prognosis of  
CC Flavivirus infection, specifically WNV-mediated encephalitis. They are  
CC also useful to raise specific antibodies, for recombinant expression of  
CC WNV proteins or peptides (for diagnosis, production of antibodies and  
CC identification of specific binding partners in cells), for identifying  
CC cellular genes implicated in resistance to viral infection, and for  
CC screening for anti-Flavivirus agents  
XX  
SQ Sequence 11029 BP; 3019 A; 2471 C; 3167 G; 2372 T; 0 U; 0 Other;  
Query Match 96.8%; Score 30; DB 8; Length 11029;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31  
|||||  
Db 10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552  
RESULT 6  
ABV74821  
ID ABV74821 standard; DNA; 11029 BP.  
XX  
AC ABV74821;  
XX  
DT 28-MAR-2003 (first entry)  
XX  
DE West Nile virus strain NY99-flamingo 382-99 complete genome.  
XX  
KW Virucide; hepatotropic; antiinflammatory; antiviral; OAS;  
KW 2'-5'-oligoadenylate synthase; Flavivirus infection; gene; ss.  
XX  
OS West Nile Virus.  
XX  
FH Key Location/Qualifiers  
FT CDS 97..10398  
FT /\*tag= a  
FT /product= "West Nile Virus protein"  
XX  
FN WO200281741-A2.  
XX  
PD 17-OCT-2002.  
XX  
PF 04-APR-2002; 2002WO-FR001169.  
XX  
PR 04-APR-2001; 2001FR-00004598.  
XX  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
XX  
XX Guenet J, Mashimo T, Simon-Chazottes D, Montagutelli X;  
PI Frenkiel M, Despres P, Deubel V, Bonhomme F, Lucas M;  
XX  
XX WPI; 2003-058566/05.  
DR P-PSDB; ABB98821.  
XX  
XX Identifying stimulators of oligoadenylate synthase family genes, useful  
PT as antiviral agents against Flavivirus, also mutated genes responsible  
PT for sensitivity to virus.  
XX  
PS Example 1; Page 52-67; 93pp; French.  
XX  
CC The present invention relates to a method for identifying compounds (I)  
CC that can stimulate a gene of the OAS (2'-5'-oligoadenylate synthase)  
CC family. The method comprises: (a) inducing expression of the OAS gene in  
CC a culture of cells from a non-human mammal (Flvr/Flvr or Flvr/Flvs;  
CC indicating resistance or sensitivity to Flavivirus infection); (b)  
CC treating cells with test compound; and (c) measuring activity of OAS gene  
CC relative to a control. (I) are potentially useful as antiviral agents for  
CC treating infections by Flaviviruses (e.g. hepatitis C; dengue; yellow  
CC fever and various forms of encephalitis). Genomic OAS DNA and derived

CC cDNA, also the encoded proteins, are useful: (a) for treating Flavivirus  
CC infection; (b) in screening for anti-flavivirus agents, and (c) for  
CC evaluating sensitivity of subjects to Flavivirus infection and their  
CC likely response to interferon treatment, e.g. to identify patients at  
CC risk of developing severe forms of such infections. The present sequence  
CC is West Nile Virus strain NY99-flamingo 382-99 (IS-98-ST1) complete  
CC genome, which was used in an example from the invention. West Nile Virus  
CC is one such Flavivirus  
XX  
SQ Sequence 11029 BP; 3019 A; 2471 C; 3167 G; 2372 T; 0 U; 0 Other;  
Query Match 96.8%; Score 30; DB 10; Length 11029;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31  
|||||  
Db 10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552  
RESULT 7  
ADN98023  
ID ADN98023 standard; DNA; 11029 BP.  
XX  
AC ADN98023;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE West Nile Virus isolate 3356 complete genome sequence.  
XX  
KW ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;  
KW Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.  
XX  
OS West Nile virus.  
XX  
FN WO2004040263-A2.  
XX  
PD 13-MAY-2004.  
XX  
PF 31-OCT-2003; 2003WO-US034823.  
XX  
PR 31-OCT-2002; 2002US-0422755P.  
PR 06-JUN-2003; 2003US-0476513P.  
XX  
PA (HEAL-) HEALTH RES INC.  
XX  
PI Wong SJ, Pei-Yong S;  
XX  
DR WPI; 2004-400223/37.  
DR GENBANK; AF404756.  
XX  
PT New diagnostic kit comprising West Nile Virus (WNV) envelope protein  
PT reactive with antibody against WNV and cross-reactive with antibody  
PT against a flavivirus, useful in diagnosing flavivirus infection caused by  
PT DENV, WNV, JEV or SLEV.  
XX  
PS Disclosure; Fig 38; 212pp; English.  
XX  
CC The invention relates to a diagnostic kit comprising at least one  
CC isolated and purified polypeptide comprising a West Nile Virus (WNV)  
CC envelope (E) protein or its immunogenic fragment having a native  
CC conformation or non-denatured structure and that is reactive with  
CC antibodies against WNV and cross-reactive with antibodies against a  
CC flavivirus. The diagnostic kit is useful in diagnosing flavivirus  
CC infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to  
CC the complete nucleotide sequence of the WNV isolate 3356.  
XX  
SQ Sequence 11029 BP; 3017 A; 2466 C; 3172 G; 2374 T; 0 U; 0 Other;  
Query Match 96.8%; Score 30; DB 12; Length 11029;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



1



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XX OS West Nile virus.
XX PN WO2004036190-A2.
XX PD 29-APR-2004.
XX PF 10-OCT-2003; 2003WO-US033639.
XX PR 16-OCT-2002; 2002US-0418891P.
XX PR 25-NOV-2002; 2002US-0429006P.
XX PR 24-FEB-2003; 2003US-0449810P.
XX PA (GENP-) GEN-PROBE INC.
XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX DR WPI; 2004-389590/36.
XX PT New hybridization assay probe comprising target-complementary sequence of
XX PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX PS Claim 26; SEQ ID NO 63; 135pp; English.
XX CC This invention relates to a novel hybridisation assay probe, for
XX CC detecting a nucleic acid, which is a probe sequence that comprises a
XX CC target-complementary sequence of bases, and optionally one or more base
XX CC sequences that are not complementary to the nucleic acid that is to be
XX CC detected. The hybridisation assay probes and the kits are useful in
XX CC detecting and amplifying a target nucleic acid sequence, for example
XX CC flavivirus like West Nile virus, that may be present in a biological
XX CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX CC birds and culex mosquitoes, with humans and horses serving as incidental
XX CC hosts. Infection of humans can lead to meningitis or encephalitis. The
XX CC invention may allow for accurate and efficient high throughput screening.
XX CC The present sequence is that of an oligonucleotide probe which is related
XX CC to the invention.
XX SQ Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 67.7%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCGCCACCGGAAGTTGAGTA 21
Db 1 TCCGCCACCGGAAGTTGAGTA 21

RESULT 11
ADN36745
ID ADN36745 standard; DNA; 21 BP.
XX AC ADN36745;
XX DT 15-JUL-2004 (first entry)
XX DE West Nile virus detection-related PCR primer SeqID67.
XX KW hybridisation assay probe; nucleic acid detection;
XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;
XX KW RNA virus; infection; meningitis; encephalitis;
XX KW high throughput screening; PCR; primer; ss.
XX OS West Nile virus.
XX PN WO2004036190-A2.
XX PD 29-APR-2004.
XX PF 10-OCT-2003; 2003WO-US033639.
XX PR 16-OCT-2002; 2002US-0418891P.
XX PR 25-NOV-2002; 2002US-0429006P.
XX PR 24-FEB-2003; 2003US-0449810P.
XX PA (GENP-) GEN-PROBE INC.
XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX DR WPI; 2004-389590/36.
XX PT New hybridization assay probe comprising target-complementary sequence of
XX PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX PS Claim 26; SEQ ID NO 63; 135pp; English.
XX CC This invention relates to a novel hybridisation assay probe, for
XX CC detecting a nucleic acid, which is a probe sequence that comprises a
XX CC target-complementary sequence of bases, and optionally one or more base
XX CC sequences that are not complementary to the nucleic acid that is to be
XX CC detected. The hybridisation assay probes and the kits are useful in
XX CC detecting and amplifying a target nucleic acid sequence, for example
XX CC flavivirus like West Nile virus, that may be present in a biological
XX CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX CC birds and culex mosquitoes, with humans and horses serving as incidental
XX CC hosts. Infection of humans can lead to meningitis or encephalitis. The
XX CC invention may allow for accurate and efficient high throughput screening.
XX CC The present sequence is that of an oligonucleotide probe which is related
XX CC to the invention.
XX SQ Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 67.7%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCGCCACCGGAAGTTGAGTA 21
Db 1 TCCGCCACCGGAAGTTGAGTA 21

RESULT 12
ADN36748
ID ADN36748 standard; DNA; 21 BP.
XX AC ADN36748;
XX DT 15-JUL-2004 (first entry)
XX DE West Nile virus detection-related PCR primer SeqID70.
XX KW hybridisation assay probe; nucleic acid detection;
XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;
XX KW RNA virus; infection; meningitis; encephalitis;
XX KW high throughput screening; PCR; primer; ss.
XX OS West Nile virus.
XX PN WO2004036190-A2.
XX PD 29-APR-2004.
XX PF 10-OCT-2003; 2003WO-US033639.
XX PR 16-OCT-2002; 2002US-0418891P.
XX PR 25-NOV-2002; 2002US-0429006P.
XX PR 24-FEB-2003; 2003US-0449810P.
XX PA (GENP-) GEN-PROBE INC.
XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX DR WPI; 2004-389590/36.
XX PT New hybridization assay probe comprising target-complementary sequence of
XX PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX PS Claim 26; SEQ ID NO 67; 135pp; English.
XX CC This invention relates to a novel hybridisation assay probe, for
XX CC detecting a nucleic acid, which is a probe sequence that comprises a
XX CC target-complementary sequence of bases, and optionally one or more base
XX CC sequences that are not complementary to the nucleic acid that is to be
XX CC detected. The hybridisation assay probes and the kits are useful in
XX CC detecting and amplifying a target nucleic acid sequence, for example
XX CC flavivirus like West Nile virus, that may be present in a biological
XX CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX CC birds and culex mosquitoes, with humans and horses serving as incidental
XX CC hosts. Infection of humans can lead to meningitis or encephalitis. The
XX CC invention may allow for accurate and efficient high throughput screening.
XX CC The present sequence is that of a PCR primer which is related to the
XX CC invention.
XX SQ Sequence 21 BP; 5 A; 2 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 67.7%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 GGAAGTTGAGTAGACGGTGCT 30
Db 1 GGAAGTTGAGTAGACGGTGCT 21

RESULT 12
ADN36748
ID ADN36748 standard; DNA; 21 BP.
XX AC ADN36748;
XX DT 15-JUL-2004 (first entry)
XX DE West Nile virus detection-related PCR primer SeqID70.
XX KW hybridisation assay probe; nucleic acid detection;
XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;
XX KW RNA virus; infection; meningitis; encephalitis;
XX KW high throughput screening; PCR; primer; ss.
XX OS West Nile virus.
XX PN WO2004036190-A2.
XX PD 29-APR-2004.
XX PF 10-OCT-2003; 2003WO-US033639.
XX PR 16-OCT-2002; 2002US-0418891P.
XX PR 25-NOV-2002; 2002US-0429006P.
XX PR 24-FEB-2003; 2003US-0449810P.
XX PA (GENP-) GEN-PROBE INC.
XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX DR WPI; 2004-389590/36.
XX PT New hybridization assay probe comprising target-complementary sequence of
XX PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX PS Claim 26; SEQ ID NO 67; 135pp; English.
XX CC This invention relates to a novel hybridisation assay probe, for
XX CC detecting a nucleic acid, which is a probe sequence that comprises a
XX CC target-complementary sequence of bases, and optionally one or more base
XX CC sequences that are not complementary to the nucleic acid that is to be
XX CC detected. The hybridisation assay probes and the kits are useful in
XX CC detecting and amplifying a target nucleic acid sequence, for example
XX CC flavivirus like West Nile virus, that may be present in a biological
XX CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX CC birds and culex mosquitoes, with humans and horses serving as incidental
XX CC hosts. Infection of humans can lead to meningitis or encephalitis. The
XX CC invention may allow for accurate and efficient high throughput screening.
XX CC The present sequence is that of a PCR primer which is related to the
XX CC invention.
XX SQ Sequence 21 BP; 5 A; 2 C; 9 G; 5 T; 0 U; 0 Other;

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PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
 XX Claim 26; SEQ ID NO 70; 135pp; English.  
 XX This invention relates to a novel hybridisation assay probe, for  
 CC detecting a nucleic acid, which is a probe sequence that comprises a  
 CC target-complementary sequence of bases, and optionally one or more base  
 CC sequences that are not complementary to the nucleic acid that is to be  
 CC detected. The hybridisation assay probes and the kits are useful in  
 CC detecting and amplifying a target nucleic acid sequence, for example  
 CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC birds and culex mosquitoes, with humans and horses serving as incidental  
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
 CC invention may allow for accurate and efficient high throughput screening.  
 CC The present sequence is that of a PCR primer which is related to the  
 CC invention.  
 XX SQ Sequence 21 BP; 5 A; 2 C; 9 G; 5 T; 0 U; 0 Other;  
 Query Match 67.7%; Score 21; DB 12; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 0.021;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 11 GAAGTTGAGTAGACGGTGCTG 31  
 |||||  
 Db 1 GAAGTTGAGTAGACGGTGCTG 21  
 |||||  
 RESULT 13  
 ADN36749  
 ID ADN36749 standard; DNA; 20 BP.  
 XX AC ADN36749;  
 XX DT 15-JUL-2004 (first entry)  
 XX DE West Nile virus detection-related PCR primer SeqID71.  
 XX KW hybridisation assay probe; nucleic acid detection;  
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;  
 KW RNA virus; infection; meningitis; encephalitis;  
 KW high throughput screening; PCR; primer; ss.  
 XX OS West Nile virus.  
 XX OS WO2004036190-A2.  
 XX PD 29-APR-2004.  
 XX PF 10-OCT-2003; 2003WO-US033639.  
 XX PR 16-OCT-2002; 2002US-0418891P.  
 XX PR 25-NOV-2002; 2002US-0429006P.  
 XX PR 24-FEB-2003; 2003US-0449810P.  
 XX PA (GENP-) GEN-PROBE INC.  
 XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;  
 XX WPI; 2004-389590/36.  
 XX New hybridization assay probe comprising target-complementary sequence of  
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
 XX Claim 26; SEQ ID NO 71; 135pp; English.  
 XX This invention relates to a novel hybridisation assay probe, for  
 CC detecting a nucleic acid, which is a probe sequence that comprises a  
 CC target-complementary sequence of bases, and optionally one or more base  
 CC sequences that are not complementary to the nucleic acid that is to be  
 CC detected. The hybridisation assay probes and the kits are useful in  
 CC detecting and amplifying a target nucleic acid sequence, for example  
 CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC birds and culex mosquitoes, with humans and horses serving as incidental  
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
 CC invention may allow for accurate and efficient high throughput screening.  
 CC The present sequence is that of a PCR primer which is related to the  
 CC invention.  
 XX SQ Sequence 21 BP; 5 A; 2 C; 9 G; 5 T; 0 U; 0 Other;  
 Query Match 67.7%; Score 21; DB 12; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 0.021;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 11 GAAGTTGAGTAGACGGTGCTG 31  
 |||||  
 Db 1 GAAGTTGAGTAGACGGTGCTG 21  
 |||||  
 RESULT 14  
 ADN36740  
 ID ADN36740 standard; DNA; 20 BP.  
 XX AC ADN36740;  
 XX DT 15-JUL-2004 (first entry)  
 XX DE West Nile virus detection-related oligonucleotide probe SeqID62.  
 XX KW hybridisation assay probe; nucleic acid detection;  
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;  
 KW RNA virus; infection; meningitis; encephalitis;  
 KW high throughput screening; probe; ss.  
 XX OS West Nile virus.  
 XX OS WO2004036190-A2.  
 XX PD 29-APR-2004.  
 XX PF 10-OCT-2003; 2003WO-US033639.  
 XX PR 16-OCT-2002; 2002US-0418891P.  
 XX PR 25-NOV-2002; 2002US-0429006P.  
 XX PR 24-FEB-2003; 2003US-0449810P.  
 XX PA (GENP-) GEN-PROBE INC.  
 XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;  
 XX WPI; 2004-389590/36.  
 XX New hybridization assay probe comprising target-complementary sequence of  
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
 XX Claim 26; SEQ ID NO 62; 135pp; English.  
 XX This invention relates to a novel hybridisation assay probe, for  
 CC detecting a nucleic acid, which is a probe sequence that comprises a  
 CC target-complementary sequence of bases, and optionally one or more base  
 CC sequences that are not complementary to the nucleic acid that is to be  
 CC detected. The hybridisation assay probes and the kits are useful in  
 CC detecting and amplifying a target nucleic acid sequence, for example  
 CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC birds and culex mosquitoes, with humans and horses serving as incidental  
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
 CC invention may allow for accurate and efficient high throughput screening.  
 CC The present sequence is that of an oligonucleotide probe which is related  
 CC to the invention.  
 XX SQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC birds and culex mosquitoes, with humans and horses serving as incidental  
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
 CC invention may allow for accurate and efficient high throughput screening.  
 CC The present sequence is that of a PCR primer which is related to the  
 CC invention.  
 XX SQ Sequence 20 BP; 5 A; 2 C; 8 G; 5 T; 0 U; 0 Other;  
 Query Match 64.5%; Score 20; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.081;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 AAGTTGAGTAGACGGTGCTG 31  
 |||||  
 Db 1 AAGTTGAGTAGACGGTGCTG 20  
 |||||  
 RESULT 14  
 ADN36740  
 ID ADN36740 standard; DNA; 20 BP.  
 XX AC ADN36740;  
 XX DT 15-JUL-2004 (first entry)  
 XX DE West Nile virus detection-related oligonucleotide probe SeqID62.  
 XX KW hybridisation assay probe; nucleic acid detection;  
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;  
 KW RNA virus; infection; meningitis; encephalitis;  
 KW high throughput screening; probe; ss.  
 XX OS West Nile virus.  
 XX OS WO2004036190-A2.  
 XX PD 29-APR-2004.  
 XX PF 10-OCT-2003; 2003WO-US033639.  
 XX PR 16-OCT-2002; 2002US-0418891P.  
 XX PR 25-NOV-2002; 2002US-0429006P.  
 XX PR 24-FEB-2003; 2003US-0449810P.  
 XX PA (GENP-) GEN-PROBE INC.  
 XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;  
 XX WPI; 2004-389590/36.  
 XX New hybridization assay probe comprising target-complementary sequence of  
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
 XX Claim 26; SEQ ID NO 62; 135pp; English.  
 XX This invention relates to a novel hybridisation assay probe, for  
 CC detecting a nucleic acid, which is a probe sequence that comprises a  
 CC target-complementary sequence of bases, and optionally one or more base  
 CC sequences that are not complementary to the nucleic acid that is to be  
 CC detected. The hybridisation assay probes and the kits are useful in  
 CC detecting and amplifying a target nucleic acid sequence, for example  
 CC flavivirus like West Nile virus, that may be present in a biological  
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
 CC birds and culex mosquitoes, with humans and horses serving as incidental  
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
 CC invention may allow for accurate and efficient high throughput screening.  
 CC The present sequence is that of an oligonucleotide probe which is related  
 CC to the invention.  
 XX SQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

```
Query Match      64.5%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCCACCGGAGTTGAGT 20
DB 1 TCGCCACCGGAGTTGAGT 20

RESULT 15
ADN36747
ID ADN36747 standard; DNA; 20 BP.
XX
AC ADN36747;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related PCR primer SeqID69.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; PCR; primer; ss.
XX
OS West Nile virus.
XX
PN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
XX
XX (GENP-) GEN-PROBE INC.
XX
PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX
DR WPI; 2004-389590/36.
XX
PT New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS Claim 26; SEQ ID NO 69; 135pp; English.
XX
CC This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of a PCR primer which is related to the
CC invention.
XX
SQ Sequence 20 BP; 5 A; 2 C; 8 G; 5 T; 0 U; 0 Other;

Query Match      64.5%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAAGTTGAGTAGACGGTGCT 30
DB 1 GAAGTTGAGTAGACGGTGCT 20

RESULT 16
ADN36748
ID ADN36748 standard; DNA; 19 BP.
XX
AC ADN36748;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID60.
XX
KW hybridisation assay probe; nucleic acid detection;
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ADN36744
ID ADN36744 standard; DNA; 19 BP.
XX
AC ADN36744;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID66.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX
OS West Nile virus.
XX
PN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
XX
XX (GENP-) GEN-PROBE INC.
XX
PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX
DR WPI; 2004-389590/36.
XX
PT New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS Claim 26; SEQ ID NO 66; 135pp; English.
XX
CC This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.
XX
SQ Sequence 19 BP; 5 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match      61.3%; Score 19; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCCACCGGAGTTGAGTA 21
DB 1 CGCCACCGGAGTTGAGTA 19

RESULT 17
ADN36738
ID ADN36738 standard; DNA; 19 BP.
XX
AC ADN36738;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID60.
XX
KW hybridisation assay probe; nucleic acid detection;
```



XX (GENP-) GEN-PROBE INC.  
XX PA Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;  
XX PT WPI; 2004-389590/36.  
XX DR  
XX PS New hybridization assay probe comprising target-complementary sequence of  
XX PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
XX PT Disclosure; SEQ ID NO 61; 135pp; English.  
XX CC This invention relates to a novel hybridisation assay probe, for  
XX CC detecting a nucleic acid, which is a probe sequence that comprises a  
XX CC target-complementary sequence of bases, and optionally one or more base  
XX CC sequences that are not complementary to the nucleic acid that is to be  
XX CC detected. The hybridisation assay probes and the kits are useful in  
XX CC detecting and amplifying a target nucleic acid sequence, for example  
XX CC flavivirus like West Nile virus, that may be present in a biological  
XX CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
XX CC birds and culex mosquitoes, with humans and horses serving as incidental  
XX CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
XX CC invention may allow for accurate and efficient high throughput screening.  
XX CC The present sequence is that of an oligonucleotide probe which is related  
XX CC to the invention.  
XX SQ Sequence 19 BP; 4 A; 6 C; 6 G; 2 T; 0 U; 1 Other;  
Query Match 58.1%; Score 18; DB 12; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 CCGCCACCGAGTTGAG 19  
DB 2 CCGCCACCGAGTTGAG 19  
RESULT 20  
ADN36825/C  
ID ADN36825 standard; RNA; 26 BP.  
XX AC  
XX AC ADN36825;  
XX DT 15-JUL-2004 (first entry)  
XX DE West Nile virus detection-related oligonucleotide probe SeqID147.  
XX KW hybridisation assay probe; nucleic acid detection;  
XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;  
XX KW RNA virus; infection; meningitis; encephalitis;  
XX KW high throughput screening; probe; ss.  
XX OS West Nile virus.  
XX FH Key Location/Qualifiers  
FT modified\_base 1..26  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= 2'-methoxyethoxy (2'-MOE) nucleotides"  
XX PN WO2004036190-A2.  
XX PD 29-APR-2004.  
XX PF 10-OCT-2003; 2003WO-US033639.  
XX PR 16-OCT-2002; 2002US-0418991P.  
XX PR 25-NOV-2002; 2002US-0429006P.  
XX PR 24-FEB-2003; 2003US-0449810P.  
XX PA (GENP-) GEN-PROBE INC.  
XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX WPI; 2004-389590/36.  
XX DR  
XX PT New hybridization assay probe comprising target-complementary sequence of  
XX PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
XX PS Example 1; SEQ ID NO 147; 135pp; English.  
XX CC This invention relates to a novel hybridisation assay probe, for  
XX CC detecting a nucleic acid, which is a probe sequence that comprises a  
XX CC target-complementary sequence of bases, and optionally one or more base  
XX CC sequences that are not complementary to the nucleic acid that is to be  
XX CC detected. The hybridisation assay probes and the kits are useful in  
XX CC detecting and amplifying a target nucleic acid sequence, for example  
XX CC flavivirus like West Nile virus, that may be present in a biological  
XX CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
XX CC birds and culex mosquitoes, with humans and horses serving as incidental  
XX CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
XX CC invention may allow for accurate and efficient high throughput screening.  
XX CC The present sequence is that of an oligonucleotide probe which is related  
XX CC to the invention.  
XX SQ Sequence 26 BP; 6 A; 10 C; 6 G; 0 T; 4 U; 0 Other;  
Query Match 58.1%; Score 18; DB 12; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 14 GTTGAGTAGACGGTGCTG 31  
DB 26 GTTGAGTAGACGGTGCTG 9  
RESULT 21  
ACN01373  
ID ACN01373 standard; RNA; 17 BP.  
XX AC  
XX AC ACN01373;  
XX DT 22-APR-2004 (first entry)  
XX DE WNV Hammerhead Ribozyme substrate SEQ ID NO 1363.  
XX KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
XX KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
XX KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
XX KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
XX KW Amberzyme; Zinzyme; ss.  
XX OS West Nile Virus.  
XX PN WO200268637-A2.  
XX PD 06-SEP-2002.  
XX PF 19-OCT-2001; 2001WO-US048350.  
XX PR 20-OCT-2000; 2000US-0242411P.  
XX PR (RIBO-) RIBOZYME PHARM INC.  
XX PA (BLAT/) BLATT L.  
XX PA (MCSW/) MCSWIGGEN J A.  
XX PI Blatt L, Mcswiggen JA;  
XX DR WPI; 2002-706994/76.  
XX PT New nucleic acid molecule that modulates replication of West Nile Virus  
XX PT (WNV), useful for treating a condition related to WNV infection e.g.  
XX PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX PS Claim 23; SEQ ID NO 1363; 495pp; English.  
XX

CC The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
CC treating a condition related to WNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention  
XX  
SQ Sequence 17 BP; 4 A; 2 C; 7 G; 0 T; 4 U; 0 Other;

Query Match 54.8%; Score 17; DB 6; Length 17;  
Best Local Similarity 76.5%; Pred. No. 4.5;  
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 13 AGTTGAGTAGACGGTGC 29  
||:||||:||||:|  
Db 1 AGUGAGUAGACGGGUC 17

RESULT 22  
ACN04650  
ID ACN04650 standard; RNA; 17 BP.  
XX  
AC ACN04650;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE WNV Zinzyme substrate SEQ ID NO 4653.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus  
PT (WNV), useful for treating a condition related to WNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 4653; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
CC treating a condition related to WNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The

CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention  
XX  
SQ Sequence 17 BP; 5 A; 1 C; 7 G; 0 T; 4 U; 0 Other;

Query Match 54.8%; Score 17; DB 6; Length 17;  
Best Local Similarity 76.5%; Pred. No. 4.5;  
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAAGTTGAGTAGACGGT 27  
||||:||||:|  
Db 1 GAAGUGAGUAGACGGU 17

RESULT 23  
ACN07292  
ID ACN07292 standard; RNA; 17 BP.  
XX  
AC ACN07292;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE WNV Amberzyme substrate SEQ ID NO 7295.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus  
PT (WNV), useful for treating a condition related to WNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 7295; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
CC treating a condition related to WNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention

```
XX SQ Sequence 17 BP; 5 A; 2 C; 7 G; 0 T; 3 U; 0 Other;
Query Match 54.8%; Score 17; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. No. 4.5;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGGAAGTTGAGTAGACG 25
DB 1 CGGAAGUUGAGUAGCG 17

RESULT 24
ACN09625/c
ID ACN09625 standard; RNA; 17 BP.
XX AC ACN09625;
XX KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX OS West Nile Virus.
XX PN WO200268637-A2.
XX PD 06-SEP-2002.
XX PF 19-OCT-2001; 2001WO-US048350.
XX PR 20-OCT-2000; 2000US-024241P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PI Blatt L, Mcswiggen JA;
XX WPI; 2002-706994/76.
XX PT New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX PS Claim 23; SEQ ID NO 9628; 495pp; English.
XX CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX SQ Sequence 17 BP; 3 A; 8 C; 1 G; 0 T; 5 U; 0 Other;
Query Match 54.8%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 10 GGAACTTGAGTAGACGG 26
DB 17 GGAACTTGAGTAGACGG 1

RESULT 25
ACN07461/c
ID ACN07461 standard; RNA; 17 BP.
XX AC ACN07461;
XX DT 22-APR-2004 (first entry)
XX DE WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7464.
XX KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX OS West Nile Virus.
XX PN WO200268637-A2.
XX PD 06-SEP-2002.
XX PF 19-OCT-2001; 2001WO-US048350.
XX PR 20-OCT-2000; 2000US-024241P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PI Blatt L, Mcswiggen JA;
XX WPI; 2002-706994/76.
XX PT New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX PS Claim 23; SEQ ID NO 7464; 495pp; English.
XX CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX SQ Sequence 17 BP; 5 A; 7 C; 2 G; 0 T; 3 U; 0 Other;
Query Match 54.8%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTGAGTAGACGGTGCT 30
DB 17 GTTGAGTAGACGGTGCT 1

RESULT 26
ACN09628/c
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ID ACN09628 standard; RNA; 17 BP.  
 XX ACN09628;  
 XX DT 22-APR-2004 (first entry)  
 XX WNV minus strand Inozyme substrate SEQ ID NO 9631.  
 XX  
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX West Nile Virus.  
 XX WO200268637-A2.  
 XX 06-SEP-2002.  
 XX 19-OCT-2001; 2001WO-US048350.  
 XX 20-OCT-2000; 2000US-0242411P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX Blatt L, Mcswiggen JA;  
 PI WPI; 2002-706994/76.  
 XX  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX Claim 23; SEQ ID NO 9631; 495pp; English.  
 XX  
 XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX  
 SQ Sequence 17 BP; 2 A; 5 C; 6 G; 0 T; 4 U; 0 Other;  
 Query Match 54.8%; Score 17; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.5;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 CCGCCACCGGAAGTTGA 18  
 Db 17 CCGCCACCGGAAGTTGA 1  
 RESULT 27  
 ACN01372  
 ID ACN01372 standard; RNA; 17 BP.  
 XX ACN01372;  
 XX DT 22-APR-2004 (first entry)  
 XX WNV Hammerhead Ribozyme substrate SEQ ID NO 1362.  
 DE

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX West Nile Virus.  
 XX WO200268637-A2.  
 XX 06-SEP-2002.  
 XX 19-OCT-2001; 2001WO-US048350.  
 XX 20-OCT-2000; 2000US-0242411P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX Blatt L, Mcswiggen JA;  
 PI WPI; 2002-706994/76.  
 XX  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX Claim 23; SEQ ID NO 1362; 495pp; English.  
 XX  
 XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX  
 SQ Sequence 17 BP; 5 A; 3 C; 6 G; 0 T; 3 U; 0 Other;  
 Query Match 54.8%; Score 17; DB 6; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 4.5;  
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 CCGGAAGTTGAGTAGAC 24  
 Db 1 CCGGAAGTTGAGTAGAC 17  
 RESULT 28  
 ACN13635/c  
 ID ACN13635 standard; RNA; 17 BP.  
 XX ACN13635;  
 XX 22-APR-2004 (first entry)  
 XX WNV minus strand DNazyme substrate SEQ ID NO 13638.  
 DE  
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX



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OS West Nile Virus.
XX WO200268637-A2.
XX
XX PD
XX
XX PF
XX 19-OCT-2001; 2001WO-US048350.
XX
XX PR
XX 20-OCT-2000; 2000US-0242411P.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX
XX PI Blatt L, Mcswiggen JA;
XX
XX DR WPI; 2002-706994/76.
XX
XX CC The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX treating a condition related to WNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention
XX
XX SQ Sequence 17 BP; 3 A; 6 C; 2 G; 0 T; 6 U; 0 Other;
XX
XX Query Match 54.8%; Score 17; DB 6; Length 17;
XX Best Local Similarity 100.0%; Pred. NO. 4.5;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCGGAAGTTGAGTAGA 23
Db 17 ACCGGAAGTTGAGTAGA 1

RESULT 29
ACN07462/c
ID ACN07462 standard; RNA; 17 BP.
XX
XX AC ACN07462;
XX
XX DT 22-APR-2004 (first entry)
XX
XX DE WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7465.
XX
XX KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyme; ss.
XX
XX OS West Nile Virus.
XX
XX PN WO200268637-A2.
XX
XX PD 06-SEP-2002.
XX
XX PF 19-OCT-2001; 2001WO-US048350.

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XX
XX PR 20-OCT-2000; 2000US-0242411P.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX
XX PI Blatt L, Mcswiggen JA;
XX
XX DR WPI; 2002-706994/76.
XX
XX CC New nucleic acid molecule that modulates replication of West Nile Virus
XX (WNV), useful for treating a condition related to WNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX PS Claim 23; SEQ ID NO 7465; 495pp; English.
XX
XX CC The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX treating a condition related to WNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention
XX
XX SQ Sequence 17 BP; 4 A; 7 C; 1 G; 0 T; 5 U; 0 Other;
XX
XX Query Match 54.8%; Score 17; DB 6; Length 17;
XX Best Local Similarity 100.0%; Pred. NO. 4.5;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AAGTTGAGTAGACGGTG 28
Db 17 AAGTTGAGTAGACGGTG 1

RESULT 30
ACN09624/c
ID ACN09624 standard; RNA; 17 BP.
XX
XX AC ACN09624;
XX
XX DT 22-APR-2004 (first entry)
XX
XX DE WNV minus strand Inozyme substrate SEQ ID NO 9627.
XX
XX KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyme; ss.
XX
XX OS West Nile Virus.
XX
XX PN WO200268637-A2.
XX
XX PD 06-SEP-2002.
XX
XX PF 19-OCT-2001; 2001WO-US048350.
XX
XX PR 20-OCT-2000; 2000US-0242411P.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.

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PI Blatt L, Mcswiggen JA;  
 XX WPI; 2002-706994/76.  
 XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX Claim 23; SEQ ID NO 9627; 495pp; English.  
 XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention  
 XX Sequence 17 BP; 4 A; 7 C; 2 G; 0 T; 4 U; 0 Other;  
 SQ Query Match 54.8%; Score 17; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.5;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 AGTGTAGTAGCGGTGC 29  
 DB 17 AGTGTAGTAGCGGTGC 1  
 RESULT 31  
 ACN05425  
 ID ACN05425 standard; RNA; 17 BP.  
 AC ACN05425;  
 XX 22-APR-2004 (first entry)  
 DE WNV DNzyme substrate SEQ ID NO 5428.  
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNzyme; Amberzyme; Zinzyme; ss.  
 XX West Nile Virus.  
 XX WO200268637-A2.  
 XX 06-SEP-2002.  
 XX 19-OCT-2001; 2001WO-US048350.  
 XX 20-OCT-2000; 2000US-0242411P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX (BLAT/) BLATT L.  
 XX (MCSW/) MCSWIGGEN J A.  
 PI Blatt L, Mcswiggen JA;  
 XX WPI; 2002-706994/76.  
 XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX Claim 23; SEQ ID NO 9627; 495pp; English.  
 XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention  
 XX Sequence 17 BP; 4 A; 7 C; 2 G; 0 T; 4 U; 0 Other;  
 SQ Query Match 54.8%; Score 17; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.5;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 AGTGTAGTAGCGGTGC 29  
 DB 17 AGTGTAGTAGCGGTGC 1  
 RESULT 32  
 ACN04649  
 ID ACN04649 standard; RNA; 17 BP.  
 AC ACN04649;  
 XX 22-APR-2004 (first entry)  
 DE WNV Zinzyme substrate SEQ ID NO 4652.  
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNzyme; Amberzyme; Zinzyme; ss.  
 XX West Nile Virus.  
 XX WO200268637-A2.  
 XX 06-SEP-2002.  
 XX 19-OCT-2001; 2001WO-US048350.  
 XX 20-OCT-2000; 2000US-0242411P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX (BLAT/) BLATT L.  
 XX (MCSW/) MCSWIGGEN J A.  
 PI Blatt L, Mcswiggen JA;  
 XX WPI; 2002-706994/76.  
 XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX Claim 23; SEQ ID NO 4652; 495pp; English.  
 XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention  
 XX Sequence 17 BP; 3 A; 2 C; 7 G; 0 T; 5 U; 0 Other;  
 SQ Query Match 54.8%; Score 17; DB 6; Length 17;  
 Best Local Similarity 70.6%; Pred. No. 4.5;  
 Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 TTGAGTAGACGGTGCTG 31  
 DB 1 UUGAGUAGACGGUGCUG 17  
 RESULT 32  
 ACN04649  
 ID ACN04649 standard; RNA; 17 BP.  
 AC ACN04649;  
 XX 22-APR-2004 (first entry)  
 DE WNV Zinzyme substrate SEQ ID NO 4652.  
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNzyme; Amberzyme; Zinzyme; ss.  
 XX West Nile Virus.  
 XX WO200268637-A2.  
 XX 06-SEP-2002.  
 XX 19-OCT-2001; 2001WO-US048350.  
 XX 20-OCT-2000; 2000US-0242411P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX (BLAT/) BLATT L.  
 XX (MCSW/) MCSWIGGEN J A.  
 PI Blatt L, Mcswiggen JA;  
 XX WPI; 2002-706994/76.  
 XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX Claim 23; SEQ ID NO 4652; 495pp; English.  
 XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention  
 XX Sequence 17 BP; 3 A; 2 C; 7 G; 0 T; 5 U; 0 Other;  
 SQ Query Match 54.8%; Score 17; DB 6; Length 17;  
 Best Local Similarity 70.6%; Pred. No. 4.5;  
 Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 TTGAGTAGACGGTGCTG 31  
 DB 1 UUGAGUAGACGGUGCUG 17

CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The CC nucleic acid molecules further comprise at least five ribose residues, at CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at CC least three of the 5' terminal nucleotides and a 3' end modification of a CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given CC in the specification. The present sequence is that of a nucleic acid CC molecule of the invention

XX Sequence 17 BP; 5 A; 3 C; 6 G; 0 T; 3 U; 0 Other;

SQ Query Match 54.8%; Score 17; DB 6; Length 17;

Best Local Similarity 82.4%; Pred. No. 4.5;

Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACCGGAAGTTGAGTAG 22

Db 1 CACCGGAAGUUGAGUAG 17

RESULT 33

ACN09626/C

ID ACN09626 standard; RNA; 17 BP.

XX ACN09626;

XX 22-APR-2004 (first entry)

DE WNV minus strand Inozyme substrate SEQ ID NO 9629.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW viricide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 23; SEQ ID NO 9629; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The CC nucleic acid molecules further comprise at least five ribose residues, at CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at CC least three of the 5' terminal nucleotides and a 3' end modification of a CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given CC in the specification. The present sequence is that of a nucleic acid CC molecule of the invention

SQ Sequence 17 BP; 3 A; 6 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 54.8%; Score 17; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.5;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCGGAAGTTGAGTAGAC 24

Db 17 CCGGAAGTTGAGTAGAC 1

RESULT 34

ACN07290

ID ACN07290 standard; RNA; 17 BP.

XX ACN07290;

XX 22-APR-2004 (first entry)

DE WNV Amberzyme substrate SEQ ID NO 7293.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW viricide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 23; SEQ ID NO 7293; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The CC nucleic acid molecules further comprise at least five ribose residues, at CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at CC least three of the 5' terminal nucleotides and a 3' end modification of a CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given CC in the specification. The present sequence is that of a nucleic acid CC molecule of the invention

XX Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;

Query Match 54.8%; Score 17; DB 6; Length 17;

|   |                        |   |  |
|---|------------------------|---|--|
| Best Local Similarity 88.2%; Pred. No. 4.5;                 |                        | Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;               |  |
| QY  | 2 CGCCACCGGAAGTTGA 18  |   |  |
| DB  | 1 CGCCACCGGAAGUUGA 17  |   |  |
| RESULT 35   |                        |   |  |
| ID  | ACN07291               | ACN07291 standard; RNA; 17 BP.  |  |
| XX  | AC                     | ACN07291;   |  |
| XX  | DT                     | 22-APR-2004 (first entry)   |  |
| XX  | DE                     | WNV Amberzyme substrate SEQ ID NO 7294.                                   |  |
| XX  | KW                     | WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;         |  |
| XX  | KW                     | virucide; neuroprotective; antibacterial; replication; pancreatitis;      |  |
| XX  | KW                     | encephalitis; myocarditis; meningitis; infection; hepatitis;              |  |
| XX  | KW                     | liver failure; cancer; cirrhosis; Hammerhead; inozyme; DNAzyme;           |  |
| XX  | KW                     | Amberzyme; Zinzyme; ss.   |  |
| XX  | OS                     | West Nile Virus.  |  |
| XX  | PN                     | WO200268637-A2.   |  |
| XX  | PD                     | 06-SEP-2002.  |  |
| XX  | PF                     | 19-OCT-2001; 2001WO-US048350.   |  |
| XX  | PR                     | 20-OCT-2000; 2000US-0242411P.   |  |
| XX  | PA                     | (RIBO-) RIBOZYME PHARM INC.   |  |
| XX  | PA                     | (BLAT/) BLATT L.  |  |
| XX  | PA                     | (MCSW/) MCSWIGGEN J A.  |  |
| XX  | PI                     | Blatt L, Mcswiggen JA;  |  |
| XX  | WPI                    | 2002-706994/76.   |  |
| XX  | DR                     | New nucleic acid molecule that modulates replication of West Nile Virus   |  |
| XX  | PT                     | (WNV), useful for treating a condition related to WNV infection e.g.      |  |
| XX  | PT                     | pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.          |  |
| XX  | PS                     | Claim 23; SEQ ID NO 7294; 495pp; English.                                 |  |
| XX  | CC                     | The invention relates to nucleic acid molecules that modulate replication |  |
| XX  | CC                     | of the West Nile Virus (WNV). The nucleic acid molecules are useful for   |  |
| XX  | CC                     | treating a condition related to WNV infection e.g. pancreatitis,          |  |
| XX  | CC                     | encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,   |  |
| XX  | CC                     | liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid    |  |
| XX  | CC                     | molecule is selected from the group of ribozymes consisting of            |  |
| XX  | CC                     | Hammerhead, inozyme, G-cleaver, DNAzyme, Amberzyme and zinzyme. The       |  |
| XX  | CC                     | nucleic acid molecules further comprise at least five ribose residues, at |  |
| XX  | CC                     | least ten 2'-O-methyl modifications, phosphorothioate linkages on at      |  |
| XX  | CC                     | least three of the 5' terminal nucleotides and a 3' end modification of a |  |
| XX  | CC                     | 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 |  |
| XX  | CC                     | are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given   |  |
| XX  | CC                     | in the specification. The present sequence is that of a nucleic acid      |  |
| XX  | CC                     | molecule of the invention   |  |
| XX  | Sequence               | 17 BP; 4 A; 5 C; 6 G; 0 T; 2 U; 0 Other;                                  |  |
| Query Match 54.8%; Score 17; DB 6; Length 17;               |                        |   |  |
| Best Local Similarity 88.2%; Pred. No. 4.5;                 |                        |   |  |
| Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0; |                        |   |  |
| QY  | 3 CGCCACCGGAAGTTGAG 19 |   |  |
| DB  | 1 CGCCACCGGAAGUUGAG 17 |   |  |
| RESULT 36   |                        |   |  |
| ID  | ACN07463/c             | ACN07463 standard; RNA; 17 BP.  |  |
| XX  | AC                     | ACN07463;   |  |
| XX  | DT                     | 22-APR-2004 (first entry)   |  |
| XX  | DE                     | WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7466.            |  |
| XX  | KW                     | WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;         |  |
| XX  | KW                     | virucide; neuroprotective; antibacterial; replication; pancreatitis;      |  |
| XX  | KW                     | encephalitis; myocarditis; meningitis; infection; hepatitis;              |  |
| XX  | KW                     | liver failure; cancer; cirrhosis; Hammerhead; inozyme; DNAzyme;           |  |
| XX  | KW                     | Amberzyme; Zinzyme; ss.   |  |
| XX  | OS                     | West Nile Virus.  |  |
| XX  | PN                     | WO200268637-A2.   |  |
| XX  | PD                     | 06-SEP-2002.  |  |
| XX  | PF                     | 19-OCT-2001; 2001WO-US048350.   |  |
| XX  | PR                     | 20-OCT-2000; 2000US-0242411P.   |  |
| XX  | PA                     | (RIBO-) RIBOZYME PHARM INC.   |  |
| XX  | PA                     | (BLAT/) BLATT L.  |  |
| XX  | PA                     | (MCSW/) MCSWIGGEN J A.  |  |
| XX  | PI                     | Blatt L, Mcswiggen JA;  |  |
| XX  | WPI                    | 2002-706994/76.   |  |
| XX  | DR                     | New nucleic acid molecule that modulates replication of West Nile Virus   |  |
| XX  | PT                     | (WNV), useful for treating a condition related to WNV infection e.g.      |  |
| XX  | PT                     | pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.          |  |
| XX  | PS                     | Claim 23; SEQ ID NO 7466; 495pp; English.                                 |  |
| XX  | CC                     | The invention relates to nucleic acid molecules that modulate replication |  |
| XX  | CC                     | of the West Nile Virus (WNV). The nucleic acid molecules are useful for   |  |
| XX  | CC                     | treating a condition related to WNV infection e.g. pancreatitis,          |  |
| XX  | CC                     | encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,   |  |
| XX  | CC                     | liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid    |  |
| XX  | CC                     | molecule is selected from the group of ribozymes consisting of            |  |
| XX  | CC                     | Hammerhead, inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The       |  |
| XX  | CC                     | nucleic acid molecules further comprise at least five ribose residues, at |  |
| XX  | CC                     | least ten 2'-O-methyl modifications, phosphorothioate linkages on at      |  |
| XX  | CC                     | least three of the 5' terminal nucleotides and a 3' end modification of a |  |
| XX  | CC                     | 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 |  |
| XX  | CC                     | are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given   |  |
| XX  | CC                     | in the specification. The present sequence is that of a nucleic acid      |  |
| XX  | CC                     | molecule of the invention   |  |
| XX  | Sequence               | 17 BP; 3 A; 7 C; 2 G; 0 T; 5 U; 0 Other;                                  |  |
| Query Match 54.8%; Score 17; DB 6; Length 17;               |                        |   |  |
| Best Local Similarity 100.0%; Pred. No. 4.5;                |                        |   |  |
| Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                        |   |  |
| QY  | 9 CGGAAGTTGAGTAGACG 25 |   |  |
| DB  | 17 CGGAAGTTGAGTAGACG 1 |   |  |
| RESULT 37   |                        |   |  |
| ID  | ACN07465/c             | ACN07465 standard; RNA; 17 BP.  |  |
| XX  | AC                     | ACN07465;   |  |
| XX  | DT                     | 22-APR-2004 (first entry)   |  |
| XX  | DE                     | WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7466.            |  |
| XX  | KW                     | WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;         |  |
| XX  | KW                     | virucide; neuroprotective; antibacterial; replication; pancreatitis;      |  |
| XX  | KW                     | encephalitis; myocarditis; meningitis; infection; hepatitis;              |  |
| XX  | KW                     | liver failure; cancer; cirrhosis; Hammerhead; inozyme; DNAzyme;           |  |
| XX  | KW                     | Amberzyme; Zinzyme; ss.   |  |
| XX  | OS                     | West Nile Virus.  |  |
| XX  | PN                     | WO200268637-A2.   |  |
| XX  | PD                     | 06-SEP-2002.  |  |
| XX  | PF                     | 19-OCT-2001; 2001WO-US048350.   |  |
| XX  | PR                     | 20-OCT-2000; 2000US-0242411P.   |  |
| XX  | PA                     | (RIBO-) RIBOZYME PHARM INC.   |  |
| XX  | PA                     | (BLAT/) BLATT L.  |  |
| XX  | PA                     | (MCSW/) MCSWIGGEN J A.  |  |
| XX  | PI                     | Blatt L, Mcswiggen JA;  |  |
| XX  | WPI                    | 2002-706994/76.   |  |
| XX  | DR                     | New nucleic acid molecule that modulates replication of West Nile Virus   |  |
| XX  | PT                     | (WNV), useful for treating a condition related to WNV infection e.g.      |  |
| XX  | PT                     | pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.          |  |
| XX  | PS                     | Claim 23; SEQ ID NO 7466; 495pp; English.                                 |  |
| XX  | CC                     | The invention relates to nucleic acid molecules that modulate replication |  |
| XX  | CC                     | of the West Nile Virus (WNV). The nucleic acid molecules are useful for   |  |
| XX  | CC                     | treating a condition related to WNV infection e.g. pancreatitis,          |  |
| XX  | CC                     | encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,   |  |
| XX  | CC                     | liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid    |  |
| XX  | CC                     | molecule is selected from the group of ribozymes consisting of            |  |
| XX  | CC                     | Hammerhead, inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The       |  |
| XX  | CC                     | nucleic acid molecules further comprise at least five ribose residues, at |  |
| XX  | CC                     | least ten 2'-O-methyl modifications, phosphorothioate linkages on at      |  |
| XX  | CC                     | least three of the 5' terminal nucleotides and a 3' end modification of a |  |
| XX  | CC                     | 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 |  |
| XX  | CC                     | are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given   |  |
| XX  | CC                     | in the specification. The present sequence is that of a nucleic acid      |  |
| XX  | CC                     | molecule of the invention   |  |
| XX  | Sequence               | 17 BP; 3 A; 7 C; 2 G; 0 T; 5 U; 0 Other;                                  |  |

DT 22-APR-2004 (first entry)  
 XX WV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7468.  
 DE  
 XX  
 XX WNV; West Nile Virus; antiinflammatory; cytotatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX  
 XX West Nile Virus.  
 OS  
 XX  
 XX WO200268637-A2.  
 PN  
 XX  
 XX 06-SEP-2002.  
 PD  
 XX  
 XX 19-OCT-2001; 2001WO-US048350.  
 XX  
 XX 20-OCT-2000; 2000US-0242411P.  
 PR  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 PA  
 XX Blatt L, Mcswiggen JA;  
 PI  
 XX WPI; 2002-706994/76.  
 DR  
 XX  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 PT  
 XX Claim 23; SEQ ID NO 7468; 495pp; English.  
 PS  
 XX  
 XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX  
 XX Sequence 17 BP; 2 A; 6 C; 5 G; 0 T; 4 U; 0 Other;  
 SQ  
 Query Match 54.8%; Score 17; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.5;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 CGCCACCGGAAGTTGAG 19  
 DB 17 CGCCACCGGAAGTTGAG 1  
 RESULT 38  
 ACN09627/C  
 ID ACN09627 standard; RNA; 17 BP.  
 AC ACN09627;  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX WV minus strand Inozyme substrate SEQ ID NO 9630.  
 DE  
 XX  
 XX WNV; West Nile Virus; antiinflammatory; cytotatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;

KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX  
 XX West Nile Virus.  
 OS  
 XX  
 XX WO200268637-A2.  
 PN  
 XX  
 XX 06-SEP-2002.  
 PD  
 XX  
 XX 19-OCT-2001; 2001WO-US048350.  
 XX  
 XX 20-OCT-2000; 2000US-0242411P.  
 PR  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 PA  
 XX Blatt L, Mcswiggen JA;  
 PI  
 XX WPI; 2002-706994/76.  
 DR  
 XX  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 PT  
 XX Claim 23; SEQ ID NO 9630; 495pp; English.  
 PS  
 XX  
 XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX  
 XX Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;  
 SQ  
 Query Match 54.8%; Score 17; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.5;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 CCACCGGAAGTTGAGTA 21  
 DB 17 CCACCGGAAGTTGAGTA 1  
 RESULT 39  
 ACN07293  
 ID ACN07293 standard; RNA; 17 BP.  
 XX  
 XX ACN07293;  
 AC  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX WNV Amberzyme substrate SEQ ID NO 7296.  
 DE  
 XX  
 XX WNV; West Nile Virus; antiinflammatory; cytotatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX  
 XX West Nile Virus.  
 OS  
 XX  
 XX WO200268637-A2.  
 PN  
 XX

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PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
PI Blatt L, Mcswiggen JA;
XX
PS Claim 23; SEQ ID NO 7296; 495pp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 2 C; 7 G; 0 T; 5 U; 0 Other;
Query Match 54.8%; Score 17; DB 6; Length 17;
Best Local Similarity 70.6%; Pred. No. 4.5;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTGAGTAGACGGTGCT 30
Db 1 GUUGAGUAGACGGUGCU 17

RESULT 40
ACN07464/C
XX ACN07464 standard; RNA; 17 BP.
XX
AC ACN07464;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7467.
XX
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
OS West Nile Virus.
XX
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Mcswiggen JA;
XX
PS Claim 23; SEQ ID NO 7296; 495pp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 2 C; 7 G; 0 T; 5 U; 0 Other;
Query Match 54.8%; Score 17; DB 6; Length 17;
Best Local Similarity 70.6%; Pred. No. 4.5;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTGAGTAGACGGTGCT 30
Db 1 GUUGAGUAGACGGUGCU 17

RESULT 41
ADN36743
ID ADN36743 standard; DNA; 18 BP.
XX
AC ADN36743;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID65.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX
OS West Nile virus.
XX
FH Key Location/Qualifiers
FT modified_base 1 /tag= a
FT /mod_base= i
XX
PN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-042906P.
PR 24-FEB-2003; 2003US-0449810P.
XX
PA (GENP-) GEN-PROBE INC.
XX

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PI Linmen JM, Pollner RB, Wu W, Dennis GG, Darby PM;  
XX WPI; 2004-389590/36.  
XX New hybridization assay probe comprising target-complementary sequence of  
PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
PT  
XX Claim 26; SEQ ID NO 65; 135pp; English.  
XX  
CC This invention relates to a novel hybridisation assay probe, for  
CC detecting a nucleic acid, which is a probe sequence that comprises a  
CC target-complementary sequence of bases, and optionally one or more base  
CC sequences that are not complementary to the nucleic acid that is to be  
CC detected. The hybridisation assay probes and the kits are useful in  
CC detecting and amplifying a target nucleic acid sequence, for example  
CC flavivirus like West Nile virus, that may be present in a biological  
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
CC birds and culex mosquitoes, with humans and horses serving as incidental  
CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
CC invention may allow for accurate and efficient high throughput screening.  
CC The present sequence is that of an oligonucleotide probe which is related  
CC to the invention.  
XX  
SQ Sequence 18 BP; 4 A; 4 C; 6 G; 3 T; 0 U; 1 Other;  
  
Query Match 54.8%; Score 17; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.5;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 GCCACCGGAGTTGAGT 20  
DB 2 GCCACCGGAGTTGAGT 18  
|||||  
RESULT 42  
ABL04952/C  
ID ABL04952 standard; cDNA; 52872 BP.  
XX  
AC ABL04952;  
XX  
XX 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 9338.  
XX  
XX Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical; gene; ss.  
XX  
OS Drosophila melanogaster.  
XX  
XX WO200171042-A2.  
XX  
XX 27-SEP-2001.  
XX  
XX 23-MAR-2001; 2001WO-US009231.  
XX  
XX 23-MAR-2000; 2000US-0191637P.  
XX  
XX 11-JUL-2000; 2000US-00614150.  
XX  
XX (PEKE ) PE CORP NY.  
XX  
XX Venter JC, Adams M, Li PWD, Myers EW;  
PI  
XX WPI; 2001-656860/75.  
XX  
XX P-PSDB; ABB60849.  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions.  
XX  
XX Claim 1; SEQ ID NO 9338; 21pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 52872 BP; 15532 A; 11487 C; 10803 G; 15050 T; 0 U; 0 Other;  
  
Query Match 54.8%; Score 17; DB 4; Length 52872;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 CACCGGAGTTGAGTAG 22  
DB 19409 CACCGGAGTTGAGTAG 19393  
|||||  
RESULT 43  
ACN14228/C  
ID ACN14228 standard; RNA; 17 BP.  
XX  
AC ACN14228;  
XX  
XX 22-APR-2004 (first entry)  
XX  
XX WNV minus strand Amberzyme substrate SEQ ID NO 14231.  
XX  
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
KW Amberzyme; Zinzyme; ss.  
XX  
XX West Nile Virus.  
XX  
XX WO200268637-A2.  
XX  
XX 06-SEP-2002.  
XX  
XX 19-OCT-2001; 2001WO-US048350.  
XX  
XX 20-OCT-2000; 2000US-0242411P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX (BLAT/) BLATT L.  
XX  
XX (MCSW/) MCSWIGGEN J A.  
XX  
XX Blatt L, Mcswiggen JA;  
XX  
XX WPI; 2002-706994/76.  
XX  
XX New nucleic acid molecule that modulates replication of West Nile Virus  
PT (WNV), useful for treating a condition related to WNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
XX Claim 23; SEQ ID NO 14231; 495pp; English.  
XX  
XX The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
CC treating a condition related to WNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid

CC molecule of the invention  
 XX Sequence 17 BP; 2 A; 5 C; 7 G; 0 T; 3 U; 0 Other;  
 SQ Query Match 51.6%; Score 16; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTG 17  
 Db 16 CCGCCACCGGAAGTTG 1  
 |||||

RESULT 44  
 ACN12344/c  
 ID ACN12344 standard; RNA; 17 BP.  
 XX AC ACN12344;  
 XX DT 22-APR-2004 (first entry)  
 XX DE WNV minus strand Zinzyne substrate SEQ ID NO 12347.  
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW viricide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; inozyme; DNAzyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX OS West Nile Virus.  
 XX PN WO200268637-A2.  
 XX PD 06-SEP-2002.  
 XX PF 19-OCT-2001; 2001WO-US048350.  
 XX PR 20-OCT-2000; 2000US-0242411P.  
 XX PA (RIBO-) RIBOZYME PHARM INC.  
 XX PA (BLAT/) BLATT L.  
 XX PA (MCSW/) MCSWIGEN J A.  
 XX PI Blatt L, Mcswiggen JA;  
 XX PI WPI; 2002-706994/76.  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX Claim 23; SEQ ID NO 12347; 495pp; English.

CC The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

SQ Sequence 17 BP; 4 A; 7 C; 3 G; 0 T; 3 U; 0 Other;  
 Query Match 51.6%; Score 16; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TGAGTAGACGGTGCTG 31  
 Db 17 TGAGTAGACGGTGCTG 2  
 |||||

RESULT 45  
 ACN03350  
 ID ACN03350 standard; RNA; 17 BP.  
 XX AC ACN03350;  
 XX DT 22-APR-2004 (first entry)  
 XX DE WNV Inozyme substrate SEQ ID NO 3353.  
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW viricide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX OS West Nile Virus.  
 XX PN WO200268637-A2.  
 XX PD 06-SEP-2002.  
 XX PF 19-OCT-2001; 2001WO-US048350.  
 XX PR 20-OCT-2000; 2000US-0242411P.  
 XX PA (RIBO-) RIBOZYME PHARM INC.  
 XX PA (BLAT/) BLATT L.  
 XX PA (MCSW/) MCSWIGEN J A.  
 XX PI Blatt L, Mcswiggen JA;  
 XX PI WPI; 2002-706994/76.  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX Claim 23; SEQ ID NO 3353; 495pp; English.

CC The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

SQ Sequence 17 BP; 3 A; 7 C; 5 G; 0 T; 2 U; 0 Other;  
 Query Match 51.6%; Score 16; DB 6; Length 17;  
 Best Local Similarity 87.5%; Pred. No. 17;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTG 17  
 Db 2 CCGCCACCGGAAGTTG 17  
 |||||

RESULT 46



AAFO8395/c  
ID AAF08395 standard; cDNA; 628 BP.  
XX AAF08395;  
AC  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE Fusarium venenatum EST SEQ ID NO:918.  
XX  
KW Multiple gene expression; filamentous fungal cell; EST;  
KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;  
KW culture condition; environmental stress; spore morphogenesis;  
KW metabolic pathway engineering; catabolic pathway engineering; ss.  
XX  
OS Fusarium venenatum.  
XX  
PN WO200056762-A2.  
XX  
PD 28-SEP-2000.  
XX  
PF 22-MAR-2000; 2000WO-US007781.  
XX  
PR 22-MAR-1999; 99US-00273623.  
XX  
PA (NOVO ) NOVO NORDISK BIOTECH INC.  
PA (NOVO ) NOVO NORDISK AS.  
XX  
PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
XX WPI; 2000-594572/56.  
XX  
PT Monitoring differential expression of genes in filamentous fungal cells  
PT uses fluorescence-labeled nucleic acids isolated from the cells and a  
PT substrate of expressed sequence tags.  
XX  
PS Claim 86; Page 734; 3161pp; English.  
XX  
CC The present invention describes a method for monitoring differential  
CC expression of genes in a first filamentous fungal (FF) cell relative to  
CC expression of the same genes in one or more second filamentous fungal  
CC cells. The method uses fluorescence-labeled nucleic acids isolated from  
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
CC are used in the methods for monitoring differential expression of genes  
CC in a first filamentous fungal (FF) cell relative to expression of the  
CC same genes in one or more second filamentous fungal cells. Monitoring the  
CC global expression of genes from FF cells allows the production potential  
CC of the microorganisms to be improved. New genes may be discovered,  
CC possible functions of unknown open reading frames can be identified and  
CC gene copy number variation and stability can be monitored. The expression  
CC of genes can be used to study how FF cells adapt to changes in culture  
CC conditions, environmental stress, spore morphogenesis, recombination,  
CC metabolic or catabolic pathway engineering. Using ESTs provides several  
CC advantages over genomic or random cDNA clones including elimination of  
CC redundancy as one spot on an array equals one gene or open reading frame,  
CC and organization of the microarrays based on function of the gene  
CC products to facilitate analysis of the results. AAF07478 to AAF11247  
CC represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents  
CC ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from  
CC Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from  
CC Trichoderma reesei, which are all specifically claimed in the present  
CC invention  
XX  
SQ Sequence 628 BP; 128 A; 175 C; 144 G; 176 T; 0 U; 5 Other;  
  
Query Match 51.6%; Score 16; DB 3; Length 628;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 14 GTTGAGTAGCGGTGC 29  
|||||  
DB 205 GTTGAGTAGCGGTGC 190  
  
RESULT 4b  
ID AAF51995/c  
XX AAF51995 standard; DNA; 1326 BP.  
XX  
AC AAF51995;  
XX  
DT 04-SEP-2001 (first entry)  
XX  
DE Mycobacterium tuberculosis potential drug target gene SEQ ID 49.  
  
Query Match 51.6%; Score 16; DB 10; Length 1323;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 GCCACCGGAAGTTGAG 19  
|||||  
DB 1037 GCCACCGGAAGTTGAG 1022  
  
RESULT 47  
ID ABZ71129/c  
XX ABZ71129 standard; DNA; 1323 BP.  
XX  
AC ABZ71129;  
XX  
DT 28-APR-2003 (first entry)  
XX  
DE Mycobacterium tuberculosis protein encoding DNA SEQ ID NO:136.  
XX  
KW Mycobacterium tuberculosis; infection; antibacterial; tuberculostatic;  
KW immunostimulant; vaccine; gene therapy; mycobacterial infection; gene;  
KW ds.  
XX  
OS Mycobacterium tuberculosis.  
XX  
PN WO2003000721-A2.  
XX  
PD 03-JAN-2003.  
XX  
PF 21-JUN-2002; 2002WO-GB002845.  
XX  
PR 22-JUN-2001; 2001GB-00015365.  
PR 07-SEP-2001; 2001GB-00021780.  
XX  
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
XX  
PI James BW, Bacon J, Marsh P;  
XX WPI; 2003-201403/19.  
DR P-PSDB; ABP57503.  
XX  
PT New mycobacterial peptide, its fragment, variant or derivative, useful as  
PT vaccine for treating or preventing mycobacterial infections, and as  
PT diagnostic reagents for identifying such infections.  
XX  
PS Claim 15; Page 243-244; 246pp; English.  
XX  
CC ABP57436 to ABP57504 represent mycobacterial amino acid sequences (I)  
CC encoded by ABZ71062 to ABZ71130 (II), which are isolated from  
CC Mycobacterium tuberculosis. (I) are encoded by genes (II) whose  
CC expression is induced or up-regulated during culture of a mycobacterium  
CC under conditions defined by a dissolved oxygen tension of at least 10%  
CC air saturation measured at 37 plus degrees Celsius when compared with a  
CC dissolved oxygen tension of at least 40% air saturation measured at 37  
CC plus degrees Celsius. (I) and (II) have antibacterial, tuberculostatic  
CC and immunostimulant activities, and can be used in vaccines and gene  
CC therapy. (I) and (II) can be used for the manufacture of a medicament for  
CC treating or preventing a mycobacterial infection. They can also be used  
CC for the manufacture of a diagnostic reagent for identifying a  
CC mycobacterial infection  
XX  
SQ Sequence 1323 BP; 228 A; 416 C; 450 G; 229 T; 0 U; 0 Other;

```
XX Drug target; growth; organism viability; characterisation; ds.
KW Mycobacterium tuberculosis.
XX WO200135317-A1.
XX 17-MAY-2001.
XX 13-NOV-2000; 2000WO-US0311152.
XX 12-NOV-1999; 99US-0165086P.
XX 12-NOV-1999; 99US-0165124P.
XX 01-FEB-2000; 2000US-0179531P.
XX (REGC ) UNIV CALIFORNIA.
XX Eisenberg D, Rotstein SH, Marcotte EM;
XX WPI; 2001-329193/34.
XX P-PSDB; AAG81144.
XX Identifying nucleotide or polypeptide sequence for use as drug target,
PT involves providing algorithm that analyzes a functional relationship
PT between nucleotide or polypeptide sequences, and comparing the sequences.
XX Disclosure; Page 82; 207pp; English.
XX This invention relates to a method for identifying a nucleotide or
CC polypeptide sequence that may be a drug target, or essential for growth
CC or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
CC represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
CC tuberculosis proteins which are potential drug targets. The DNA and
CC protein sequences are used to illustrate the method of the invention. The
CC method involves providing an unknown nucleotide or polypeptide sequences,
CC and comparing it to a number of sequences along with at least one
CC algorithm capable of analysing a functional relationship between
CC nucleotide and polypeptide sequences. The method is useful for
CC characterizing the function of nucleic acids and polypeptides that may be
CC useful as a target for a drug or essential for the growth or viability of
CC an organism
XX Sequence 1326 BP; 229 A; 416 C; 451 G; 230 T; 0 U; 0 Other;
SQ Query Match 51.6%; Score 16; DB 4; Length 1326;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GCCACCGGAAGTTGAG 19
|||||
DB 1037 GCCACCGGAAGTTGAG 1022
RESULT 49
ABL28588/c
ID ABL28588 standard; DNA; 31068 BP.
XX ABL28588;
AC ABL28588;
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 37237.
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX Drosophila melanogaster.
OS WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009231.
```

```
XX 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX (PEKE ) PE CORP NY.
XX Venter JC, Adams M, Li FWD, Myers EW;
XX WPI; 2001-656860/75.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
XX Claim 1; SEQ ID NO 37237; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent,
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
CC AB872072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 31068 BP; 8424 A; 6977 C; 7023 G; 8644 T; 0 U; 0 Other;
SQ Query Match 51.6%; Score 16; DB 4; Length 31068;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CGCCACCGGAAGTTGA 18
|||||
DB 2641 CGCCACCGGAAGTTGA 2626
RESULT 50
AAI99682_14/c
Continuation (15 of 45) of AAI99682 from base 1400001 (Mycobacterium tuberculosis strain
WP Sequence split into 45 fragments LOCUS AAI99682 Accession AAI99682
WP Fragment Name Begin End
WP AAI99682_00 1 110000
WP AAI99682_01 100001 210000
WP AAI99682_02 200001 310000
WP AAI99682_03 300001 410000
WP AAI99682_04 400001 510000
WP AAI99682_05 500001 610000
WP AAI99682_06 600001 710000
WP AAI99682_07 700001 810000
WP AAI99682_08 800001 910000
WP AAI99682_09 900001 1010000
WP AAI99682_10 1000001 1110000
WP AAI99682_11 1100001 1210000
WP AAI99682_12 1200001 1310000
WP AAI99682_13 1300001 1410000
WP AAI99682_14 1400001 1510000
WP AAI99682_15 1500001 1610000
WP AAI99682_16 1600001 1710000
WP AAI99682_17 1700001 1810000
WP AAI99682_18 1800001 1910000
WP AAI99682_19 1900001 2010000
WP AAI99682_20 2000001 2110000
WP AAI99682_21 2100001 2210000
WP AAI99682_22 2200001 2310000
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WP AAI99682_26 2600001 2710000
WP AAI99682_27 2700001 2810000
WP AAI99682_28 2800001 2910000
WP AAI99682_29 2900001 3010000
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|----|------------|---------|---------|
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| WP | AAI9682_31 | 3100001 | 3210000 |
| WP | AAI9682_32 | 3200001 | 3310000 |
| WP | AAI9682_33 | 3300001 | 3410000 |
| WP | AAI9682_34 | 3400001 | 3510000 |
| WP | AAI9682_35 | 3500001 | 3610000 |
| WP | AAI9682_36 | 3600001 | 3710000 |
| WP | AAI9682_37 | 3700001 | 3810000 |
| WP | AAI9682_38 | 3800001 | 3910000 |
| WP | AAI9682_39 | 3900001 | 4010000 |
| WP | AAI9682_40 | 4000001 | 4110000 |
| WP | AAI9682_41 | 4100001 | 4210000 |
| WP | AAI9682_42 | 4200001 | 4310000 |
| WP | AAI9682_43 | 4300001 | 4410000 |
| WP | AAI9682_44 | 4400001 | 4411529 |

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Best Local Similarity 100.0%; Pred. No. 14;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACCGGAAGTTGAG 19  
|||||  
Db 50409 GCCACCGGAAGTTGAG 50394

Search completed: March 25, 2005, 08:12:57  
Job time : 210.747 secs

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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 04:27:15 ; Search time 1236.08 Seconds  
(without alignments)  
954.628 Million cell updates/sec

Title: US-10-688-489-59  
Perfect score: 31  
Sequence: 1 tcgcaccggaagttagtagacggtgctg 31

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsel1:\*  
9: gb\_gsel2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1          | 18    | 58.1        | 731    | 8  | BZ992042 PUFIP307B |
| 2          | 17    | 54.8        | 545    | 6  | CD309228 StrPu691. |
| 3          | 17    | 54.8        | 737    | 8  | BH794414 ME MBA000 |
| 4          | 17    | 54.8        | 895    | 7  | CF824029           |
| 5          | 17    | 54.8        | 3008   | 3  | AK029674           |
| 6          | 16    | 51.6        | 334    | 2  | BF545230           |
| 7          | 16    | 51.6        | 410    | 1  | AI029009 UI-R-CO-1 |
| 8          | 16    | 51.6        | 434    | 6  | CD174634           |
| 9          | 16    | 51.6        | 587    | 7  | CF895091           |
| 10         | 16    | 51.6        | 470    | 8  | AQ951732 Sheared D |
| 11         | 16    | 51.6        | 480    | 5  | BQ559427           |
| 12         | 16    | 51.6        | 520    | 8  | AZ952856           |
| 13         | 16    | 51.6        | 539    | 6  | CA542435           |
| 14         | 16    | 51.6        | 587    | 7  | CF895091           |
| 15         | 16    | 51.6        | 590    | 8  | BZ179360           |
| 16         | 16    | 51.6        | 602    | 2  | AW338466           |
| 17         | 16    | 51.6        | 604    | 8  | AQ447015           |
| 18         | 16    | 51.6        | 607    | 7  | CO430950           |
| 19         | 16    | 51.6        | 612    | 2  | AW173515           |
| 20         | 16    | 51.6        | 614    | 2  | AW173560           |
| 21         | 16    | 51.6        | 626    | 2  | AW168911           |
| 22         | 16    | 51.6        | 627    | 2  | AW172834           |
| 23         | 16    | 51.6        | 671    | 9  | CE654959           |
| 24         | 16    | 51.6        | 691    | 8  | BZ281548           |

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| AI884543  | vm34a04.x   | 707  | 1 | AI884543  | 51.6 | 16 | C 26 |
| CB244514  | UI-M-FYO-   | 736  | 6 | CB244514  | 51.6 | 16 | C 27 |
| CV223901  | CS_hyp_06   | 743  | 7 | CV223901  | 51.6 | 16 | C 28 |
| AL051573  | Drosophila  | 823  | 9 | CNS0088X  | 51.6 | 16 | C 29 |
| BG440946  | GA_Ea001    | 837  | 4 | BG440946  | 51.6 | 16 | C 30 |
| AL050582  | Drosophila  | 897  | 9 | CNS00C0Q  | 51.6 | 16 | C 31 |
| CD048769  | AGENCYCOURT | 1021 | 6 | CD048769  | 51.6 | 16 | C 32 |
| CA467417  | AGENCYCOURT | 1357 | 3 | CA467417  | 51.6 | 16 | C 33 |
| AK040525  | Mus muscu   | 4639 | 3 | AK040525  | 51.6 | 16 | C 34 |
| AW222053  | EST298864   | 189  | 2 | AW222053  | 48.4 | 15 | C 35 |
| AW576128  | UI-HF-BN0   | 201  | 2 | AW576128  | 48.4 | 15 | C 36 |
| CL981863  | OBIFSC046   | 225  | 9 | CL981863  | 48.4 | 15 | C 37 |
| BB587059  | BB587059    | 229  | 2 | BB587059  | 48.4 | 15 | C 38 |
| BY309989  | BY309989    | 260  | 5 | BY309989  | 48.4 | 15 | C 39 |
| BF412428  | UI-R-BT1-   | 296  | 2 | BF412428  | 48.4 | 15 | C 40 |
| AU196235  | AU196235    | 304  | 1 | AU196235  | 48.4 | 15 | C 41 |
| CA190223  | SCCULRIC1   | 326  | 6 | CA190223  | 48.4 | 15 | C 42 |
| CA118676  | SCBGR111    | 336  | 6 | CA118676  | 48.4 | 15 | C 43 |
| BY106179  | BY106179    | 337  | 5 | BY106179  | 48.4 | 15 | C 44 |
| BY215955  | BY215955    | 339  | 5 | BY215955  | 48.4 | 15 | C 45 |
| BY223847  | BY223847    | 351  | 5 | BY223847  | 48.4 | 15 | C 46 |
| BY219248  | BY219248    | 352  | 5 | BY219248  | 48.4 | 15 | C 47 |
| BY037625  | BY037625    | 369  | 5 | BY037625  | 48.4 | 15 | C 48 |
| BY042524  | BY042524    | 369  | 5 | BY042524  | 48.4 | 15 | C 49 |
| BB841964  | BB841964    | 371  | 2 | BB841964  | 48.4 | 15 | C 50 |
| BY005819  | BY005819    | 374  | 5 | BY005819  | 48.4 | 15 | C 51 |
| BY052803  | BY052803    | 374  | 5 | BY052803  | 48.4 | 15 | C 52 |
| BY047494  | BY047494    | 380  | 5 | BY047494  | 48.4 | 15 | C 53 |
| BB842123  | BB842123    | 388  | 2 | BB842123  | 48.4 | 15 | C 54 |
| BY019218  | BY019218    | 392  | 5 | BY019218  | 48.4 | 15 | C 55 |
| BY053908  | BY053908    | 393  | 5 | BY053908  | 48.4 | 15 | C 56 |
| CA294233  | SCSGLV101   | 395  | 6 | CA294233  | 48.4 | 15 | C 57 |
| BY217696  | BY217696    | 396  | 5 | BY217696  | 48.4 | 15 | C 58 |
| BB770230  | BB770230    | 409  | 8 | BB770230  | 48.4 | 15 | C 59 |
| CC011670  | PUDH039TD   | 412  | 8 | CC011670  | 48.4 | 15 | C 60 |
| BY040350  | BY040350    | 432  | 5 | BY040350  | 48.4 | 15 | C 61 |
| CA704862  | wk1c.pk0    | 436  | 6 | CA704862  | 48.4 | 15 | C 62 |
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Strongylocentrotidae; Strongylocentrotus.
1 (bases 1 to 545)
Poustka,A.J., Groth,D., Hennig,S., Thamm,S., Cameron,A., Beck,A.,
Reinhardt,R., Herwig,R., Panopoulou,G. and Lehrach,H.
Generation, annotation, evolutionary analysis, and database
integration of 20,000 unique sea urchin EST clusters
Genome Res. 13 (12), 2736-2746 (2003)
Contact: Poustka AJ
Laboraty 145, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Innestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
Email: poustka@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF
procedure, clones that display the same hybridisation matrix with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per ONF cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well as the coordinates of
the other clones assigned to the same ONF cluster as the clone from
which the above EST is generated is available at the sea urchin
project web site at: http://www.molgen.mpg.de/ag_seaurchin/. cDNA
clones and filters are distributed via the Resource Center/Primary
Database of the German Human Genome Project (http://www.rzpd.de)
PCR PRIMERS
FORWARD: 5' CCCAGGCTTACACTTATGCTCCGGCTCG 3' (M13RSP) 5'-seq
BACKWARD: 5' GCTATTACGCGAGTGGCGAAGGGGATGTG 3' (M13FSP) 3'-seq
Seq primer: 5'-CCGCTCGGAATCCCGGGT-3' pSport3/86
High quality sequence stop: 545.
FEATURES
Location/Qualifiers
1..545
/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
/clone="MPMGP691H07137;MPI_SURUDI_137H7"
/tissue_type="whole larva"
/dev_stage="larva 2-3 weeks"
/lab_host="E.coli, XLI blue"
/clone_lib="Sea urchin larva cDNA library MPMGP691"

/notes="Vector: pSport1; Site_1: NotI; Site_2: SalI; Rand
primed and directionally cloned in pSport1 vector using a
NotI 5'-PGACTAGTTCTAGATCGGCGGCCCC (T)15-3' and a
SalI 5'-TCGACCCACCGGTCGCG-3' adapters (Gibco BRL)"

ORIGIN
Query Match          54.8%; Score 17; DB 6; Length 545;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAAGTTGAGTAGACGGT 27
|||||
DB 130 GAAGTTGAGTAGACGGT 114

RESULT 3
BH794414/c
LOCUS
DEFINITION
ME_MBa0002N14r Manihot esculenta Manihot esculenta genomic clone
BH794414
BH794414.1 GI:19892462
GSS.
Manihot esculenta (cassava)
Manihot esculenta
Manihot esculenta
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
Manihoteae; Manihot.
1 (bases 1 to 737)
Tomkins,J.P., Fregene,M., Main,D., Goicoechea,J.L., Blackmon,B.,
Atkins,M., Tohme,J. and Wing,R.A.
New Genomic Resources for Cassava (Manihot esculenta): Development
of a Deep-Coverage BAC Library and Preliminary STC Analysis
Unpublished (2002)
Contact: Tomkins J
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634, USA
Tel: 864 656 6419
Fax: 864 656 4293
Email: jtomkins@clemson.edu
Total High Quality bases = 383
Seq primer: TAATACGACTCACTATAGG
Class: BAC ends
High quality sequence start: 130
High quality sequence stop: 737.
FEATURES
Location/Qualifiers
1..737
/organism="Manihot esculenta"
/mol_type="genomic DNA"
/strain="MECW72"
/db_xref="taxon:3983"
/clone="ME_MBa0002N14r"
/tissue_type="Leaf"
/lab_host="E. coli"
/clone_lib="Manihot esculenta"
/notes="Vector: pCUGIBAC-1; Site_1: HindIII; Site_2: NotI;
For more details on library preparation and sequence
analysis see
http://www.genome.clemson.edu/projects/stc/cassava/ME_MBa
to order clones from this library see
http://www.genome.clemson.edu/orders"

ORIGIN
Query Match          54.8%; Score 17; DB 8; Length 737;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCCACCGGAAGTTGAG 19
|||||
DB 254 CGCCACCGGAAGTTGAG 238

```

```

RESULT 4
CF824029 LOCUS      CF824029      895 bp      mRNA      linear      EST 01-APR-2004
DEFINITION EST701411 Coccidioides posadasii saprobic phase cDNA library, 2 to
4 kb Coccidioides posadasii cDNA clone CIDAP04 5' end, mRNA
sequence.
ACCESSION CF824029
VERSION    CF824029.1 GI:45930086
KEYWORDS  EST.
SOURCE    Coccidioides posadasii
ORGANISM  Coccidioides posadasii
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE 1 (bases 1 to 895)
AUTHORS   Gardner,M.J. and Cole,G.T.
TITLE     Analysis of gene expression in Coccidioides posadasii mycelia and
            spherules via expressed sequence tags
JOURNAL   Unpublished (2003)
COMMENT   Other ESTs: EST701410
            Contact: Gardner MJ
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org
            Seq primer: M13 Reverse
            Location/Qualifiers
                1..895
                /organism="Coccidioides posadasii"
                /mol_type="mRNA"
                /strain="C735"
                /db_xref="taxon:199306"
                /clone="CIDAP04"
                /dev_stage="saprobic phase (mycelia)"
                /lab_host="E. coli DH10B, T1 phage resistant"
                /clone_lib="Coccidioides posadasii saprobic phase cDNA
                library, 2 to 4 kb"
                /note="Vector: pExpress 1; Site 1: Not 1; Site 2: Eco RV;
                Coccidioides posadasii saprobic phase cDNA library, size
                fractionated cDNA 2 to 4 kb"
ORIGIN
Query Match      54.8%; Score 17; DB 7; Length 895;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4      GCCACCGGAAGTTGAGT 20
        |||||
        829 GCCACCGGAAGTTGAGT 845

RESULT 5
AK029674/c LOCUS      AK029674      3008 bp      mRNA      linear      HTC 03-APR-2004
DEFINITION Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4930452119 product:unclassifiable, full insert
sequence.
ACCESSION AK029674
VERSION    AK029674.1 GI:26081467
KEYWORDS  HTC; CAP trapper.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS   Carninci,P. and Hayashizaki,Y.
TITLE     High-efficiency full-length cDNA cloning
JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
MEDLINE   99279253
PUBMED    10349636
REFERENCE 2
AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

```

```

TITLE
JOURNAL    Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
MEDLINE    Normalization and subtraction of cap-trapper-selected cDNAs to
PUBMED     Prepare full-length cDNA libraries for rapid discovery of new genes
REFERENCE  Genome Res. 10 (10), 1617-1630 (2000)
AUTHORS     20499374
            11042159
3
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Teshikawa,T., Ozawa,K., Tanaka,T., Matsumura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL    20530913
MEDLINE
PUBMED
REFERENCE  11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE     Functional annotation of a full-length mouse cDNA collection
JOURNAL    Nature 409, 685-690 (2001)
MEDLINE
PUBMED
REFERENCE  5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE     Analysis of the mouse transcriptome based on functional annotation
JOURNAL    of 60,770 full-length cDNAs
MEDLINE    Nature 420, 563-573 (2002)
PUBMED
REFERENCE  6 (bases 1 to 3008)
AUTHORS     Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saitoh,K., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
            Direct Submission
            Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physiscal and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES
            Location/Qualifiers
                1..3008
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="C57BL/6J"
                /db_xref="FANTOM,DB:4930452119"
                /db_xref="taxon:10090"
                /clone="4930452119"
                /sex="male"
                /tissue type="testis"
                /clone_lib="RIKEN full-length enriched mouse cDNA library"
                /dev stage="adult"
                1..3008
            misc_feature
            /note="unclassifiable"

```

## ORIGIN

Query Match 54.8%; Score 17; DB 3; Length 3008;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AAGTTGAGTAGACGGTG 28  
 |||||  
 Db 317 AAGTTGAGTAGACGGTG 301

## RESULT 6

BF545230/c 334 bp mRNA linear EST 11-DEC-2000  
 LOCUS UI-R-CO-10-f-06-0-UI-r1 UI-R-CO Rattus norvegicus cDNA clone  
 DEFINITION UI-R-CO-10-f-06-0-UI 5', mRNA sequence.

ACCESSION BF545230  
 VERSION BF545230.1 GI:11636337  
 KEYWORDS EST.

## SOURCE

ORGANISM Rattus norvegicus (Norway rat)  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

## REFERENCE

AUTHORS 1 (bases 1 to 334)  
 TITLE Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 8889548

## COMMENT

Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565

Email: bento-soares@uiowa.edu  
 cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
 clones will be available through Research Genetics (www.resgen.com)  
 This clone is also available through the I.M.A.G.E. Consortium at  
 LLNL (info@image.llnl.gov). IMAGE ID= 1782453 The following  
 repetitive elements were found in this cDNA sequence: 27-117,  
 >PB1D10#SINE/Alu 61-138, >B4A#SINE/B4 61-204, >B4#SINE/B4  
 Seq primer: M13 Forward.

## FEATURES

## Source

Location/Qualifiers  
 1..334  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-CO-10-f-06-0-UI"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="UI-R-CO"

/notes="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CO  
 library is a subtracted library derived from the UI-R-A1  
 and UI-R-E1 libraries. The UI-R-A1 library consisted of a  
 mixture of individually tagged normalized libraries  
 constructed from rat placenta, adult lung, brain, liver,  
 kidney, heart, spleen, ovary, and muscle. The UI-R-E1  
 library consisted of a mixture of individually tagged  
 normalized libraries constructed from 8, 12 and 18-day  
 embryo. The tag is a string of 3-5 nucleotides present  
 between the Not I site and the oligo-dr track which  
 allows identification of the library of origin of a clone  
 within the mixture. The subtracted library (UI-R-CO) was  
 constructed as follows: PCR amplified cDNA inserts from a  
 pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had  
 been derived was used as a driver in a hybridization with  
 the pooled UI-R-A1 and UI-R-E1 library in the form of  
 single-stranded circles. The remaining single-stranded

## ORIGIN

Query Match 51.6%; Score 16; DB 2; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 69;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AGTTGAGTAGACGGTG 28  
 |||||  
 Db 191 AGTTGAGTAGACGGTG 176

## RESULT 7

AI029009 410 bp mRNA linear EST 04-JUL-1999  
 LOCUS UI-R-CO-10-f-06-0-UI-s1 UI-R-CO Rattus norvegicus cDNA clone  
 DEFINITION UI-R-CO-10-f-06-0-UI 3', mRNA sequence.

ACCESSION AI029009  
 VERSION AI029009.1 GI:4295595  
 KEYWORDS EST.

## SOURCE

ORGANISM Rattus norvegicus (Norway rat)  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

## REFERENCE

AUTHORS 1 (bases 1 to 410)  
 TITLE Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 8889548

## COMMENT

On Jun 22, 1998 this sequence version replaced gi:3246835.  
 Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu

cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone  
 distribution: clones will be available through Research Genetics  
 This clone is also available through the I.M.A.G.E. Consortium at  
 LLNL (info@image.llnl.gov). IMAGE ID=1782453 The following  
 repetitive elements were found in this cDNA sequence: 204-347,  
 >B4#SINE/B4 270-347, >B4A#SINE/B4 291-381, >PB1D10#SINE/Alu  
 Seq primer: M13 Forward

## POLYA=No.

## Location/Qualifiers

1..410  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-CO-10-f-06-0-UI"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="UI-R-CO"

/notes="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CO  
 library is a subtracted library derived from the UI-R-A1  
 and UI-R-E1 libraries. The UI-R-A1 library consisted of a  
 mixture of individually tagged normalized libraries  
 constructed from rat placenta, adult lung, brain, liver,  
 kidney, heart, spleen, ovary, and muscle. The UI-R-E1  
 library consisted of a mixture of individually tagged  
 normalized libraries constructed from 8, 12 and 18-day

circles (subtracted library) was purified by  
 hydroxyapatite column chromatography, converted to  
 double-stranded circles and electroporated into DH10B  
 bacteria (Life Technologies) to generate the UI-R-CO  
 library. This procedure has been previously described  
 (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,  
 1996)"

embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-CO) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the pooled UI-R-A1 and UI-R-E1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-CO library. This procedure has been previously described (Bonaldi, Lennon and Soares, Genome Research 6: 791-806, 1996)"

## ORIGIN

Query Match 51.6%; Score 16; DB 1; Length 410;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AGTTCAGTAGACGGTG 28  
|||||  
Db 217 AGTTCAGTAGACGGTG 232

## RESULT 8

CD174634/c  
LOCUS  
DEFINITION AGENCOURT\_13961755 NIH\_MGC\_172 Homo sapiens cDNA 5', mRNA linear EST 19-MAY-2003  
ACCESSION CD174634  
VERSION CD174634.1 GI:30858406  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 434)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Dr. Jamie Thompson, University of WI  
cDNA Library Preparation: Gina Zastrow-Hayes  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDKW42 row: f column: 23  
High quality sequence start: 3  
High quality sequence stop: 434.

## FEATURES

Location/Qualifiers  
1..434  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="embryonic stem cells, WA01, passage 38"  
/lab\_host="DH10B Tona"  
/clone\_lib="NIH MGC 172"  
/note="Vector: pDONR201; Site 1: attP2; Site 2: attP1;  
LIBR PRIMING - oligo dT; METHOD - full-length enriched;  
Embryonic Stem Cells HI; LIBR PROVIDER - Bradfield"

## ORIGIN

Query Match 51.6%; Score 16; DB 6; Length 434;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTT 16  
|||||

## Db

31 TCCGCCACCGGAAGTT 16

## RESULT 9

CD177046/c  
LOCUS  
DEFINITION AGENCOURT\_13975662 NIH\_MGC\_173 Homo sapiens cDNA 5', mRNA linear EST 19-MAY-2003  
ACCESSION CD177046  
VERSION CD177046.1 GI:30863289  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 438)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Dr. Jamie Thompson, University of WI  
cDNA Library Preparation: Gina Zastrow-Hayes  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDKM35 row: o column: 01  
High quality sequence start: 14  
High quality sequence stop: 438.

## FEATURES

Location/Qualifiers  
1..438  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="embryonic trophoblasts, made from WA01 stem cells"  
/lab\_host="DH10B Tona"  
/clone\_lib="NIH MGC 173"  
/note="Vector: pDONR201; Site 1: attP2; Site 2: attP1;  
LIBR PRIMING - oligo dT; METHOD - full-length enriched;  
LIBR PROVIDER - Bradfield"

## ORIGIN

Query Match 51.6%; Score 16; DB 6; Length 438;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTT 16  
|||||

Db 37 TCCGCCACCGGAAGTT 22

## RESULT 10

AQ951732/c  
LOCUS  
DEFINITION AQ951732 Sheared DNA-48L4, TR Sheared DNA Trypanosoma brucei genomic clone  
ACCESSION AQ951732  
VERSION AQ951732.1 GI:6774997  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
1 (bases 1 to 470)  
El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C., Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J., Fraser,C. and Adams,M.  
Determination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library  
Unpublished (1999)  
Contact: Najib M. El-Sayed

Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: nelsayed@tigr.org  
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared  
DNA library constructed at TIGR. Clones will be available for  
distribution through ATCC. Sheared DNA end sequences search page:  
<http://www.tigr.org/tcdb/mbd/tbdb/>.  
Seq primer: M13-Reverse  
Class: shotgun.

# FEATURES

source

## Location/Qualifiers

```
1. .470
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
/clone_lib="Sheared DNA-48L4"
/clone="Sheared DNA"
/Note="Vector: pUC18; Site 1: SmaI; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
sheared to give a tight size distribution (approx 2 kb).
The v + i method used for the library construction is
described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun
sequencing projects. In Genome Sequencing: A Practical
Approach, eds. M. Vaudin and B. Borell, Oxford University
Press, 1999)."
```

## ORIGIN

```
Query Match 51.6%; Score 16; DB 8; Length 470;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 11 GAAGTTGAGTAGACGG 26

Db 246 GAAGTTGAGTAGACGG 231

## RESULT 11

BQ559427/c

LOCUS

DEFINITION BQ559427 480 bp mRNA linear EST 20-JUN-2002

H4058B07-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone

H4058B07 5', mRNA sequence.

ACCESSION BQ559427

VERSION BQ559427.1 GI:21460312

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 480)

AUTHORS VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G.,

Martin, P.R., Stagg, C.A., Bassev, U., Alba, K., Hanatani, T.,

Kargul, G.J., Luo, A.G., Kelso, J., Hide, W. and Ko, M.S.H.

Assembly, verification, and initial annotation of NIA 7.4K mouse

cDNA clone set

Genome Res. 12 (12), 1999-2003 (2002)

22354164

PUBMED 12466305

COMMENT Other\_ESTs: H4058B07-3

Contact: Yong Qian

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA

Email: cdna@lgsun.grc.nia.nih.gov

This clone set has been freely distributed to the community. Please

visit [http://lgsun.grc.nia.nih.gov/cDNA/NIA\\_7.4K.html](http://lgsun.grc.nia.nih.gov/cDNA/NIA_7.4K.html) for details.

Plate: H4058 row: B column: 07

Seq primer: -21M13 Reverse

High quality sequence stop: 480  
POLYA=No.

## FEATURES

source

## Location/Qualifiers

```
1. 480
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="niaEST:H4058B07-5"
/db_xref="taxon:10090"
/clone="H4058B07"
/sex="mixed"
/dev_stage="mixed"
/lab_host="DH10B"
/clone_lib="NIA Mouse 7.4K cDNA Clone Set"
/Note="Vector: pSPORT1; Site 1: Sall; Site 2: NotI; This
clone is among a rearranged set of 7,407 clones from more
than 20 cDNA libraries."
```

## ORIGIN

```
Query Match 51.6%; Score 16; DB 5; Length 480;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 4 GCCACCGGAAGTTGAG 19

Db 440 GCCACCGGAAGTTGAG 425

## RESULT 12

AZ952856

LOCUS

DEFINITION

2M0217A22R Mouse 10kb plasmid UUGC2M library Mus musculus genomic

clone UUGC2M0217A22 R, genomic survey sequence.

ACCESSION AZ952856

VERSION AZ952856.1 GI:13824083

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 520)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Bescorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0217 row: A column: 22

Seq primer: CACACGAGAACGATGAC

Class: plasmid ends

High quality sequence stop: 520.

Location/Qualifiers

1. 520

ORGANISM="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0217A22"

/sex="Female"

/lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 51.6%; Score 16; DB 8; Length 520;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 AAGTTGAGTAGACGGT 27  
|||||  
Db 432 AAGTTGAGTAGACGGT 447

RESULT 13  
CA542435/c  
LOCUS  
DEFINITION  
C0618H12-5N NIA Mouse Trophoblast Stem Cell cDNA Library (Long) Mus musculus cDNA clone NIA:C0618H12 IMAGE:30021983 5', mRNA sequence.  
CA542435  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Lim, M.K., Luo, A., Tanaka, T., Kunath, R., Rossant, J. and Ko, M.S.H.  
Systematic Analyses of NIA Mouse Trophoblast Stem Cell cDNA Library (Long)  
Unpublished (2001)  
Other ESTs: C0618H12-3  
Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: [cdna@lgaun.grc.nia.nih.gov](mailto:cdna@lgaun.grc.nia.nih.gov)  
Plate: C0618 row: H column: 12  
Seq primer: M13 Reverse  
High quality sequence stop: 539  
POLYA=NO.

## FEATURES

## source

1. .539  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="B5/EGFP transgenic ICR mice"  
/db\_xref="niaEST:C0618H12-5N"  
/db\_xref="taxon:10090"  
/clone="NIA:C0618H12 IMAGE:30021983"  
/tissue\_type="Trophoblast stem cell"  
/dev\_stage="3.5-dpc"  
/lab\_host="DH10B"  
/clone\_lib="NIA Mouse Trophoblast Stem Cell cDNA Library (Long)"  
/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (<http://lgaun.grc.nia.nih.gov/cdna>). This is

## ORIGIN

Query Match 51.6%; Score 16; DB 6; Length 539;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCCACCGGAAGTTGAG 19  
|||||  
Db 440 GCCACCGGAAGTTGAG 425

RESULT 14  
CF895091/c  
LOCUS

DEFINITION  
A0143H02-5 NIA Mouse Undifferentiated ES Cell cDNA Library (Long 1)

CF895091 587 bp mRNA linear EST 04-NOV-2003  
Mus musculus cDNA clone NIA:A0143H02 IMAGE:30727765 5', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE

CF895091  
EST.  
Mus musculus (house mouse)

ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS  
TITLE

1 (bases 1 to 587)  
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.  
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification method

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Genome Res. 11 (9), 1553-1558 (2001)  
21429098  
11544199

Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: [cdna@lgaun.grc.nia.nih.gov](mailto:cdna@lgaun.grc.nia.nih.gov)  
Plate: A0143 row: H column: 02  
Seq primer: M13 Reverse  
High quality sequence stop: 587  
POLYA=NO.

Location/Qualifiers  
1. .587  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129/Sv x 129/Sv-CP"  
/db\_xref="niaEST:A0143H02-5"  
/db\_xref="taxon:10090"  
/clone="NIA:A0143H02 IMAGE:30727765"  
/dev\_stage="r1 ES cells"  
/lab\_host="DH10B"  
/clone\_lib="NIA Mouse Undifferentiated ES Cell cDNA Library (Long 1)"

a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Dr. Janet Rossant and Tilo Kunath (Samuel Lunenfeld Research Institute, Canada). Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen).

5'-pGACAGATCTAGATCGGAGCGCCCTTTT-3' from 4 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lona-linker L1-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B *E. coli* host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.6 kb. The library was constructed by Yulan Piao (NIA)."

/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: Sali; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (<http://lgsun.grc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]. Total RNAs were obtained from Dr. Kenneth R. Boheler (National Institute on Aging, USA). ES cells were cultured without feeder cells in the presence of LIF and BRL-conditioned media. Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen).  
 5'-PACTAGTCTCAGACGCGAGCGCCCTTTTCTTTT-3' from 14.2 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Loxe-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sali and NotI enzymes and cloned into Sali/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.4 kb. The library was constructed by Yulan Piao."

ORIGIN  
 Query Match 51.6%; Score 16; DB 7; Length 587;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCCACCGGAAGTTGAG 19

Db 214 GCCACCGGAAGTTGAG 199

RESULT 15  
 BZ179360  
 LOCUS  
 DEFINITION CH230-44419, TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone  
 CH230-44419, genomic survey sequence.

ACCESSION BZ179360

VERSION BZ179360.1 GI:23823491

KEYWORDS GSS.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 590)

AUTHORS Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, P., de Jong, P. and Fraser, C.M.

TITLE Rat BAC End Sequences from Library CHORI-230 MboI segment

JOURNAL Unpublished (1999)

COMMENT Other GSSs: CH230-44419.TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230 (<http://www.chori.org/bacpac/rat230.htm>). For BAC library availability, please contact Pieter de Jong ([pdejong@mail.cho.org](mailto:pdejong@mail.cho.org)).

Clones may be purchased from BACPAC Resources

([http://www.chori.org/bacpac/or\\_xing/information.html](http://www.chori.org/bacpac/or_xing/information.html)). BAC end

page: [http://www.tigr.org/tdb/bac\\_ends/rat/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html)

Plate: 444 row: 1 column: 9

Seq.primer: SP6

Class: BAC ends.

Location/Qualifiers

source

1. 590  
 /organism="Rattus norvegicus"  
 /mol\_type="genomic DNA"  
 /strain="BN/SENHsd/MCW"  
 /db\_xref="taxon:10116"  
 /clone="CH230-44419"  
 /sex="Female"  
 /cell\_type="Brain"  
 /clone\_lib="CHORI-230 Segment 2"  
 /note="Vector: pTARBA1.3; Site 1: MboI; Site 2: MboI;  
 CHORI-230 Rat (BN/SENHsd/MCW) BAC library produced by  
 Pieter de Jong"

ORIGIN

Query Match 51.6%; Score 16; DB 8; Length 590;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCGGAAGTTGAGTAGA 23

Db 489 CCGGAAGTTGAGTAGA 504

RESULT 16

AW338466/c

LOCUS

DEFINITION

AW338466 602 bp mRNA linear EST 31-JAN-2000  
 xw78h03.x1 NCI CGAP Panel Homo sapiens cDNA clone IMAGE:2834165 3'  
 similar to SM:ACDV HUMAN P49748 ACYL-COA DEHYDROGENASE,  
 VERY-LONG-CHAIN SPECIFIC PRECURSOR ;contains Alu repetitive  
 element;; mRNA sequence.

ACCESSION AW338466

VERSION AW338466.1 GI:6835092

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 602)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Life Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.lnl.gov/bbrp/image/image.html](http://www-bio.lnl.gov/bbrp/image/image.html)

Seq primer: -40UP from Gibco

High quality sequence stop: 359.

Location/Qualifiers

source

1. 602

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2834165"

/tissue\_type="adenocarcinoma"

/lab\_host="DH10B"

/clone\_lib="NCI-CGAP\_Panel"

/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Sali;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.

Average insert size 1.72 kb. Life Technologies catalog #:  
 11548-013"

ORIGIN

Query Match 51.6%; Score 16; DB 2; Length 602;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCGGAAGTTGAGT 20

Db 564 CCACCGGAAGTTGAGT 549



RESULT 17  
 AQ447015/c  
 LOCUS  
 DEFINITION  
 604 bp DNA linear GSS 08-APR-1999  
 mgxb0002M12f CUGI Rice Blast BAC Library Magnaporthe grisea genomic  
 clone mgxb0002M12f, genomic survey sequence.  
 AQ447015  
 AQ447015.1 GI:4576152  
 GSS.  
 MAGNAPORTHE GRISEA (anamorph: Pyricularia grisea)  
 ORGANISM  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.  
 1 (bases 1 to 604)  
 Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,  
 Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.  
 A BAC End Sequencing Framework to Sequence the Magnaporthe grisea  
 Genome  
 UNPUBLISHED (1998)  
 JOURNAL  
 COMMENT  
 Contact: Dean RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson University, Clemson, SC 29634  
 Tel: 864 656 5737  
 Fax: 864 656 4293  
 Email: rdean@clemson.edu  
 Seq primer: TAATACGACTCATATAGGG  
 Class: BAC ends  
 High quality sequence start: 61  
 High quality sequence stop: 455.  
 Location/Qualifiers  
 1..604  
 /organism="Magnaporthe grisea"  
 /mol\_type="genomic DNA"  
 /strain="70-15"  
 /db\_xref="taxon:148305"  
 /clone="mgxb0002M12f"  
 /tissue\_type="Protoplasts"  
 /lab\_host="B. coli DH10B"  
 /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;  
 Rice blast is one of the most devastating fungal diseases  
 of rice world wide. It is a filamentous ascomycete with  
 a haploid genome (n=7) of approximately 40 Mbp. Rice  
 blast is an important model pathogen for studying  
 numerous aspects of the fungal-host interaction. In  
 order to facilitate genome wide analysis, a BAC library  
 containing 9216 clones with an average insert size of 130  
 kbp was constructed. This library represents greater  
 than 25X genome coverage. High density colony filters  
 are available upon request."

# FEATURES source

1..604  
 /organism="Magnaporthe grisea"  
 /mol\_type="genomic DNA"  
 /strain="70-15"  
 /db\_xref="taxon:148305"  
 /clone="mgxb0002M12f"  
 /tissue\_type="Protoplasts"  
 /lab\_host="B. coli DH10B"  
 /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;  
 Rice blast is one of the most devastating fungal diseases  
 of rice world wide. It is a filamentous ascomycete with  
 a haploid genome (n=7) of approximately 40 Mbp. Rice  
 blast is an important model pathogen for studying  
 numerous aspects of the fungal-host interaction. In  
 order to facilitate genome wide analysis, a BAC library  
 containing 9216 clones with an average insert size of 130  
 kbp was constructed. This library represents greater  
 than 25X genome coverage. High density colony filters  
 are available upon request."

## ORIGIN

Query Match 51.6%; Score 16; DB 8; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 CCACCGGAAGTTGAGT 20  
 |||||  
 DB 558 CCACCGGAAGTTGAGT 543

RESULT 18  
 CO430950/c  
 LOCUS  
 DEFINITION  
 607 bp mRNA linear EST 06-JUL-2004  
 UI-M-HX0-csc-e-14-0-UI.r1 NIH BMAP\_HX0 Mus musculus cDNA clone  
 IMAGE:30685069 5', mRNA sequence.  
 CO430950  
 CO430950.1 GI:49677244  
 EST.  
 KEYWORDS  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

# REFERENCE AUTHORS TITLE JOURNAL COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 607)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 UNPUBLISHED (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. James Lin University of Iowa  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/mousefl.html>  
 This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)

Seq primer: PYX-5.

# FEATURES source

Location/Qualifiers  
 1..607  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:30685069"  
 /tissue\_type="whole eye"  
 /dev\_stage="newborn (1, 5, 15 days) and embryonic (15, 16,  
 17, 18 dpc)"  
 /lab\_host="DH10B (T1 phage resistant)"  
 /clone\_lib="NIH BMAP HX0"  
 /note="Organ: Eye; Vector: PYX-Asc; Site 1: EcoR I;  
 Site 2: Not I; The library was constructed according  
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
 1996. Denatured RNA was size fractionated on a 1% agarose  
 gel. First strand cDNA synthesis was primed with oligo-dT  
 primer containing a Not I site. Double strand cDNA was  
 size selected according to mRNA size fraction, ligated  
 with EcoR I adaptor, digested with NotI and then cloned  
 directionally into PYX-Asc vector. The library tag  
 sequence located between the Not I site and the polyA tail  
 is AATAATTACG. This library was created for the University  
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
 Developing Mouse Nervous System', supported by National  
 Institute of Mental Health (NIMH)."

## ORIGIN

Query Match 51.6%; Score 16; DB 7; Length 607;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 GCCACCGGAAGTTGAG 19  
 |||||  
 DB 101 GCCACCGGAAGTTGAG 86

# RESULT 19 AW173515/c LOCUS DEFINITION

612 bp mRNA linear EST 16-NOV-1999  
 XJ08a06.x1 NCI CGAP U2c Homo sapiens cDNA clone IMAGE:2656594 3'  
 similar to SW:ACDV HUMAN P49748 ACYL-COA DEHYDROGENASE,  
 VERY-LONG-CHAIN SPECIFIC PRECURSOR 1, mRNA sequence.

AW173515

## ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AW173515.1 GI:6439463  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 612)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 UNPUBLISHED (1997)  
 Contact: Robert Strausberg, Ph.D.



Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 416.  
 Location/Qualifiers  
 1. .612  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2656594"  
 /tissue\_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut2"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

## ORIGIN

Query Match 51.6%; Score 16; DB 2; Length 612;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAAGTTGAGT 20  
 |||||  
 Db 571 CCACCGGAAGTTGAGT 556

## RESULT 20

AW173560/c  
 LOCUS  
 DEFINITION  
 xj08g06.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2656666 3', similar to SW-ACDV HUMAN P49748 ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR ;, mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

AW173560  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 614)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 Unpublished (1997)

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 415.  
 Location/Qualifiers  
 1. .614  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2656666"  
 /tissue\_type="moderately-differentiated endometrial

## FEATURES

source  
 5 CCACCGGAAGTTGAGT 20  
 |||||  
 Db 565 CCACCGGAAGTTGAGT 550

adenocarcinoma, 3 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut2"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

## ORIGIN

Query Match 51.6%; Score 16; DB 2; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAAGTTGAGT 20  
 |||||  
 Db 570 CCACCGGAAGTTGAGT 555

## RESULT 21

AW168911/c  
 LOCUS  
 DEFINITION  
 xj15b06.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2657267 3', similar to SW-ACDV HUMAN P49748 ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR ;, mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

AW168911  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 626)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 Unpublished (1997)

JOURNAL  
 COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 425.  
 Location/Qualifiers  
 1. .626  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2657267"  
 /tissue\_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut2"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

## FEATURES

source

5 CCACCGGAAGTTGAGT 20  
 |||||  
 Db 565 CCACCGGAAGTTGAGT 550

## ORIGIN

Query Match 51.6%; Score 16; DB 2; Length 626;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAAGTTGAGT 20  
 |||||  
 Db 565 CCACCGGAAGTTGAGT 550

```

RESULT 22
AW172834/c
LOCUS
DEFINITION
  XJ0403.x1 NCI CGAP Ut-2 Homo sapiens cDNA clone IMAGE:2656229 3'
  similar to SW:ACDV_HUMAN P49748 ACYL-COA DEHYDROGENASE,
  VERY-LONG-CHAIN SPECIFIC PRECURSOR ;, mRNA sequence.
ACCESSION
AW172834
VERSION
AW172834.1 GI:6438782
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 627)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 401.
Location/Qualifiers
1..627
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2656229"
/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP Ut-2"
/notes="Organ: uterus; Vector: pCMV-SPORT6; Site 1: Salt;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
ORIGIN
Query Match 51.6%; Score 16; DB 2; Length 627;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAAGTTGAGT 20
| | | | | | | | | |
Db 562 CCACCGGAAGTTGAGT 547

RESULT 23
CE654959/c
LOCUS
DEFINITION
  tigr-gas-dog-17000368030354 Dog Library Canis familiaris genomic,
  genomic survey sequence.
ACCESSION
CE654959
VERSION
CE654959.1 GI:36973823
KEYWORDS
GSS.
SOURCE
Canis familiaris (dog)
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 671)
AUTHORS
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE
The dog genome: survey sequencing and comparative analysis
JOURNAL
Science 301 (5641), 1898-1903 (2003)

```

```

MEDLINE
22875432
PUBMED
14512627
COMMENT
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1..671
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BstXI; Libraries were prepared from
peripheral blood"
ORIGIN
Query Match 51.6%; Score 16; DB 9; Length 671;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCGAAGTTGAGTAG 22
| | | | | | | | | |
Db 512 ACCCGAAGTTGAGTAG 497

RESULT 24
BZ281548
LOCUS
DEFINITION
  CH230-384M7.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
  CH230-384M7, genomic survey sequence.
ACCESSION
BZ281548
VERSION
BZ281548.1 GI:24008985
KEYWORDS
GSS.
ORGANISM
Rattus norvegicus (Norway rat)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 691)
AUTHORS
Zhao,S., Shetty,J., Shatsman,S., Tsengaye,G., Geer,K.,
Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other GSSs: CH230-384M7.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 384 row: M column: 7
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
1..691
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SENhd/MCW"
/db_xref="taxon:10116"
/clone="CH230-384M7"
FEATURES
source

```

/sex="Female"  
 /cell\_type="Brain"  
 /clone\_lib="CHORI-230 Segment 2"  
 /notes="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
 CHORI-230 Rat (BN/SsnHed/MCW) BAC library produced by  
 Pieter de Jong"

## ORIGIN

Query Match 51.6%; Score 16; DB 8; Length 691;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAGTT 16  
 |||  
 Db 350 TCCGCCACCGGAGTT 365

## RESULT 25

AI871886/c  
 LOCUS  
 DEFINITION  
 wm53a05.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2439632 3',  
 similar to SW:ACDV HUMAN P49748 ACYL-COA DEHYDROGENASE,  
 VERY-LONG-CHAIN SPECIFIC PRECURSOR ;, mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

AI871886 697 bp mRNA linear EST 07-MAR-2000  
 wm53a05.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2439632 3',  
 similar to SW:ACDV HUMAN P49748 ACYL-COA DEHYDROGENASE,  
 VERY-LONG-CHAIN SPECIFIC PRECURSOR ;, mRNA sequence.

REFERENCE  
 AUTHORS  
 TITLE

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)

COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Greg Lennon, Ph.D.  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1198 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 414.  
 Location/Qualifiers

## FEATURES

source

1..697  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2439632"  
 /tissue\_type="moderately-differentiated endometrial  
 adenocarcinoma, 3 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut2"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.  
 Average insert size 1.85 kb. Life Technologies catalog #:  
 11539-012"

## ORIGIN

Query Match 51.6%; Score 16; DB 1; Length 697;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAGGTTGAGT 20  
 |||  
 Db 564 CCACCGGAGGTTGAGT 549

RESULT 26  
 AI884543/c  
 LOCUS  
 DEFINITION

wm34a04.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2437806 3',  
 similar to SW:ACDV HUMAN P49748 ACYL-COA DEHYDROGENASE,  
 VERY-LONG-CHAIN SPECIFIC PRECURSOR ;, mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE

ORGANISM

Homo sapiens (human)

REFERENCE  
 AUTHORS  
 TITLE

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)

COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Greg Lennon, Ph.D.  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1252 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 410.  
 Location/Qualifiers

## FEATURES

source

1..707  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2437806"  
 /tissue\_type="serous papillary carcinoma, high grade, 2  
 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut4"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.  
 Average insert size 1.48 kb. Life Technologies catalog #:  
 11542-016"

## ORIGIN

Query Match 51.6%; Score 16; DB 1; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAGTTGAGT 20  
 |||  
 Db 568 CCACCGGAGTTGAGT 553

RESULT 27  
 CB244514/c  
 LOCUS

UI-M-FY0-cdq-i-20-0-UI.r1 NIH-BMAP\_FY0 Mus musculus cDNA clone  
 IMAGE:6833085 5', mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE  
 AUTHORS  
 TITLE

NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)

JOURNAL  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.

AI884543 707 bp mRNA linear EST 07-MAR-2000  
 wm34a04.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2437806 3',  
 similar to SW:ACDV HUMAN P49748 ACYL-COA DEHYDROGENASE,  
 VERY-LONG-CHAIN SPECIFIC PRECURSOR ;, mRNA sequence.

AI884543  
 AI884543.1 GI:5589707  
 EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 707)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)

COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Greg Lennon, Ph.D.  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1252 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 410.  
 Location/Qualifiers

## FEATURES

source

1..707  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2437806"  
 /tissue\_type="serous papillary carcinoma, high grade, 2  
 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut4"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.  
 Average insert size 1.48 kb. Life Technologies catalog #:  
 11542-016"

## ORIGIN

Query Match 51.6%; Score 16; DB 1; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAGTTGAGT 20  
 |||  
 Db 568 CCACCGGAGTTGAGT 553

RESULT 27  
 CB244514/c  
 LOCUS

UI-M-FY0-cdq-i-20-0-UI.r1 NIH-BMAP\_FY0 Mus musculus cDNA clone  
 IMAGE:6833085 5', mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE  
 AUTHORS  
 TITLE

NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)

JOURNAL  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.

Email: cgaabs-r@mail.nih.gov  
 Tissue Procurement: Dr. Jim Lin, University of Iowa  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 DNA sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)

Seq primer: pYX-5.

## FEATURES

source  
 Location/Qualifiers  
 1. .736  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:6833085"  
 /tissue\_type="whole brain"  
 /dev\_stage="embryo 13.5,14.5,16.5,17.5dpc"  
 /lab\_host="DH10B (TI phage resistant)"  
 /clone\_lib="NIH BMAP\_FY0"  
 /notes="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;  
 Site 2: Not I; The library was constructed according  
 to Bernaldo, Lennon and Soares, Genome Research, 6:791-806,  
 1996. Denatured RNA was size fractionated on a 1% agarose  
 gel. First strand cDNA synthesis was primed with oligo-dT  
 primer containing a Not I site. Double strand cDNA was  
 size selected according to mRNA size fraction, ligated  
 with EcoR I adaptor, digested with NotI and then cloned  
 directionally into pYX-Asc vector. The library tag  
 sequence located between the Not I site and the polyA tail  
 is AGCGACAGC. This library was created for the University  
 of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
 Developing Mouse Nervous System', supported by National  
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,  
 program coordinator."

## ORIGIN

Query Match 51.6%; Score 16; DB 6; Length 736;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 GCCACCGGAAGTTGAG 19  
 |||||  
 Db 438 GCCACCGGAAGTTGAG 423

## RESULT 28

CV2233901  
 LOCUS CS\_hyp\_06c11\_M13Reverse Blue crab hypodermis, normalized  
 DEFINITION Callinectes sapidus cDNA clone CS\_hyp\_06c11\_5', similar to  
 ref|XP\_285910.2| similar to crossveinless 2 CGI5671-PA - Mus  
 musculus. Score = 35.8 bits (81), Expect = 0.95, mRNA sequence.  
 CV2233901  
 ACCESSION CV2233901.1 GI:52370487  
 VERSION EST  
 KEYWORDS  
 SOURCE Callinectes sapidus (blue crab)  
 ORGANISM  
 Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 Eubrachyura; Portunoidae; Portunidae; Callinectes.  
 REFERENCE 1 (bases 1 to 743)  
 AUTHORS Shafer,T.H., Coblenz,F.E. and Towle,D.W.  
 TITLE Expressed sequence tags from normalized cDNA libraries prepared  
 from gill and hypodermis tissues of the blue crab, Callinectes  
 sapidus  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Thomas H. Shafer  
 Department of Biological Sciences  
 University of North Carolina Wilmington  
 601 S. College Rd, Wilmington, NC 28403, USA

Tel: 910-962-7275  
 Fax: 910-962-4066

Email: shafert@uncw.edu

Plate: 06 row: c column: 11

Seq primer: M13 Reverse

High quality sequence stop: 491.

## FEATURES

source  
 Location/Qualifiers  
 1. .743  
 /organism="Callinectes sapidus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6763"  
 /clone="CS\_hyp\_06c11"  
 /tissue\_type="Pooled hypodermal epithelium from the  
 mid-dorsal region and arthrodial membrane of premolt  
 (stage D2) and 3-hour postmolt crabs"  
 /dev\_stage="Adult"  
 /clone\_lib="Blue crab hypodermis, normalized"  
 /note="Vector: pCMV Sport 6.1; Total RNA samples were  
 prepared individually from each tissue, checked for  
 quality, and then pooled for construction and  
 normalization of a cDNA library by Invitrogen. Plasmids  
 were isolated and inserts sequenced from their 5'-ends by  
 the Blue Crab Molecular Genetics Laboratory at the  
 University of North Carolina Wilmington. Traces were  
 trimmed, compared (BLASTx) to NCBI non-redundant protein  
 database as of 19 July 2004, and processed for submission  
 to dBEST by trace2dbEST software (Parkinson, Anthony and  
 Blaxter, unpublished software)."

## ORIGIN

Query Match 51.6%; Score 16; DB 7; Length 743;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 CCGGAAGTTGAGTAGA 23  
 |||||  
 Db 632 CCGGAAGTTGAGTAGA 647

## RESULT 29

CNS0088X/c  
 LOCUS CNS0088X  
 DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #  
 BACR1618 of RPCI-98 library from Drosophila melanogaster (fruit  
 fly), genomic survey sequence.  
 AL051573  
 ACCESSION AL051573.1 GI:4933425  
 VERSION GSS.  
 KEYWORDS  
 SOURCE Drosophila melanogaster (fruit fly)  
 ORGANISM  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
 REFERENCE 1 (bases 1 to 823)  
 AUTHORS Genoscope.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 COMMENT Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the Berkeley Drosophila Genome Project (BDGP).  
 The BDGP is constructing a physical map of the Drosophila  
 melanogaster genome using these BACs. For further information  
 please see <http://www.fruitfly.org> The BDGP Drosophila  
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
 Aaron Mamoosier in Piter de Jong's laboratory in the Department of  
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
 NY. The library is named RPCI-98 and was constructed by partial  
 EcoRI digestion of Drosophila DNA provided by the BDGP from the  
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's  
 P1 and EST libraries. A more detailed description of the library  
 and how to order individual BAC clones, the entire library, or  
 filters for hybridization from the BACPAC Resource Center can be

found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
source  
Location/Qualifiers  
1..823  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone\_lib="BACR16G18"  
/clone\_lib="RPCI-98"  
/notes="end : TET3"

ORIGIN

Query Match 51.6%; Score 16; DB 9; Length 823;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCCACCGGAAGTTGA 18  
|||||  
Db 418 CGCCACCGGAAGTTGA 403

RESULT 30  
BG440946  
LOCUS  
DEFINITION  
GA\_Ea0011B07f Gossypium arboreum 7-10 dpa fiber library Gossypium  
arboreum cDNA clone GA\_Ea0011B07f, mRNA sequence.

ACCESSION  
BG440946  
VERSION  
BG440946.1 GI:13350598  
KEYWORDS  
EST.  
SOURCE  
Gossypium arboreum  
ORGANISM  
Gossypium arboreum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

1 (bases 1 to 837)  
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,  
Henry,B., Wood,R.C., Leslie,A. and Wilkins,T.A.

An integrated analysis of the genetics, development, and evolution  
of the cotton fiber  
Unpublished (2000)

CONTACT: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: [rwing@clemson.edu](mailto:rwing@clemson.edu)  
Seq primer: TAATAGACTACTATAGG  
High quality sequence stop: 273.

FEATURES  
source  
Location/Qualifiers  
1..837  
/organism="Gossypium arboreum"  
/mol\_type="mRNA"  
/strain="AKA"  
/cultivar="8400"  
/db\_xref="taxon:29729"  
/clone="GA\_Ea0011B07f"  
/tissue\_type="Fibers isolated from bolls harvested 7-10  
dpa"  
/lab\_host="E. coli"  
/clone\_lib="Gossypium arboreum 7-10 dpa fiber library"  
/notes="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

Query Match 51.6%; Score 16; DB 4; Length 837;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGTTGAGTAGACG 25  
|||||  
Db 643 GGAAGTTGAGTAGACG 658

RESULT 31

CNS00C0Q  
LOCUS  
DEFINITION  
Drosophila melanogaster genome survey sequence TET3 end of BAC #  
BAC24G05 of RPCI-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

ACCESSION  
AL058582  
VERSION  
AL058582.1 GI:4946160  
KEYWORDS  
GSS.  
SOURCE  
Drosophila melanogaster (fruit fly)

ORGANISM  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 897)  
Genoscope.  
Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr))  
- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

TITLE  
JOURNAL

COMMENT

Determination of this BAC-end sequence was carried out as part of a  
collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila  
melanogaster genome using these BACs. For further information  
please see <http://www.fruitfly.org> The BDGP Drosophila  
melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
Aaron Mammoser in Pieter de Jong's laboratory in the Department of  
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
NY. The library is named RPCI-98 and was constructed by partial  
EcoRI digestion of Drosophila DNA provided by the BDGP from the  
isogenic strain y2; cn bw sp, the same strain used for the BDGP's  
P1 and EST libraries. A more detailed description of the library  
and how to order individual BAC clones, the entire library, or  
filters for hybridization from the BACPAC Resource Center can be  
found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
source  
Location/Qualifiers  
1..897  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BAC24G05"  
/clone\_lib="RPCI-98"  
/note="end : TET3"

ORIGIN

Query Match 51.6%; Score 16; DB 9; Length 897;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCCACCGGAAGTTGA 18  
|||||  
Db 372 CGCCACCGGAAGTTGA 387

RESULT 32  
CD048769/c  
LOCUS  
DEFINITION  
AGENCOURT\_13965886 NIH\_MGC\_172 Homo sapiens cDNA 5', mRNA sequence.  
ACCESSION  
CD048769  
VERSION  
CD048769.1 GI:30484080  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1021)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Jamie Thompson, University of WI  
cDNA Library Preparation: Gina Zastrow-Hayes  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: NDKM47 row: b column: 05  
 High quality sequence start: 13  
 High quality sequence stop: 315.  
 Location/Qualifiers

#### FEATURES

source

1..1021

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/tissue\_type="embryonic stem cells, WA01, passage 38"

/lab\_host="DH10B Tona"

/clone\_lib="NIH MGC 172"

/notes="Vector: pDONR201; Site 1: attP2; Site 2: attP1;

LIBR\_PRIMING - Oligo dT; METHOD - full-length enriched;

Embryonic Stem Cells HI; LIBR PROVIDER - Bradfield"

#### ORIGIN

Query Match 51.6%; Score 16; DB 6; Length 1021;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAGTT 16

|||||

Db 32 TCCGCCACCGGAAGTT 17

#### RESULT 33

CA467417/c

LOCUS

DEFINITION CA467417 1357 bp mRNA linear EST 09-MAR-2004

IMAGE:30118765 5', mRNA sequence.

ACCESSION CA467417.1 GI:24923769

VERSION EST.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 1357)

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Bradfield Laboratory

CDNA Library Preparation: Mark Bittinger

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDKM016 row: a column: 14

High quality sequence stop: 312.

Location/Qualifiers

1..1357

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGE:30118765"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC 154"

/note="Organ: Kidney; TCDD (DMSO vehicle) Treated 48

Hours IP injections; Vector: pDONR201; Site 1: attP2;

Site 2: attP1; CDNA made by oligo-dT with attB2 site and

directionally cloned. Priming sequence:

5'-TTTCTCGAGGCGCCACCTTGTACAGAAAGCTGGTGTGTTTTTTTTTT

TTT-3'. Full-length enriched library was constructed

using the GeneRacer kit by Invitrogen, library

amplification 16 cycles. Library constructed by Mark

Bittinger in the Bradfield laboratory (McArdle Laboratory

for Cancer Research, University of Wisconsin). Note: this  
 is a NIH\_MGC Library."

#### ORIGIN

Query Match 51.6%; Score 16; DB 6; Length 1357;  
 Best Local Similarity 100.0%; Pred. No. 66;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAGTT 16

|||||

Db 51 TCCGCCACCGGAAGTT 36

#### RESULT 34

AK040525/c

LOCUS

DEFINITION AK040525 4639 bp mRNA linear HTC 03-APR-2004

Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched

library, clone:A430105D10 product:hypothetical protein, full insert

sequence.

ACCESSION AK040525

VERSION AK040525.1 GI:26087907

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 Carninci, P. and Hayashizaki, Y.

AUTHORS High-efficiency full-length cDNA cloning

TITLE Meth. Enzymol. 303, 19-44 (1999)

JOURNAL 99279253

MEDLINE 10349636

REFERENCE 2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

3 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the

FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 4639)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,

Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,

Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Oono, M., Ohsato, N.,

Okazaki, Y., Saito, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,

Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
 COMMENT  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: <http://genome.gsc.riken.jp/>  
 URL: <http://fantom.gsc.riken.jp/>

## FEATURES

source

1. 4639  
 /location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="FANTOM DB:A430105D10"  
 /db\_xref="taxon:10090"  
 /clone="A430105D10"  
 /tissue\_type="thymus"  
 /clone\_lib="RIKEN full-length enriched mouse cDNA library"  
 /dev\_stage="0 day neonate"  
 misc\_feature  
 1. 4639  
 /note="hypothetical protein (evidence: rscds)"

## ORIGIN

Query Match 51.6%; Score 16; DB 3; Length 4639;  
 Best Local Similarity 100.0%; Pred. NO. 63;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 GCCACCGGAAGTTGAG 19  
 |||||||  
 Db 830 GCCACCGGAAGTTGAG 815

RESULT 35  
 AW222053  
 LOCUS  
 DEFINITION  
 EST298864 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA clone cLENG64, mRNA sequence.  
 ACCESSION  
 AW222053  
 VERSION  
 AW222053.1 GI:6533737  
 KEYWORDS  
 EST.  
 SOURCE  
 Lycopersicon esculentum (tomato)  
 ORGANISM  
 Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.  
 REFERENCE  
 1 (bases 1 to 189)  
 AUTHORS  
 Alcala, J., Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Roming, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.  
 TITLE  
 Generation of ESTs from tomato fruit tissue  
 JOURNAL  
 Unpublished (1999)  
 COMMENT  
 Contact: CUGI  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 5 prime sequence.  
 /location/Qualifiers  
 1. 189  
 /organism="Lycopersicon esculentum"

## ORIGIN

Query Match 48.4%; Score 15; DB 2; Length 189;  
 Best Local Similarity 100.0%; Pred. NO. 2.8e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 CCCACCGGAAGTTG 17  
 |||||||  
 Db 19 CCCACCGGAAGTTG 33  
 RESULT 36  
 AW576128/c  
 LOCUS  
 DEFINITION  
 IMAGE:3064232 3', mRNA sequence.  
 ACCESSION  
 AW576128  
 VERSION  
 AW576128.1 GI:7247667  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1 (bases 1 to 201)  
 AUTHORS  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL  
 Unpublished (1999)  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: M.B. Soares Lab  
 cDNA Library Arrayed by: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)  
 The following repetitive elements were found in this cDNA sequence:  
 28-62, >AT-richLow\_complexity  
 Seq primer: M13 Forward  
 POLYA=yes.

## FEATURES

source

1. 201  
 /location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3064232"  
 /tissue\_type="lymph"  
 /cell\_type="germinal center B cells"  
 /cell\_line="MGC85"  
 /lab\_host="DH10B (LT1)"  
 /clone\_lib="NIH MGC\_50"  
 /note="Vector: pT7T3-Pac; Site\_1: NotI; Site\_2: Eco RI;  
 Constructed from size fractionated cytoplasmic mRNA

/mol\_type="mRNA"  
 /cultivar="TA496"  
 /db\_xref="taxon:4081"  
 /clone="cLENG64"  
 /tissue\_type="pericarp"  
 /dev\_stage="red ripe (7-20 days post-breaker)"  
 /clone\_lib="tomato fruit red ripe, TAMU"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI; supplier: Giovannoni; Fruit were tagged at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit) and harvested 7 days post-breaker (fully red-ripe), 10 days post breaker, and 20 days post-breaker (over-ripe). 20 day fruit which showed external or internal signs of pathogenesis were discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."







RESULT 39  
BY309989/c

LOCUS  
DEFINITION

ACCESSION  
VERSION

KEYWORDS  
SOURCE

ORGANISM

REFERENCE

AUTHORS

BY309989 260 bp mRNA linear EST 11-DEC-2002  
BY309989 RIKEN full-length enriched, stroma cell Mus musculus cDNA  
clone J320012H13 5', mRNA sequence.  
BY309989  
BY309989.1 GI:26500326  
EST.

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 260)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
Nikaido, I., Oatono, N., Saito, R., Suzuki, H., Yamana, I.,  
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,  
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,  
Batalov, S., Baisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,  
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,  
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,  
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,  
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,  
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,  
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,  
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,  
Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G.,  
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,  
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,  
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,  
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,  
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,  
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,  
Yang, L., Yuan, Z., Zvolan, M., Zhu, Y., Zimmer, A., Carninci, P.,  
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,  
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,  
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,  
Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

12466851  
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Email: genome-res@gsr.riken.jp, URL: http://genome-gsc.riken.jp/  
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,  
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,  
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,  
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,  
Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, M. and  
Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Tissues were provided by Takashi Ishikawa (Department of Surgery  
2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama  
236-0004 Japan) whose assistance we gratefully acknowledge.  
Please visit our web site (<http://genome-gsc.riken.go.jp>) for  
further details.

FEATURES  
Location/Qualifiers

1..260  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="I320012H13"  
/cell\_type="stroma cell"  
/clone\_lib="RIKEN full-length enriched, stroma cell"

ORIGIN

Query Match 48.4%; Score 15; DB 5; Length 260;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 CCGCCACCGGAAGTT 16  
|||||  
Db 31 CCGCCACCGGAAGTT 17  
|||||

RESULT 40  
BF412428/c

LOCUS  
DEFINITION

BF412428 296 bp mRNA linear EST 28-NOV-2000  
UI-R-BT1-bnd-b-06-0-UI-s1 UI-R-BT1 Rattus norvegicus cDNA clone  
UI-R-BT1-bnd-b-06-0-UI 3', mRNA sequence.

ACCESSION  
VERSION

BF412428  
BF412428.1 GI:11400417

KEYWORDS  
SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

1 (bases 1 to 296)  
Normalizaton and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)

97044477  
8889548  
Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565

Email: bento-soares@uiowa.edu  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
clones will be available through Research Genetics ([www.resgen.com](http://www.resgen.com))  
Seq primer: M13 Forward  
POLYA=Yes.

Location/Qualifiers  
1..296  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-BT1-bnd-b-06-0-UI"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="UI-R-BT1"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The library UI-R-FT1 is a substracted library derived from a mixture of the following tissues: hippocampus, thalamus, mid-brain, medulla, corpus striatum, cerebral cortex and testis. For a detailed description of the library from which this clone was derived, please visit our web site at [ratest.eng.uiowa.edu](http://ratest.eng.uiowa.edu). The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)  
TAG\_SEQ=None found"

## ORIGIN

Query Match 48.4%; Score 15; DB 2; Length 296;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCCACCGGAAGTTGA 18  
|||||  
Db 86 GCCACCGGAAGTTGA 72

## RESULT 41

AU196235/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

304 bp mRNA linear EST 15-OCT-2003  
CDNA clone PFL086h02\_r 5', mRNA sequence.

AU196235.1 GI:31938671

Porphyra yezoensis

Porphyra yezoensis

Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.

1 (bases 1 to 304)

Asamizu,E., Nakajima,M., Kitade,Y., Saga,N., Nakamura,Y. and Tabata,S.

COMPARISON OF RNA EXPRESSION PROFILES BETWEEN THE TWO GENERATIONS OF PORPHYRA YEZOENSIS (RHODOPHYTA), BASED ON EXPRESSED SEQUENCE TAG FREQUENCY ANALYSIS

J. Phycol. 39 (5), 923-930 (2003)

Contact: Erika Asamizu

The First Laboratory for Plant Gene Research

Kazusa DNA Research Institute

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan

Email: [asamizu@kazusa.or.jp](mailto:asamizu@kazusa.or.jp), URL:<http://www.kazusa.or.jp/en/plant/>.

Location/Qualifiers

1..304

/organism="Porphyra yezoensis"

/mol\_type="mRNA"

/strain="TU-1"

/db\_xref="taxon:2788"

/clone="PFL086h02\_r"

/dev\_stage="sporophytes"

/clone\_lib="Porphyra yezoensis TU-1 sporophytes"

ORIGIN

Query Match 48.4%; Score 15; DB 1; Length 304;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAGT 15

|||||

Db 39 TCCGCCACCGGAAGT 25

RESULT 42

CA190223/c

LOCUS

DEFINITION

ACCESSION

VERSION

326 bp mRNA linear EST 24-SEP-2003  
SCCCLR1C10D04.g LRI Saccharum officinarum cDNA clone SCCCLR1C10D04 5', mRNA sequence.

CA190223.1 GI:35134164

## KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 326)

Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

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Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: [parnuda@unicamp.br](mailto:parnuda@unicamp.br)

Clone distribution: clone distribution information can be found

through the Brazilian Clone Collection Center (BCCC) at

<http://www.bcccenter.fcav.unesp.br>

Plate: C10 row: D column: 04

Seq primer: T7 Promoter Primer.

Location/Qualifiers

1..326

/organism="Saccharum officinarum"

/mol\_type="mRNA"

/db\_xref="taxon:4547"

/clone="SCCCLR1C10D04"

/lab\_host="DH10B"

/clone\_lib="LRI1"

/note="Organ: Leaf roll from field grown adult plants

(large insert library); Vector: pSport1; Site 1: Sali;

Site 2: NotI; An unidirectional cDNA library generated

from [leaf roll from field grown adult plants (large

insert library)]. cDNA was prepared from polyA+ mRNA

using SuperScript Plasmid System Kit (Invitrogen). The

double-strand cDNAs were fractionated in a sepharose

CL-2B 40cm-columns and fragments sizing between 0.8 and

1.5 Kb were directionally cloned into the vector. Details

of each source of RNA and library construction can be

obtained at <http://sucest.lad.ic.unicamp.br/public>"

ORIGIN

Query Match 48.4%; Score 15; DB 6; Length 326;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CGGAAGTTGAGTAGA 23

|||||

Db 197 CGGAAGTTGAGTAGA 183

|||||

CA118676/c

LOCUS

DEFINITION

5', mRNA sequence.

CA118676

CA118676.1 GI:34971984

EST.

Saccharum officinarum

Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum

complex.

1 (bases 1 to 336)

Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

## EST.

Saccharum officinarum

Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum

complex.

1 (bases 1 to 326)

Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

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Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: [parnuda@unicamp.br](mailto:parnuda@unicamp.br)

Clone distribution: clone distribution information can be found

through the Brazilian Clone Collection Center (BCCC) at

<http://www.bcccenter.fcav.unesp.br>

Plate: C10 row: D column: 04

Seq primer: T7 Promoter Primer.

Location/Qualifiers

1..326

/organism="Saccharum officinarum"

/mol\_type="mRNA"

/db\_xref="taxon:4547"

/clone="SCCCLR1C10D04"

/lab\_host="DH10B"

/clone\_lib="LRI1"

/note="Organ: Leaf roll from field grown adult plants

(large insert library); Vector: pSport1; Site 1: Sali;

Site 2: NotI; An unidirectional cDNA library generated

from [leaf roll from field grown adult plants (large

insert library)]. cDNA was prepared from polyA+ mRNA

using SuperScript Plasmid System Kit (Invitrogen). The

double-strand cDNAs were fractionated in a sepharose

CL-2B 40cm-columns and fragments sizing between 0.8 and

1.5 Kb were directionally cloned into the vector. Details

of each source of RNA and library construction can be

obtained at <http://sucest.lad.ic.unicamp.br/public>"

ORIGIN

Query Match

Best Local Similarity

Matches

Qy

Db

CA118676/c

LOCUS

DEFINITION

5', mRNA sequence.

CA118676

CA118676.1

EST.

Saccharum officinarum

Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum

complex.

1 (bases 1 to 336)

Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

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Fax: 55 19 3788 1089  
Email: parruda@unicamp.br  
Clone distribution: clone distribution information can be found  
through the Brazilian Clone Collection Center (BCCC) at  
http://www.bcccenter.fcav.unesp.br  
Plate: 112 row: D column: 03  
Seq primer: T7 Promoter Primer.

## FEATURES

Location/Qualifiers

source

1..336

/organism="Saccharum officinarum"

/mol\_type="mRNA"

/db\_xref="taxon:4547"

/clone="SCBGLR1112D03"

/lab\_host="DH10B"

/clone\_lib="LRI"

/notes="Organ: Leaf roll from field grown adult plants (large insert library); Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [leaf roll from field grown adult plants (large insert library)]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucet.lad.ic.unicamp.br/public>"

## ORIGIN

Query Match

Best Local Similarity 48.4%; Score 15; DB 6; Length 336;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGGAGTTGAGTAGA 23

|||||

Db 197 CGGAGTTGAGTAGA 183

## RESULT 44

BY106179/c

LOCUS

BY106179 RIKEN full-length enriched, 15 days embryo whole body Mus  
musculus cDNA clone L330001H23 5', mRNA sequence.

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

337 bp mRNA linear EST 07-DEC-2002  
musculus cDNA clone L330001H23 5', mRNA sequence.

BY106179

BY106179.1 GI:26216796

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 337)

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,  
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,  
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,  
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,  
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,  
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,  
Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dregani,T.A.,  
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,  
Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,  
Kawaji,H., Kawasawa,Y., Kedziercki,R.M., King,B.L., Konagaya,A.,  
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,  
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,  
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,  
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,  
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,  
Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,  
Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,  
Verardo,R., Wagner,L., Wahlstedt,C., Wang,Y., Watanabe,Y.,  
Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,

Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,  
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,  
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,  
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,  
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,  
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,  
Rogers,J., Birney,E. and Hayashizaki,Y.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

## JOURNAL

MEDLINE

PUBMED

COMMENT

12466851

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Email: genome-res@gsr.riken.jp, URL: <http://genome.gsc.riken.jp/>

Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,

Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,

Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,

Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,

Shiraki,T., Tsgami,M., Waki,K., Watanishi,A., Muramatsu,M. and

Hayashizaki,Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for

further details.

FEATURES

source

1..337

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="CS7BL/6J"

/db\_xref="taxon:10090"

/clone="L330001H23"

/tissue type="whole body"

/dev stage="15 days embryo"

/clone\_lib="RIKEN full-length enriched, 15 days embryo

whole body"

ORIGIN

Query Match

Best Local Similarity 48.4%; Score 15; DB 5; Length 337;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGGCCACCGGAAGTT 16

|||||

Db 168 CGGCCACCGGAAGTT 154

## RESULT 45

BY215955

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BY215955 339 bp mRNA linear EST 10-DEC-2002  
BY215955 RIKEN full-length enriched, activated spleen Mus musculus  
cDNA clone F830039P10 5', mRNA sequence.  
BY215955  
BY215955.1 GI:26396697



Email: genome-res@gsr.riken.jp, URL: <http://genome.gsc.riken.jp/>  
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,  
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,  
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,  
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,  
 Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and  
 Hayashizaki, Y. Direct Submission  
 Computational Analysis of Full-Length Mouse cDNAs Compared with  
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics  
 Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome  
 Trust/MRC building Addenbrookes Hospital Cambridge) whose  
 assistance we gratefully acknowledge.  
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for  
 further details.

## FEATURES

source

Location/Qualifiers  
 1. .351  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="NOD"  
 /db\_xref="taxon:10090"  
 /clone="F830305P17"  
 /tissue\_type="activated spleen"  
 /clone\_lib="RIKEN full-length enriched, activated spleen"

## ORIGIN

Query Match 48.4%; Score 15; DB 5; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GAGTAGACGGTGCTG 31

DB 213 GAGTAGACGGTGCTG 227

## RESULT 47

LOCUS

BY219248 352 bp mRNA linear EST 10-DEC-2002  
 BY219248 RIKEN full-length enriched, activated spleen Mus musculus  
 cDNA clone F830113N13 5', mRNA sequence.

ACCESSION

VERSION

BY219248.1

KEYWORDS

EST.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 352)

AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
 Nikaudo, I., Oatso, N., Saito, R., Suzuki, H., Yamanaka, I.,  
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,  
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,  
 Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,  
 Chotia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,  
 Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,  
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,  
 Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,  
 Kawaji, H., Kawasaki, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,

Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,  
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,  
 Numata, K., Okido, T., Pavan, W.J., Perle, G., Pesole, G.,  
 Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,  
 Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,  
 Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,  
 Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,  
 Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,  
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 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,  
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 22354683  
 12466851

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Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics

Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome

Trust/MRC building Addenbrookes Hospital Cambridge) whose

assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for

further details.

FEATURES

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MEDLINE  
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source

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Search completed: March 25, 2005, 09:06:01  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

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| Sequence 87, Appl  | 87     | 41.9 | 87 | 2 US-08-483-5288-87  | Sequence 87, Appl  |
| Sequence 87, Appl  | 87     | 41.9 | 87 | 2 US-08-673-799C-87  | Sequence 87, Appl  |
| Sequence 14219, A  | 216    | 41.9 | 4  | US-09-252-991A-14219 | Sequence 14219, A  |
| Sequence 8307, Ap  | 363    | 41.9 | 4  | US-09-270-767-8307   | Sequence 8307, Ap  |
| Sequence 23589, A  | 363    | 41.9 | 4  | US-09-270-767-23589  | Sequence 23589, A  |
| Sequence 90, Appl  | 390    | 41.9 | 3  | US-08-483-5288-90    | Sequence 90, Appl  |
| Sequence 132, App  | 390    | 41.9 | 3  | US-08-673-799C-90    | Sequence 132, App  |
| Sequence 1, Appli  | 424    | 41.9 | 3  | US-09-397-787-132    | Sequence 1, Appli  |
| Sequence 1, Appli  | 435    | 41.9 | 1  | US-09-634-238-154    | Sequence 1, Appli  |
| Sequence 1, Appli  | 499    | 41.9 | 1  | US-07-935-311A-1     | Sequence 1, Appli  |
| Sequence 1, Appli  | 499    | 41.9 | 5  | US-08-368-079-1      | Sequence 1, Appli  |
| Sequence 25455, A  | 504    | 41.9 | 4  | PCT-US93-07996-1     | Sequence 25455, A  |
| Sequence 6408, Ap  | 513    | 41.9 | 4  | US-09-270-767-25455  | Sequence 6408, Ap  |
| Sequence 10074, A  | 528    | 41.9 | 4  | US-09-902-540-6408   | Sequence 10074, A  |
| Sequence 10402, A  | 598    | 41.9 | 4  | US-09-270-767-10074  | Sequence 10402, A  |
| Sequence 32726, A  | 601    | 41.9 | 4  | US-09-949-016-32726  | Sequence 32726, A  |
| Sequence 42365, A  | 601    | 41.9 | 4  | US-09-949-016-42365  | Sequence 42365, A  |
| Sequence 78587, A  | 601    | 41.9 | 4  | US-09-949-016-78587  | Sequence 78587, A  |
| Sequence 88613, A  | 601    | 41.9 | 4  | US-09-949-016-88613  | Sequence 88613, A  |
| Sequence 142339, A | 601    | 41.9 | 4  | US-09-949-016-89710  | Sequence 142339, A |
| Sequence 198373, A | 601    | 41.9 | 4  | US-09-949-016-198373 | Sequence 198373, A |
| Sequence 198374, A | 601    | 41.9 | 4  | US-09-949-016-198374 | Sequence 198374, A |
| Sequence 198375, A | 601    | 41.9 | 4  | US-09-949-016-198375 | Sequence 198375, A |
| Sequence 1172, Ap  | 603    | 41.9 | 4  | US-09-543-681A-1172  | Sequence 1172, Ap  |
| Sequence 2272, Ap  | 624    | 41.9 | 4  | US-09-252-991A-2272  | Sequence 2272, Ap  |
| Sequence 54, Appl  | 636    | 41.9 | 4  | US-09-902-540-54     | Sequence 54, Appl  |
| Sequence 14176, A  | 651    | 41.9 | 4  | US-09-252-991A-14176 | Sequence 14176, A  |
| Sequence 3219, Ap  | 651    | 41.9 | 4  | US-09-134-000C-3219  | Sequence 3219, Ap  |
| Sequence 2747, Ap  | 654    | 41.9 | 4  | US-09-107-532A-2747  | Sequence 2747, Ap  |
| Sequence 10362, A  | 654    | 41.9 | 4  | US-09-270-767-10362  | Sequence 10362, A  |
| Sequence 792, App  | 657    | 41.9 | 4  | US-09-543-681A-792   | Sequence 792, App  |
| Sequence 377, App  | 667    | 41.9 | 4  | US-09-602-777A-377   | Sequence 377, App  |
| Sequence 10111, A  | 669    | 41.9 | 4  | US-09-270-767-10111  | Sequence 10111, A  |
| Sequence 11566, A  | 752    | 41.9 | 4  | US-09-270-767-11566  | Sequence 11566, A  |
| Sequence 14092, A  | 780    | 41.9 | 4  | US-09-252-991A-14092 | Sequence 14092, A  |
| Sequence 535, App  | 822    | 41.9 | 4  | US-09-673-395A-535   | Sequence 535, App  |
| Sequence 9578, Ap  | 825    | 41.9 | 4  | US-09-902-540-9578   | Sequence 9578, Ap  |
| Sequence 12027, A  | 849    | 41.9 | 4  | US-09-252-991A-12027 | Sequence 12027, A  |
| Sequence 14131, A  | 945    | 41.9 | 4  | US-09-252-991A-14131 | Sequence 14131, A  |
| Sequence 5, Appli  | 1089   | 41.9 | 2  | US-08-704-931-5      | Sequence 5, Appli  |
| Sequence 4137, Ap  | 1104   | 41.9 | 4  | US-09-252-991A-4137  | Sequence 4137, Ap  |
| Sequence 892, App  | 1257   | 41.9 | 4  | US-09-252-991A-892   | Sequence 892, App  |
| Sequence 2483, Ap  | 1278   | 41.9 | 4  | US-09-252-991A-2483  | Sequence 2483, Ap  |
| Sequence 12056, A  | 1359   | 41.9 | 4  | US-09-252-991A-12056 | Sequence 12056, A  |
| Sequence 1, Appli  | 1360   | 41.9 | 2  | US-08-704-931-1      | Sequence 1, Appli  |
| Sequence 4118, Ap  | 1404   | 41.9 | 2  | US-09-252-991A-4118  | Sequence 4118, Ap  |
| Sequence 3, Appli  | 1530   | 41.9 | 2  | US-08-704-931-3      | Sequence 3, Appli  |
| Sequence 764, App  | 1558   | 41.9 | 4  | US-09-949-016-764    | Sequence 764, App  |
| Sequence 4025, Ap  | 1563   | 41.9 | 4  | US-09-949-016-4025   | Sequence 4025, Ap  |
| Sequence 2566, Ap  | 1563   | 41.9 | 4  | US-09-252-991A-2566  | Sequence 2566, Ap  |
| Sequence 2352, Ap  | 1671   | 41.9 | 4  | US-09-252-991A-2352  | Sequence 2352, Ap  |
| Sequence 219, App  | 1671   | 41.9 | 4  | US-09-602-787A-219   | Sequence 219, App  |
| Sequence 4087, Ap  | 1680   | 41.9 | 4  | US-09-252-991A-4087  | Sequence 4087, Ap  |

|     |    |      |        |   |                      |                    |       |    |      |        |   |                     |                   |
|-----|----|------|--------|---|----------------------|--------------------|-------|----|------|--------|---|---------------------|-------------------|
| 101 | 13 | 41.9 | 1826   | 3 | US-09-282-305-1      | Sequence 1, Appl1  | C 174 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14552 | Sequence 14552, A |
| 102 | 13 | 41.9 | 1826   | 4 | US-09-883-720-1      | Sequence 1, Appl1  | C 175 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14553 | Sequence 14553, A |
| 103 | 13 | 41.9 | 1833   | 3 | US-08-704-966-3      | Sequence 3, Appl1  | C 176 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14554 | Sequence 14554, A |
| 104 | 13 | 41.9 | 1833   | 3 | US-08-705-438-3      | Sequence 3, Appl1  | C 177 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14555 | Sequence 14555, A |
| 105 | 13 | 41.9 | 1833   | 4 | US-09-489-039A-1045  | Sequence 1045, Ap  | C 178 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14556 | Sequence 14556, A |
| 106 | 13 | 41.9 | 1935   | 4 | US-09-252-991A-5783  | Sequence 5783, Ap  | C 179 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14557 | Sequence 14557, A |
| 107 | 13 | 41.9 | 2385   | 4 | US-09-252-991A-11998 | Sequence 11998, A  | C 180 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14558 | Sequence 14558, A |
| 108 | 13 | 41.9 | 2811   | 5 | PCT-US94-05905-21    | Sequence 21, Appl  | C 181 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14559 | Sequence 14559, A |
| 109 | 13 | 41.9 | 2820   | 2 | US-08-306-488-1      | Sequence 1, Appl1  | C 182 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14560 | Sequence 14560, A |
| 110 | 13 | 41.9 | 2820   | 5 | PCT-US94-05905-19    | Sequence 19, Appl  | C 183 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14561 | Sequence 14561, A |
| 111 | 13 | 41.9 | 2839   | 1 | US-07-814-964-6      | Sequence 6, Appl1  | C 184 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14562 | Sequence 14562, A |
| 112 | 13 | 41.9 | 2839   | 1 | US-08-258-442-6      | Sequence 1, Appl1  | C 185 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14565 | Sequence 14565, A |
| 113 | 13 | 41.9 | 2839   | 1 | US-08-328-809-1      | Sequence 1, Appl1  | C 186 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14566 | Sequence 14566, A |
| 114 | 13 | 41.9 | 2839   | 3 | US-09-015-003-1      | Sequence 1, Appl1  | C 187 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14567 | Sequence 14567, A |
| 115 | 13 | 41.9 | 2839   | 4 | US-08-866-840-1      | Sequence 6, Appl1  | C 188 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14568 | Sequence 14568, A |
| 116 | 13 | 41.9 | 2839   | 5 | PCT-US92-11107-6     | Sequence 6, Appl1  | C 189 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14569 | Sequence 14569, A |
| 117 | 13 | 41.9 | 2859   | 4 | US-09-252-991A-944   | Sequence 944, Ap   | C 190 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14570 | Sequence 14570, A |
| 118 | 13 | 41.9 | 2887   | 4 | US-09-949-016-2186   | Sequence 2186, Ap  | C 191 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14571 | Sequence 14571, A |
| 119 | 13 | 41.9 | 3459   | 4 | US-09-902-540-433    | Sequence 433, Ap   | C 192 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14572 | Sequence 14572, A |
| 120 | 13 | 41.9 | 3487   | 3 | US-09-453-702B-164   | Sequence 164, Ap   | C 193 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14573 | Sequence 14573, A |
| 121 | 13 | 41.9 | 4776   | 2 | US-08-852-401-1      | Sequence 1, Appl1  | C 194 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14574 | Sequence 14574, A |
| 122 | 13 | 41.9 | 8051   | 2 | US-08-576-626A-2     | Sequence 2, Appl1  | C 195 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14575 | Sequence 14575, A |
| 123 | 13 | 41.9 | 1026   | 4 | US-09-949-016-16680  | Sequence 16680, A  | C 196 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14576 | Sequence 14576, A |
| 124 | 13 | 41.9 | 11358  | 4 | US-09-902-540-1075   | Sequence 1075, Ap  | C 197 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14577 | Sequence 14577, A |
| 125 | 13 | 41.9 | 11808  | 4 | US-09-949-016-15281  | Sequence 15281, A  | C 198 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14578 | Sequence 14578, A |
| 126 | 13 | 41.9 | 13259  | 4 | US-09-949-016-16454  | Sequence 16454, A  | C 199 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14579 | Sequence 14579, A |
| 127 | 13 | 41.9 | 13466  | 4 | US-09-902-540-1007   | Sequence 1007, Ap  | C 200 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14580 | Sequence 14580, A |
| 128 | 13 | 41.9 | 14823  | 4 | US-09-902-540-1087   | Sequence 1087, Ap  | C 201 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14581 | Sequence 14581, A |
| 129 | 13 | 41.9 | 16541  | 4 | US-09-902-540-1165   | Sequence 1165, Ap  | C 202 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14582 | Sequence 14582, A |
| 130 | 13 | 41.9 | 19253  | 4 | US-09-949-016-15131  | Sequence 15131, Ap | C 203 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14583 | Sequence 14583, A |
| 131 | 13 | 41.9 | 19728  | 4 | US-09-949-016-12506  | Sequence 12506, A  | C 204 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14584 | Sequence 14584, A |
| 132 | 13 | 41.9 | 19728  | 4 | US-09-949-016-15767  | Sequence 15767, A  | C 205 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14585 | Sequence 14585, A |
| 133 | 13 | 41.9 | 20495  | 4 | US-09-949-016-17198  | Sequence 17198, A  | C 206 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14586 | Sequence 14586, A |
| 134 | 13 | 41.9 | 23445  | 4 | US-09-949-016-12955  | Sequence 12955, A  | C 207 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14587 | Sequence 14587, A |
| 135 | 13 | 41.9 | 24459  | 4 | US-09-902-540-5004   | Sequence 5004, Ap  | C 208 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14588 | Sequence 14588, A |
| 136 | 13 | 41.9 | 25686  | 4 | US-09-902-540-1246   | Sequence 1246, Ap  | C 209 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14589 | Sequence 14589, A |
| 137 | 13 | 41.9 | 26933  | 4 | US-09-949-016-12045  | Sequence 12045, A  | C 210 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14590 | Sequence 14590, A |
| 138 | 13 | 41.9 | 26933  | 4 | US-09-949-016-15972  | Sequence 15972, A  | C 211 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14591 | Sequence 14591, A |
| 139 | 13 | 41.9 | 29321  | 4 | US-09-949-016-14257  | Sequence 14257, A  | C 212 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14592 | Sequence 14592, A |
| 140 | 13 | 41.9 | 29321  | 4 | US-09-949-016-14258  | Sequence 14258, A  | C 213 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14593 | Sequence 14593, A |
| 141 | 13 | 41.9 | 32441  | 4 | US-09-902-540-1247   | Sequence 1247, Ap  | C 214 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14594 | Sequence 14594, A |
| 142 | 13 | 41.9 | 32573  | 4 | US-09-949-016-13359  | Sequence 13359, A  | C 215 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14595 | Sequence 14595, A |
| 143 | 13 | 41.9 | 39754  | 4 | US-09-949-016-14689  | Sequence 14689, A  | C 216 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14596 | Sequence 14596, A |
| 144 | 13 | 41.9 | 41171  | 4 | US-08-311-731A-122   | Sequence 122, Ap   | C 217 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14597 | Sequence 14597, A |
| 145 | 13 | 41.9 | 45862  | 4 | US-09-949-016-13928  | Sequence 13928, A  | C 218 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14598 | Sequence 14598, A |
| 146 | 13 | 41.9 | 50453  | 4 | US-09-949-016-16642  | Sequence 16642, A  | C 219 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14599 | Sequence 14599, A |
| 147 | 13 | 41.9 | 51242  | 4 | US-09-949-016-12486  | Sequence 12486, A  | C 220 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14600 | Sequence 14600, A |
| 148 | 13 | 41.9 | 55298  | 4 | US-09-491-356C-1     | Sequence 1, Appl1  | C 221 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14601 | Sequence 14601, A |
| 149 | 13 | 41.9 | 61663  | 3 | US-09-453-702B-62    | Sequence 62, Appl1 | C 222 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14602 | Sequence 14602, A |
| 150 | 13 | 41.9 | 68719  | 4 | US-09-949-016-12799  | Sequence 12799, A  | C 223 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14603 | Sequence 14603, A |
| 151 | 13 | 41.9 | 68720  | 4 | US-09-949-016-14296  | Sequence 14296, A  | C 224 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14604 | Sequence 14604, A |
| 152 | 13 | 41.9 | 113042 | 4 | US-09-949-016-12343  | Sequence 12343, A  | C 225 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14605 | Sequence 14605, A |
| 153 | 13 | 41.9 | 113042 | 4 | US-09-949-016-15246  | Sequence 15246, A  | C 226 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14606 | Sequence 14606, A |
| 154 | 13 | 41.9 | 118999 | 4 | US-09-791-105B-32    | Sequence 32, Appl  | C 227 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14607 | Sequence 14607, A |
| 155 | 13 | 41.9 | 118999 | 4 | US-09-791-105B-32    | Sequence 32, Appl  | C 228 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14608 | Sequence 14608, A |
| 156 | 13 | 41.9 | 127771 | 4 | US-09-949-016-14982  | Sequence 14982, A  | C 229 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14609 | Sequence 14609, A |
| 157 | 13 | 41.9 | 134292 | 4 | US-09-949-016-12158  | Sequence 12158, A  | C 230 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14610 | Sequence 14610, A |
| 158 | 13 | 41.9 | 161652 | 4 | US-09-497-858A-40    | Sequence 40, Appl  | C 231 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14611 | Sequence 14611, A |
| 159 | 13 | 41.9 | 174359 | 4 | US-09-949-016-11968  | Sequence 11968, A  | C 232 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14612 | Sequence 14612, A |
| 160 | 13 | 41.9 | 174362 | 4 | US-09-949-016-14259  | Sequence 14259, A  | C 233 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14613 | Sequence 14613, A |
| 161 | 13 | 41.9 | 194790 | 4 | US-09-949-016-15393  | Sequence 15393, A  | C 234 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14614 | Sequence 14614, A |
| 162 | 13 | 41.9 | 209210 | 4 | US-09-949-016-15094  | Sequence 15094, A  | C 235 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14615 | Sequence 14615, A |
| 163 | 13 | 41.9 | 636591 | 4 | US-09-949-016-11808  | Sequence 11808, A  | C 236 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14616 | Sequence 14616, A |
| 164 | 13 | 41.9 | 636591 | 4 | US-09-949-016-13388  | Sequence 13388, A  | C 237 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14617 | Sequence 14617, A |
| 165 | 13 | 41.9 | 767677 | 4 | US-09-949-016-12147  | Sequence 12147, A  | C 238 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14618 | Sequence 14618, A |
| 166 | 13 | 41.9 | 767677 | 4 | US-09-949-016-17361  | Sequence 17361, A  | C 239 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14619 | Sequence 14619, A |
| 167 | 13 | 41.9 | 784019 | 4 | US-09-949-016-14033  | Sequence 14033, A  | C 240 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14620 | Sequence 14620, A |
| 168 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14546  | Sequence 14546, A  | C 241 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14621 | Sequence 14621, A |
| 169 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14547  | Sequence 14547, A  | C 242 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14622 | Sequence 14622, A |
| 170 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14548  | Sequence 14548, A  | C 243 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14623 | Sequence 14623, A |
| 171 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14549  | Sequence 14549, A  | C 244 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14624 | Sequence 14624, A |
| 172 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14550  | Sequence 14550, A  | C 245 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14625 | Sequence 14625, A |
| 173 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14551  | Sequence 14551, A  | C 246 | 13 | 41.9 | 818128 | 4 | US-09-949-016-14626 | Sequence 14626, A |

|     |    |      |     |   |                      |                    |       |    |      |      |   |                      |                    |
|-----|----|------|-----|---|----------------------|--------------------|-------|----|------|------|---|----------------------|--------------------|
| 247 | 12 | 38.7 | 431 | 4 | US-09-670-314-377    | Sequence 377, App  | c 320 | 12 | 38.7 | 903  | 3 | US-08-762-227A-66    | Sequence 66, Appl  |
| 248 | 12 | 38.7 | 432 | 4 | US-09-902-540-1638   | Sequence 1638, Ap  | c 321 | 12 | 38.7 | 903  | 4 | US-09-328-352-1510   | Sequence 1510, Ap  |
| 249 | 12 | 38.7 | 433 | 4 | US-09-270-767-6917   | Sequence 6917, Ap  | c 322 | 12 | 38.7 | 903  | 4 | US-09-902-540-4584   | Sequence 4584, Ap  |
| 250 | 12 | 38.7 | 436 | 4 | US-09-270-767-22199  | Sequence 22199, A  | c 323 | 12 | 38.7 | 903  | 5 | PCT-US95-01185-66    | Sequence 66, Appl  |
| 251 | 12 | 38.7 | 452 | 4 | US-09-322-357-47     | Sequence 47, Appl  | c 324 | 12 | 38.7 | 936  | 4 | US-09-248-796A-912   | Sequence 912, App  |
| 252 | 12 | 38.7 | 459 | 3 | US-09-199-637A-268   | Sequence 268, App  | c 325 | 12 | 38.7 | 951  | 4 | US-09-134-000C-1037  | Sequence 1037, App |
| 253 | 12 | 38.7 | 465 | 4 | US-09-621-976-3332   | Sequence 3332, Ap  | c 326 | 12 | 38.7 | 969  | 4 | US-09-328-352-1763   | Sequence 1763, Ap  |
| 254 | 12 | 38.7 | 468 | 4 | US-09-621-976-13677  | Sequence 13677, A  | c 327 | 12 | 38.7 | 983  | 4 | US-09-640-211A-15    | Sequence 15, Appl  |
| 255 | 12 | 38.7 | 494 | 4 | US-09-621-976-18300  | Sequence 18300, A  | c 328 | 12 | 38.7 | 998  | 2 | US-08-105-989-6      | Sequence 6, Appl   |
| 256 | 12 | 38.7 | 495 | 4 | US-09-710-279-5      | Sequence 5, Appl   | c 329 | 12 | 38.7 | 998  | 3 | US-09-138-922-6      | Sequence 6, Appl   |
| 257 | 12 | 38.7 | 495 | 4 | US-09-710-279-473    | Sequence 473, App  | c 330 | 12 | 38.7 | 1001 | 3 | US-09-641-638-198    | Sequence 198, App  |
| 258 | 12 | 38.7 | 495 | 4 | US-09-248-796A-9077  | Sequence 9077, App | c 331 | 12 | 38.7 | 1001 | 3 | US-09-170-097-198    | Sequence 198, App  |
| 259 | 12 | 38.7 | 504 | 3 | US-09-370-838-250    | Sequence 250, App  | c 332 | 12 | 38.7 | 1017 | 3 | US-08-469-318-67     | Sequence 67, Appl  |
| 260 | 12 | 38.7 | 504 | 3 | US-09-854-133-250    | Sequence 250, App  | c 333 | 12 | 38.7 | 1017 | 3 | US-08-468-609A-67    | Sequence 67, Appl  |
| 261 | 12 | 38.7 | 510 | 3 | US-09-134-001C-2594  | Sequence 2594, Ap  | c 334 | 12 | 38.7 | 1017 | 3 | US-08-446-872A-67    | Sequence 67, Appl  |
| 262 | 12 | 38.7 | 528 | 4 | US-09-621-976-3331   | Sequence 3331, Ap  | c 335 | 12 | 38.7 | 1017 | 3 | US-08-762-227A-67    | Sequence 67, Appl  |
| 263 | 12 | 38.7 | 567 | 4 | US-09-252-991A-3149  | Sequence 3149, Ap  | c 336 | 12 | 38.7 | 1017 | 4 | US-09-902-540-9102   | Sequence 9102, Ap  |
| 264 | 12 | 38.7 | 570 | 4 | US-09-248-796A-5804  | Sequence 5804, Ap  | c 337 | 12 | 38.7 | 1017 | 5 | PCT-US95-01185-67    | Sequence 67, Appl  |
| 265 | 12 | 38.7 | 573 | 4 | US-09-328-352-1033   | Sequence 1033, Ap  | c 338 | 12 | 38.7 | 1047 | 3 | US-08-469-318-65     | Sequence 65, Appl  |
| 266 | 12 | 38.7 | 601 | 4 | US-09-949-016-22002  | Sequence 22002, A  | c 339 | 12 | 38.7 | 1047 | 3 | US-08-469-318-74     | Sequence 74, Appl  |
| 267 | 12 | 38.7 | 601 | 4 | US-09-949-016-22003  | Sequence 22003, A  | c 340 | 12 | 38.7 | 1047 | 3 | US-08-469-318-76     | Sequence 76, Appl  |
| 268 | 12 | 38.7 | 601 | 4 | US-09-949-016-22004  | Sequence 22004, A  | c 341 | 12 | 38.7 | 1047 | 3 | US-08-468-609A-65    | Sequence 65, Appl  |
| 269 | 12 | 38.7 | 601 | 4 | US-09-949-016-25005  | Sequence 25005, A  | c 342 | 12 | 38.7 | 1047 | 3 | US-08-468-609A-74    | Sequence 74, Appl  |
| 270 | 12 | 38.7 | 601 | 4 | US-09-949-016-25006  | Sequence 25006, A  | c 343 | 12 | 38.7 | 1047 | 3 | US-08-468-609A-76    | Sequence 76, Appl  |
| 271 | 12 | 38.7 | 601 | 4 | US-09-949-016-4450   | Sequence 4450, A   | c 344 | 12 | 38.7 | 1047 | 3 | US-08-446-872A-65    | Sequence 65, Appl  |
| 272 | 12 | 38.7 | 601 | 4 | US-09-949-016-52288  | Sequence 52288, A  | c 345 | 12 | 38.7 | 1047 | 3 | US-08-446-872A-74    | Sequence 74, Appl  |
| 273 | 12 | 38.7 | 601 | 4 | US-09-949-016-53918  | Sequence 53918, A  | c 346 | 12 | 38.7 | 1047 | 3 | US-08-446-872A-76    | Sequence 76, Appl  |
| 274 | 12 | 38.7 | 601 | 4 | US-09-949-016-57347  | Sequence 57347, A  | c 347 | 12 | 38.7 | 1047 | 3 | US-08-762-227A-65    | Sequence 65, Appl  |
| 275 | 12 | 38.7 | 601 | 4 | US-09-949-016-60149  | Sequence 60149, A  | c 348 | 12 | 38.7 | 1047 | 3 | US-08-762-227A-74    | Sequence 74, Appl  |
| 276 | 12 | 38.7 | 601 | 4 | US-09-949-016-60150  | Sequence 60150, A  | c 349 | 12 | 38.7 | 1047 | 3 | US-08-762-227A-76    | Sequence 76, Appl  |
| 277 | 12 | 38.7 | 601 | 4 | US-09-949-016-60646  | Sequence 60646, A  | c 350 | 12 | 38.7 | 1047 | 5 | PCT-US95-01185-65    | Sequence 65, Appl  |
| 278 | 12 | 38.7 | 601 | 4 | US-09-949-016-83423  | Sequence 83423, A  | c 351 | 12 | 38.7 | 1047 | 5 | PCT-US95-01185-74    | Sequence 74, Appl  |
| 279 | 12 | 38.7 | 601 | 4 | US-09-949-016-83459  | Sequence 83459, A  | c 352 | 12 | 38.7 | 1047 | 5 | PCT-US95-01185-76    | Sequence 76, Appl  |
| 280 | 12 | 38.7 | 601 | 4 | US-09-949-016-84323  | Sequence 84323, A  | c 353 | 12 | 38.7 | 1074 | 3 | US-09-134-001C-542   | Sequence 542, App  |
| 281 | 12 | 38.7 | 601 | 4 | US-09-949-016-84325  | Sequence 84325, A  | c 354 | 12 | 38.7 | 1078 | 4 | US-09-522-689A-1     | Sequence 1, Appl   |
| 282 | 12 | 38.7 | 601 | 4 | US-09-949-016-84325  | Sequence 84325, A  | c 355 | 12 | 38.7 | 1089 | 5 | PCT-US95-03866-31    | Sequence 31, Appl  |
| 283 | 12 | 38.7 | 601 | 4 | US-09-949-016-86532  | Sequence 86532, A  | c 356 | 12 | 38.7 | 1092 | 4 | US-09-489-039A-6864  | Sequence 6864, Ap  |
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| 285 | 12 | 38.7 | 601 | 4 | US-09-949-016-86534  | Sequence 86534, A  | c 358 | 12 | 38.7 | 1100 | 3 | US-09-152-060-23     | Sequence 23, Appl  |
| 286 | 12 | 38.7 | 601 | 4 | US-09-949-016-128409 | Sequence 128409, A | c 359 | 12 | 38.7 | 1106 | 5 | PCT-US92-02977-5     | Sequence 5, Appl   |
| 287 | 12 | 38.7 | 601 | 4 | US-09-949-016-140349 | Sequence 140349, A | c 360 | 12 | 38.7 | 1106 | 5 | PCT-US95-03032-4     | Sequence 4, Appl   |
| 288 | 12 | 38.7 | 601 | 4 | US-09-949-016-140350 | Sequence 140350, A | c 361 | 12 | 38.7 | 1107 | 4 | US-09-252-991A-14565 | Sequence 14565, A  |
| 289 | 12 | 38.7 | 601 | 4 | US-09-949-016-142625 | Sequence 142625, A | c 362 | 12 | 38.7 | 1110 | 4 | US-09-489-039A-416   | Sequence 416, App  |
| 290 | 12 | 38.7 | 601 | 4 | US-09-949-016-162628 | Sequence 162628, A | c 363 | 12 | 38.7 | 1140 | 4 | US-09-252-991A-2912  | Sequence 2912, App |
| 291 | 12 | 38.7 | 601 | 4 | US-09-949-016-162629 | Sequence 162629, A | c 364 | 12 | 38.7 | 1170 | 4 | US-09-491-577-49     | Sequence 49, Appl  |
| 292 | 12 | 38.7 | 601 | 4 | US-09-949-016-169472 | Sequence 169472, A | c 365 | 12 | 38.7 | 1173 | 3 | US-08-706-216-5      | Sequence 5, Appl   |
| 293 | 12 | 38.7 | 601 | 4 | US-09-949-016-176054 | Sequence 176054, A | c 366 | 12 | 38.7 | 1173 | 4 | US-09-650-284B-5     | Sequence 5, Appl   |
| 294 | 12 | 38.7 | 601 | 4 | US-09-949-016-176055 | Sequence 176055, A | c 367 | 12 | 38.7 | 1230 | 4 | US-09-902-540-7025   | Sequence 7025, Ap  |
| 295 | 12 | 38.7 | 601 | 4 | US-09-949-016-186031 | Sequence 186031, A | c 368 | 12 | 38.7 | 1245 | 4 | US-09-252-991A-4537  | Sequence 4537, Ap  |
| 296 | 12 | 38.7 | 601 | 4 | US-09-949-016-199453 | Sequence 199453, A | c 369 | 12 | 38.7 | 1291 | 1 | US-07-952-755-2      | Sequence 2, Appl   |
| 297 | 12 | 38.7 | 601 | 4 | US-09-949-016-199454 | Sequence 199454, A | c 370 | 12 | 38.7 | 1291 | 1 | US-08-443-679-2      | Sequence 2, Appl   |
| 298 | 12 | 38.7 | 603 | 4 | US-09-252-991A-4238  | Sequence 4238, Ap  | c 371 | 12 | 38.7 | 1304 | 4 | US-09-270-767-678    | Sequence 678, App  |
| 299 | 12 | 38.7 | 610 | 4 | US-09-270-767-15117  | Sequence 15117, A  | c 372 | 12 | 38.7 | 1304 | 4 | US-09-270-767-15960  | Sequence 15960, A  |
| 300 | 12 | 38.7 | 640 | 4 | US-09-854-133-431    | Sequence 431, App  | c 373 | 12 | 38.7 | 1311 | 4 | US-09-248-796A-5537  | Sequence 5537, Ap  |
| 301 | 12 | 38.7 | 647 | 5 | PCT-US94-0417A-651   | Sequence 27, Appl  | c 374 | 12 | 38.7 | 1320 | 1 | US-07-681-704A-1     | Sequence 1, Appl   |
| 302 | 12 | 38.7 | 657 | 4 | US-09-489-039A-67    | Sequence 67, Appl  | c 375 | 12 | 38.7 | 1320 | 4 | US-09-602-787A-159   | Sequence 159, App  |
| 303 | 12 | 38.7 | 658 | 3 | US-08-476-120-7      | Sequence 7, Appl   | c 376 | 12 | 38.7 | 1326 | 4 | US-09-328-352-2243   | Sequence 2243, App |
| 304 | 12 | 38.7 | 672 | 4 | US-09-252-991A-3957  | Sequence 3957, Ap  | c 377 | 12 | 38.7 | 1341 | 3 | US-09-199-637A-266   | Sequence 266, App  |
| 305 | 12 | 38.7 | 702 | 4 | US-09-489-039A-6546  | Sequence 6546, Ap  | c 378 | 12 | 38.7 | 1347 | 3 | US-09-342-681C-13    | Sequence 13, Appl  |
| 306 | 12 | 38.7 | 744 | 4 | US-09-270-767-13516  | Sequence 13516, A  | c 379 | 12 | 38.7 | 1353 | 4 | US-09-252-991A-4921  | Sequence 4921, Ap  |
| 307 | 12 | 38.7 | 771 | 4 | US-09-543-681A-2936  | Sequence 2936, Ap  | c 380 | 12 | 38.7 | 1368 | 4 | US-09-270-767-5066   | Sequence 5066, Ap  |
| 308 | 12 | 38.7 | 832 | 4 | US-09-270-767-12770  | Sequence 12770, A  | c 381 | 12 | 38.7 | 1368 | 4 | US-09-270-767-20348  | Sequence 20348, A  |
| 309 | 12 | 38.7 | 840 | 4 | US-09-348-796A-6353  | Sequence 6353, Ap  | c 382 | 12 | 38.7 | 1374 | 4 | US-09-252-991A-4024  | Sequence 4024, Ap  |
| 310 | 12 | 38.7 | 840 | 4 | US-09-949-016-5446   | Sequence 5446, Ap  | c 383 | 12 | 38.7 | 1382 | 2 | US-08-596-387B-123   | Sequence 123, App  |
| 311 | 12 | 38.7 | 858 | 4 | US-09-248-796A-8715  | Sequence 8715, Ap  | c 384 | 12 | 38.7 | 1382 | 2 | US-09-067-615-123    | Sequence 123, App  |
| 312 | 12 | 38.7 | 862 | 1 | US-08-379-280-4      | Sequence 4, Appl   | c 385 | 12 | 38.7 | 1382 | 5 | PCT-US95-09816A-123  | Sequence 123, App  |
| 313 | 12 | 38.7 | 889 | 2 | US-08-832-883-52     | Sequence 52, Appl  | c 386 | 12 | 38.7 | 1385 | 2 | US-08-596-387B-121   | Sequence 121, App  |
| 314 | 12 | 38.7 | 889 | 2 | US-08-832-877-52     | Sequence 52, Appl  | c 387 | 12 | 38.7 | 1385 | 3 | US-09-067-615-121    | Sequence 121, App  |
| 315 | 12 | 38.7 | 891 | 4 | US-09-543-681A-204   | Sequence 204, App  | c 388 | 12 | 38.7 | 1385 | 5 | PCT-US95-09816A-121  | Sequence 121, App  |
| 316 | 12 | 38.7 | 894 | 4 | US-09-902-540-6908   | Sequence 6908, Ap  | c 389 | 12 | 38.7 | 1393 | 4 | US-09-902-540-9055   | Sequence 9055, Ap  |
| 317 | 12 | 38.7 | 903 | 3 | US-08-469-318-66     | Sequence 66, Appl  | c 390 | 12 | 38.7 | 1395 | 4 | US-10-029-180-43     | Sequence 43, Appl  |
| 318 | 12 | 38.7 | 903 | 3 | US-08-468-609A-66    | Sequence 66, Appl  | c 391 | 12 | 38.7 | 1400 | 1 | US-07-989-845-1      | Sequence 1, Appl   |
| 319 | 12 | 38.7 | 903 | 3 | US-08-446-872A-66    | Sequence 66, Appl  | c 392 | 12 | 38.7 | 1400 | 5 | PCT-US93-11298-1     | Sequence 1, Appl   |



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RESULT 2
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      51.6%; Score 16; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GCACCGGAAGTTGAG 19
DB      1450409 GCACCGGAAGTTGAG 1450394

RESULT 3
US-09-313-294A-1931/c
; Sequence 1931, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 1931
; LENGTH: 214
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700551761H1
US-09-313-294A-1931

Query Match      48.4%; Score 15; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCCGCCACCGGAAGT 15
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RESULT 4
US-09-464-535-13/c
; Sequence 13, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McGonigle, Brian
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB1306 US NA
; CURRENT APPLICATION NUMBER: US/09/464,535
; CURRENT FILING DATE: 1999-12-15
; EARLIER APPLICATION NUMBER: 60/112,555
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-464-535-13

Query Match      48.4%; Score 15; DB 4; Length 436;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      157 CCACCGGAAGTTGAG 143

RESULT 5
US-09-464-535-39/c
; Sequence 39, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McGonigle, Brian
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB1306 US NA
; CURRENT APPLICATION NUMBER: US/09/464,535
; CURRENT FILING DATE: 1999-12-15
; EARLIER APPLICATION NUMBER: 60/112,555
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 39
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-464-535-39

Query Match      48.4%; Score 15; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CCACCGGAAGTTGAG 19
DB      164 CCACCGGAAGTTGAG 150

RESULT 6
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; Sequence 33, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McGonigle, Brian
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB1306 US NA
; CURRENT APPLICATION NUMBER: US/09/464,535
; CURRENT FILING DATE: 1999-12-15
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; EARLIER APPLICATION NUMBER: 60/112,555
; CURRENT FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 33
; LENGTH: 616
; TYPE: DNA
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US-09-464-535-33

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5 CCACCGGAAGTTGAG 19
Db 376 CCACCGGAAGTTGAG 362

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; Sequence 31, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McGonigle, Brian
; APPLICANT: Rafaleki, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB1306 US NA

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; CURRENT APPLICATION NUMBER: US/09/464,535
; CURRENT FILING DATE: 1999-12-15
; EARLIER APPLICATION NUMBER: 60/112,555
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 31
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Zea mays
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; NAME/KEY: unsure
; LOCATION: (3)
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; NAME/KEY: unsure
; LOCATION: (41)
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; NAME/KEY: unsure
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US-09-464-535-31

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Query Match 48.4%; Score 15; DB 4; Length 673;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5 CCACCGGAAGTTGAG 19
Db 362 CCACCGGAAGTTGAG 348

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RESULT 8

PCT-US95-08354A-1  
 ; Sequence 1, Application PC/TUS9508354A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Temple University - Of The  
 ; APPLICANT: Commonwealth System of Higher Education  
 ; TITLE OF INVENTION: JAK3 PROTEIN TYROSINE  
 ; TITLE OF INVENTION: KINASE AND DNA ENCODING THE SAME  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Seidel, Gonda, Lavorgna  
 ; ADDRESSEE: & Monaco, P.C.  
 ; STREET: Suite 1800, Two Penn Center  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19102  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: WordPerfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/08354A  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/272,368  
 ; FILING DATE: 8 July 1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Monaco, Daniel A.  
 ; REGISTRATION NUMBER: 30,480  
 ; REFERENCE/DOCKET NUMBER: 6056-203 PC  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 568-8383  
 ; TELEFAX: (215) 568-5549  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4016 nucleotides  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single stranded  
 ; TOPOLOGY: linear  
 ; PCT-US95-08354A-1

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 Best Local Similarity 100.0%; Pred. No. 18;  
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 Db 2033 GAGTAGACGGTGCTG 2047  
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 ; Sequence 12182, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 12182  
 ; LENGTH: 92581

; TYPE: DNA  
 ; ORGANISM: Human  
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 Query Match 48.4%; Score 15; DB 4; Length 92581;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 GGAAGTTGAGTAGAC 24  
 Db 55600 GGAAGTTGAGTAGAC 55586  
 RESULT 10  
 US-09-949-016-16542/c  
 ; Sequence 16542, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 16542  
 ; LENGTH: 92581  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-16542

Query Match 48.4%; Score 15; DB 4; Length 92581;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 GGAAGTTGAGTAGAC 24  
 Db 55600 GGAAGTTGAGTAGAC 55586  
 RESULT 11  
 US-09-621-976-17715/c  
 ; Sequence 17715, Application US/09621976  
 ; Patent No. 6639063  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Jobert, S.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
 ; FILE REFERENCE: GENSET.054PR2  
 ; CURRENT APPLICATION NUMBER: US/09/621,976  
 ; CURRENT FILING DATE: 2000-07-21  
 ; NUMBER OF SEQ ID NOS: 19335  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 17715  
 ; LENGTH: 223  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc.feature  
 ; LOCATION: 208  
 ; OTHER INFORMATION: n=a, g, c o r t  
 US-09-621-976-17715  
 Query Match 45.2%; Score 14; DB 4; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 74;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAG 14  
Db 15 TCCGCCACCGGAAG 2

## RESULT 12

US-09-471-276-430/c  
; Sequence 430, Application US/09471276  
; Patent No. 6822072  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6822072  
; FILE REFERENCE: GENSET.025CP1  
; CURRENT APPLICATION NUMBER: US/09/471,276  
; CURRENT FILING DATE: 1999-12-21  
; EARLIER APPLICATION NUMBER: 09/057,719  
; EARLIER FILING DATE: 1998-04-09  
; EARLIER APPLICATION NUMBER: 09/069,047  
; EARLIER FILING DATE: 1998-04-28  
; EARLIER APPLICATION NUMBER: PCT/IB99/00712  
; EARLIER FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 1622  
; SOFTWARE: Patent.pm

; SEQ ID NO 430  
; LENGTH: 236

; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

; NAME/KEY: CDS  
; LOCATION: 52..234  
; NAME/KEY: sig\_peptide  
; LOCATION: 52..159  
; OTHER INFORMATION: Von Heijne matrix  
; OTHER INFORMATION: score 4.8000019073486  
; OTHER INFORMATION: seq VLLAIGMFFTAWF/FV  
US-09-471-276-430

## Query Match

Best Local Similarity 45.2%; Score 14; DB 4; Length 236;  
Best Local Similarity 100.0%; Pred. No. 74;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAG 14  
Db 25 TCCGCCACCGGAAG 12

## RESULT 13

US-09-247-155-137/c  
; Sequence 137, Application US/09247155A  
; Patent No. 6312922  
; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: Complementary DNAs  
; FILE REFERENCE: GENSET.021A  
; CURRENT APPLICATION NUMBER: US/09/247,155A  
; CURRENT FILING DATE: 1999-02-09  
; EARLIER APPLICATION NUMBER: 60/074,121  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/081,563  
; EARLIER FILING DATE: 1998-04-13  
; EARLIER APPLICATION NUMBER: 60/096,116  
; EARLIER FILING DATE: 1998-08-10  
; EARLIER APPLICATION NUMBER: 60/099,273  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: Patent.pm

; SEQ ID NO 137  
; LENGTH: 419  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 50..286  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 50..157  
; OTHER INFORMATION: Von Heijne matrix  
; OTHER INFORMATION: score 4.8000019073486  
; OTHER INFORMATION: seq VLLAIGMFFTAWF/FV  
; FEATURE:  
; NAME/KEY: polyA signal  
; LOCATION: 385..390  
; FEATURE:  
; NAME/KEY: polyA site  
; LOCATION: 405..416  
US-09-247-155-137

Query Match 45.2%; Score 14; DB 3; Length 419;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAG 14  
Db 23 TCCGCCACCGGAAG 10

## RESULT 14

US-09-247-155-73/c  
; Sequence 73, Application US/09247155A  
; Patent No. 6312922  
; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: Complementary DNAs  
; FILE REFERENCE: GENSET.021A  
; CURRENT APPLICATION NUMBER: US/09/247,155A  
; CURRENT FILING DATE: 1999-02-09  
; EARLIER APPLICATION NUMBER: 60/074,121  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/081,563  
; EARLIER FILING DATE: 1998-04-13  
; EARLIER APPLICATION NUMBER: 60/096,116  
; EARLIER FILING DATE: 1998-08-10  
; EARLIER APPLICATION NUMBER: 60/099,273  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: Patent.pm

; SEQ ID NO 73  
; LENGTH: 425

; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 55..291  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 55..255  
; OTHER INFORMATION: Von Heijne matrix  
; OTHER INFORMATION: score 4.4  
; OTHER INFORMATION: seq LISLVASLFMGFG/VL  
; FEATURE:  
; NAME/KEY: polyA signal  
; LOCATION: 390..395  
; FEATURE:  
; NAME/KEY: polyA site  
; LOCATION: 410..425  
US-09-247-155-73



Query Match 45.2%; Score 14; DB 3; Length 425;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGCCACCGGAAG 14  
DB 27 TCCGCCACCGGAAG 14

RESULT 15  
US-09-621-976-17717/c  
; Sequence 17717, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 17717  
; LENGTH: 440  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-621-976-17717

Query Match 45.2%; Score 14; DB 4; Length 440;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGCCACCGGAAG 14  
DB 29 TCCGCCACCGGAAG 16

RESULT 16  
US-09-270-767-14483  
; Sequence 14483, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14483  
; LENGTH: 443  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-14483

Query Match 45.2%; Score 14; DB 4; Length 443;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GCCACCGGAAGTTG 17  
DB 334 GCCACCGGAAGTTG 347

RESULT 17  
US-09-621-976-17361  
; Sequence 17361, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 17361  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-621-976-17361

Query Match 45.2%; Score 14; DB 4; Length 468;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGCCACCGGAAG 14  
DB 259 TCCGCCACCGGAAG 272

RESULT 18  
US-09-621-976-17716/c  
; Sequence 17716, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 17716  
; LENGTH: 536  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 300,454,457  
; OTHER INFORMATION: n=a, g, c or t  
US-09-621-976-17716

Query Match 45.2%; Score 14; DB 4; Length 536;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGCCACCGGAAG 14  
DB 15 TCCGCCACCGGAAG 2

RESULT 19  
US-09-513-989C-12104/c  
; Sequence 12104, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 12104  
; LENGTH: 564

```
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 21
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 33
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 57
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 187
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-12104

Query Match          45.2%; Score 14; DB 4; Length 564;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAG 14
   |||||
Db 56 TCCGCCACCGGAAG 43

RESULT 20
US-09-621-976-1822/c
; Sequence 1822, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 1822
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 243..479
; NAME/KEY: sig_peptide
; LOCATION: 243..443
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 4.40000009536743
; OTHER INFORMATION: seq LISLVASLFMGFG/VL
US-09-621-976-1822

Query Match          45.2%; Score 14; DB 4; Length 579;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAG 14
   .|||||
Db 29 TCCGCCACCGGAAG 16

RESULT 21
US-09-949-016-29329
; Sequence 29329, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 21
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 33
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 57
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 187
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-12104

Query Match          45.2%; Score 14; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAG 14
   |||||
Db 98 TCCGCCACCGGAAG 111

RESULT 22
US-09-949-016-86408
; Sequence 86408, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86408
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-86408

Query Match          45.2%; Score 14; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AAGTTGAGTAGACG 25
   |||||
Db 434 AAGTTGAGTAGACG 447

RESULT 23
US-09-949-016-173059
; Sequence 173059, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
```

; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 173059  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-173059

Query Match 45.2%; Score 14; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAG 14  
|||||  
DB 98 TCCGCCACCGGAAG 111

RESULT 24  
US-09-902-540-4310/c  
; Sequence 4310, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 4310  
; LENGTH: 663  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-4310

Query Match 45.2%; Score 14; DB 4; Length 663;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TGAGTAGACGGTGC 29  
|||||  
DB 288 TGAGTAGACGGTGC 275

RESULT 25  
US-09-127-219B-2/c  
; Sequence 2, Application US/09127219B  
; Patent No. 637272  
; GENERAL INFORMATION:  
; APPLICANT: KIRKPATRICK, D. LYNN  
; APPLICANT: POWIS, GARTH  
; TITLE OF INVENTION: INHIBITORS OF REDOX SIGNALING AND METHODS OF USING SAME  
; FILE REFERENCE: 98-571-us  
; CURRENT APPLICATION NUMBER: US/09/127,219B  
; CURRENT FILING DATE: 1998-07-31  
; PRIOR APPLICATION NUMBER: 60/054,566  
; PRIOR FILING DATE: 1997-08-01  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 2187  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-127-219B-2

Query Match 45.2%; Score 14; DB 3; Length 2187;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAG 14  
|||||  
DB 251 TCCGCCACCGGAAG 238

RESULT 26  
US-09-252-991A-10206/c  
; Sequence 10206, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 10206  
; LENGTH: 2310  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-10206

Query Match 45.2%; Score 14; DB 4; Length 2310;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGT 15  
|||||  
DB 1292 CCGCCACCGGAAGT 1279

RESULT 27  
US-09-902-540-8535/c  
; Sequence 8535, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 8535  
; LENGTH: 2850  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-8535

Query Match 45.2%; Score 14; DB 4; Length 2850;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCCACCGGAAGTT 16  
|||||  
DB 1752 CGCCACCGGAAGTT 1739

RESULT 28

```
US-09-949-016-12296
; Sequence 12296, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12296
; LENGTH: 2913
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12296

Query Match          45.2%; Score 14; DB 4; Length 2913;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCCACCGGAAGTT 16
DB 758 CGCCACCGGAAGTT 771

RESULT 29
US-09-949-016-12327
; Sequence 12327, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12327
; LENGTH: 8073
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12327

Query Match          45.2%; Score 14; DB 4; Length 8073;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAG 14
DB 1909 TCCGCCACCGGAAG 1922

RESULT 30
US-09-949-016-16645
; Sequence 16645, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16645
; LENGTH: 8074
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16645

Query Match          45.2%; Score 14; DB 4; Length 8074;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAG 14
DB 1909 TCCGCCACCGGAAG 1922

RESULT 31
US-09-902-540-899
; Sequence 899, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 899
; LENGTH: 8518
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-899

Query Match          45.2%; Score 14; DB 4; Length 8518;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCCACCGGAAGTT 16
DB 6766 CGCCACCGGAAGTT 6779

RESULT 32
US-09-902-540-1219
; Sequence 1219, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
```

;; PRIOR FILING DATE: 2000-07-10  
;; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 1219  
; LENGTH: 22761  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(22761)  
; OTHER INFORMATION: unsure at all n locations  
US-09-902-540-1219

Query Match 45.2%; Score 14; DB 4; Length 22761;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGT 15  
Db 18791 CCGCCACCGGAAGT 18804  
|||||

## RESULT 33

US-09-902-540-1214/C  
; Sequence 1214, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 1214  
; LENGTH: 22807  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-1214

Query Match 45.2%; Score 14; DB 4; Length 22807;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TGAGTAGACGGTGC 29  
Db 21474 TGAGTAGACGGTGC 21461  
|||||

## RESULT 34

US-09-902-540-1214/C  
; Sequence 1214, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 1214  
; LENGTH: 22807  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-1214

;; FILING DATE: 20-JAN-1988  
;; APPLICATION NUMBER: 485,614  
; FILING DATE: 15-APR-1983  
; APPLICATION NUMBER: 713,624  
; FILING DATE: 10-JUN-1991  
; APPLICATION NUMBER: 260,574  
; FILING DATE: 21-OCT-1988  
; APPLICATION NUMBER: 848,733  
; FILING DATE: 01-APR-1986  
; APPLICATION NUMBER: 535,354  
; FILING DATE: 26-SEP-1983  
; SEQ ID NO:1:  
; LENGTH: 24595  
5428147-1

Query Match 45.2%; Score 14; DB 6; Length 24595;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGT 15  
Db 22666 CCGCCACCGGAAGT 22679  
|||||

## RESULT 35

US-09-902-540-1214/C  
; Sequence 1214, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 1214  
; LENGTH: 22807  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-1214

Query Match 45.2%; Score 14; DB 6; Length 24595;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGT 15  
Db 22666 CCGCCACCGGAAGT 22679  
|||||

## RESULT 36

US-09-949-016-13407  
; Sequence 13407, Application US/09949016  
; Patent No. 6812339

```
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13407
; LENGTH: 32616
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13407

Query Match          45.2%; Score 14; DB 4; Length 32616;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 CGGAAGTTGAGTAG 22
        |||||
Db      8287 CGGAAGTTGAGTAG 8300

RESULT 37
US-09-949-016-16785/c
; Sequence 16785, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16785
; LENGTH: 35784
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16785
```

```
Query Match          45.2%; Score 14; DB 4; Length 35784;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCCGCCACCGGAAG 14
        |||||
Db      1184 TCCGCCACCGGAAG 1171

RESULT 38
US-09-949-016-16786/c
; Sequence 16786, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
```

```
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16786
; LENGTH: 35784
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16786

Query Match          45.2%; Score 14; DB 4; Length 35784;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCCGCCACCGGAAG 14
        |||||
Db      1184 TCCGCCACCGGAAG 1171

RESULT 39
US-09-949-016-15846
; Sequence 15846, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15846
; LENGTH: 40951
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)...(40951)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15846
```

```
Query Match          45.2%; Score 14; DB 4; Length 40951;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 GGAAGTTGAGTAGA 23
        |||||
Db      15796 GGAAGTTGAGTAGA 15809

RESULT 40
US-09-949-016-15794
; Sequence 15794, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
```

;/ CURRENT FILING DATE: 2000-04-14  
;/ PRIOR APPLICATION NUMBER: 60/241,755  
;/ PRIOR FILING DATE: 2000-10-20  
;/ PRIOR APPLICATION NUMBER: 60/237,768  
;/ PRIOR FILING DATE: 2000-10-03  
;/ PRIOR APPLICATION NUMBER: 60/231,498  
;/ PRIOR FILING DATE: 2000-09-08  
;/ NUMBER OF SEQ ID NOS: 207012  
;/ SOFTWARE: FastSeq for Windows Version 4.0  
;/ SEQ ID NO 15794  
;/ LENGTH: 123513  
;/ TYPE: DNA  
;/ ORGANISM: Human  
;/ FEATURE:  
;/ NAME/KEY: misc\_feature  
;/ LOCATION: (1)...(123513)  
;/ OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15794

Query Match 45.2%; Score 14; DB 4; Length 123513;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAGTTGA 18  
Db 118414 CCACCGGAGTTGA 118427

RESULT 41  
US-09-949-016-15444/c  
;/ Sequence 15444, Application US/09949016  
;/ Patent No. 6812339  
;/ GENERAL INFORMATION:  
;/ APPLICANT: VENTER, J. Craig et al.  
;/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
;/ FILE REFERENCE: CL001307  
;/ CURRENT APPLICATION NUMBER: US/09/949,016  
;/ CURRENT FILING DATE: 2000-04-14  
;/ PRIOR APPLICATION NUMBER: 60/241,755  
;/ PRIOR FILING DATE: 2000-10-20  
;/ PRIOR APPLICATION NUMBER: 60/237,768  
;/ PRIOR FILING DATE: 2000-10-03  
;/ PRIOR APPLICATION NUMBER: 60/231,498  
;/ PRIOR FILING DATE: 2000-09-08  
;/ NUMBER OF SEQ ID NOS: 207012  
;/ SOFTWARE: FastSeq for Windows Version 4.0  
;/ SEQ ID NO 15444  
;/ LENGTH: 145928  
;/ TYPE: DNA  
;/ ORGANISM: Human  
;/ FEATURE:  
;/ NAME/KEY: misc\_feature  
;/ LOCATION: (1)...(145928)  
;/ OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15444

Query Match 45.2%; Score 14; DB 4; Length 145928;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGTTGAGTAGA 23  
Db 1160 GGAAGTTGAGTAGA 1147

RESULT 42  
US-09-949-016-14182/c  
;/ Sequence 14182, Application US/09949016  
;/ Patent No. 6812339  
;/ GENERAL INFORMATION:  
;/ APPLICANT: VENTER, J. Craig et al.  
;/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

;/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
;/ FILE REFERENCE: CL001307  
;/ CURRENT APPLICATION NUMBER: US/09/949,016  
;/ CURRENT FILING DATE: 2000-04-14  
;/ PRIOR APPLICATION NUMBER: 60/241,755  
;/ PRIOR FILING DATE: 2000-10-20  
;/ PRIOR APPLICATION NUMBER: 60/237,768  
;/ PRIOR FILING DATE: 2000-10-03  
;/ PRIOR APPLICATION NUMBER: 60/231,498  
;/ PRIOR FILING DATE: 2000-09-08  
;/ NUMBER OF SEQ ID NOS: 207012  
;/ SOFTWARE: FastSeq for Windows Version 4.0  
;/ SEQ ID NO 14182  
;/ LENGTH: 422592  
;/ TYPE: DNA  
;/ ORGANISM: Human  
;/ FEATURE:  
;/ NAME/KEY: misc\_feature  
;/ LOCATION: (1)...(422592)  
;/ OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14182

Query Match 45.2%; Score 14; DB 4; Length 422592;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AAGTTGAGTAGACG 25  
Db 402008 AAGTTGAGTAGACG 401995

RESULT 43  
US-08-483-528B-87  
;/ Sequence 87, Application US/08483528B  
;/ Patent No. 5939532  
;/ GENERAL INFORMATION:  
;/ APPLICANT: NAKAMURA, KAZUYASU  
;/ APPLICANT: KOIKE, MASAMICHI  
;/ APPLICANT: SHITARA, KENYA  
;/ APPLICANT: HANAI, NOBUO  
;/ APPLICANT: KUWANA, YOSHIHISA  
;/ APPLICANT: HASEGAWA, MAMORU  
;/ TITLE OF INVENTION: HUMANIZED ANTIBODIES  
;/ NUMBER OF SEQUENCES: 103  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: NIXON & VANDERHVE P.C.  
;/ STREET: 1100 NORTH GLEBE ROAD  
;/ CITY: ARLINGTON  
;/ STATE: VIRGINIA  
;/ COUNTRY: U.S.A.  
;/ ZIP: 22201-4714  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Patent In Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/483,528B  
;/ FILING DATE: 07-JUN-95  
;/ CLASSIFICATION: 536  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (703)816-4000  
;/ TELEFAX: (703)816-4100  
;/ INFORMATION FOR SEQ ID NO: 87:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 87 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: other nucleic acid  
;/ DESCRIPTION: /desc = "synthetic DNA"  
US-08-483-528B-87

Query Match 41.9%; Score 13; DB 2; Length 87;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAAGTTGAGTAGA 23  
|||||  
Db 57 GAAGTTGAGTAGA 69

## RESULT 44

US-08-673-799C-87  
; Sequence 87, Application US/08673799C  
; Patent No. 6042828  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: KOIKE, MASAMICHI  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: KUWANA, YOSHITHISA  
; APPLICANT: HASEGAWA, MAMORU  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/673,799C  
; FILING DATE: 27-JUN-96

CLASSIFICATION: 536  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)816-4000  
; TELEFAX: (703)816-4100  
; INFORMATION FOR SEQ ID NO: 87:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 87 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "synthetic DNA"  
US-08-673-799C-87

Query Match 41.9%; Score 13; DB 3; Length 87;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAAGTTGAGTAGA 23  
|||||  
Db 57 GAAGTTGAGTAGA 69

## RESULT 45

US-09-393-385B-87  
; Sequence 87, Application US/09393385B  
; Patent No. 6423511  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: KOIKE, MASAMICHI  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: KUWANA, YOSHITHISA  
; APPLICANT: HASEGAWA, MAMORU  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; NUMBER OF SEQUENCES: 113

## CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/393,385B  
; FILING DATE: 27-JUN-96

## CLASSIFICATION:

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)816-4000  
; TELEFAX: (703)816-4100  
; INFORMATION FOR SEQ ID NO: 87:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 87 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "synthetic DNA"  
US-09-393-385B-87

Query Match 41.9%; Score 13; DB 3; Length 87;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAAGTTGAGTAGA 23  
|||||  
Db 57 GAAGTTGAGTAGA 69

## RESULT 46

US-09-252-991A-14219/c  
; Sequence 14219, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 14219  
; LENGTH: 216  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14219

Query Match 41.9%; Score 13; DB 4; Length 216;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GTAGACGGTGCTG 31  
|||||  
Db 203 GTAGACGGTGCTG 191

## RESULT 47

US-09-270-767-8307/c  
; Sequence 8307, Application US/09270767  
; Patent No. 6703491



GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8307  
LENGTH: 363  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-8307

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Sequence 23589, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 23589  
LENGTH: 363  
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US-09-270-767-23589

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DB 18 CCGCCACCGGAG 6

RESULT 49  
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Sequence 90, Application US/08483528B  
Patent No. 5939532  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KUWANA, YOSHIHISA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,528B  
FILING DATE: 07-JUN-95  
CLASSIFICATION: 536  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 90:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 390 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens and mouse  
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US-08-483-528B-90

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Sequence 90, Application US/08673799C  
Patent No. 6042828  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KUWANA, YOSHIHISA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; FILING DATE: 27-JUN-96
; CLASSIFICATION: 536
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
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; US-08-673-799C-90

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Best Local Similarity 100.0%; Pred. NO. 2.8e+02;
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Scoring table: OLIGO\_NUC  
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Searched: 5552208 seqs, 297965951 residues

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Minimum DB seq length: 0

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| 151 | 13 | 41.9 | 390     | 14 | US-10-195-752-90      | GENERAL INFORMA   | c 224 | 13 | 41.9 | 659 | 17 | US-10-027-632-270307 | Sequence 270307,  |
| 152 | 13 | 41.9 | 405     | 18 | US-10-425-115-96801   | Sequence 96801, A | c 225 | 13 | 41.9 | 659 | 17 | US-10-424-599-108133 | Sequence 108133,  |
| 153 | 13 | 41.9 | 413     | 9  | US-09-960-352-9322    | Sequence 9322, Ap | c 226 | 13 | 41.9 | 665 | 9  | US-09-796-692-7275   | Sequence 7275, Ap |
| 154 | 13 | 41.9 | 423     | 18 | US-10-437-963-49282   | Sequence 49282, A | c 227 | 13 | 41.9 | 665 | 14 | US-10-040-862-7275   | Sequence 7275, Ap |
| 155 | 13 | 41.9 | 424     | 9  | US-09-876-889-132     | Sequence 132, App | c 228 | 13 | 41.9 | 665 | 17 | US-10-057-475B-7275  | Sequence 7275, Ap |
| 156 | 13 | 41.9 | 425     | 18 | US-10-425-115-46417   | Sequence 46417, A | c 229 | 13 | 41.9 | 665 | 17 | US-10-154-884B-7275  | Sequence 7275, Ap |
| 157 | 13 | 41.9 | 429     | 9  | US-09-960-352-1727    | Sequence 1727, Ap | c 230 | 13 | 41.9 | 665 | 18 | US-10-764-324-7275   | Sequence 7275, Ap |

|       |    |      |      |    |                      |                   |       |    |      |      |    |                      |                   |
|-------|----|------|------|----|----------------------|-------------------|-------|----|------|------|----|----------------------|-------------------|
| 231   | 13 | 41.9 | 666  | 18 | US-10-363-345A-8955  | Sequence 8955, Ap | 304   | 13 | 41.9 | 1252 | 13 | US-10-027-632-123357 | Sequence 123357,  |
| c 232 | 13 | 41.9 | 666  | 18 | US-10-363-345A-8956  | Sequence 8956, Ap | 305   | 13 | 41.9 | 1252 | 13 | US-10-027-632-123358 | Sequence 123358,  |
| c 233 | 13 | 41.9 | 666  | 18 | US-10-437-963-79916  | Sequence 79916, A | 306   | 13 | 41.9 | 1252 | 17 | US-10-027-632-123357 | Sequence 123357,  |
| c 234 | 13 | 41.9 | 672  | 17 | US-10-424-599-82366  | Sequence 82366, A | 307   | 13 | 41.9 | 1252 | 17 | US-10-027-632-123358 | Sequence 123358,  |
| c 235 | 13 | 41.9 | 674  | 18 | US-10-425-115-40172  | Sequence 40172, A | c 308 | 13 | 41.9 | 1267 | 17 | US-10-424-599-26192  | Sequence 26192, A |
| c 236 | 13 | 41.9 | 677  | 9  | US-09-770-149-366    | Sequence 366, App | c 309 | 13 | 41.9 | 1278 | 18 | US-10-437-963-100800 | Sequence 100800,  |
| c 237 | 13 | 41.9 | 684  | 9  | US-09-765-205-41     | Sequence 41, Appl | c 310 | 13 | 41.9 | 1287 | 9  | US-09-938-842A-2429  | Sequence 2429, Ap |
| c 238 | 13 | 41.9 | 686  | 18 | US-10-653-047-7286   | Sequence 7286, Ap | c 311 | 13 | 41.9 | 1287 | 11 | US-09-938-842A-2429  | Sequence 2429, Ap |
| c 239 | 13 | 41.9 | 700  | 17 | US-10-424-599-137955 | Sequence 137955,  | c 312 | 13 | 41.9 | 1288 | 18 | US-10-363-345A-1103  | Sequence 1103, Ap |
| c 240 | 13 | 41.9 | 717  | 15 | US-10-265-689-11     | Sequence 11, Appl | c 313 | 13 | 41.9 | 1288 | 18 | US-10-363-345A-1104  | Sequence 1104, Ap |
| c 241 | 13 | 41.9 | 732  | 16 | US-10-029-386-20641  | Sequence 20641, A | c 314 | 13 | 41.9 | 1301 | 17 | US-10-424-599-37991  | Sequence 37991, A |
| c 242 | 13 | 41.9 | 737  | 18 | US-10-437-963-98813  | Sequence 98813, A | c 315 | 13 | 41.9 | 1320 | 15 | US-10-230-026-21     | Sequence 21, Appl |
| c 243 | 13 | 41.9 | 749  | 18 | US-10-425-115-138765 | Sequence 138765,  | c 316 | 13 | 41.9 | 1320 | 18 | US-10-486-307-21     | Sequence 21, Appl |
| c 244 | 13 | 41.9 | 750  | 17 | US-10-425-114-341    | Sequence 341, App | c 317 | 13 | 41.9 | 1322 | 18 | US-10-767-701-11866  | Sequence 11866, A |
| c 245 | 13 | 41.9 | 754  | 18 | US-10-425-115-170641 | Sequence 170641,  | c 318 | 13 | 41.9 | 1326 | 9  | US-09-738-626-3349   | Sequence 3349, Ap |
| c 246 | 13 | 41.9 | 758  | 18 | US-10-425-115-85436  | Sequence 85436, A | c 319 | 13 | 41.9 | 1332 | 17 | US-10-369-493-37336  | Sequence 37336, A |
| c 247 | 13 | 41.9 | 761  | 18 | US-10-363-345A-18977 | Sequence 18977, A | c 320 | 13 | 41.9 | 1333 | 17 | US-10-424-599-402    | Sequence 402, App |
| c 248 | 13 | 41.9 | 761  | 18 | US-10-363-345A-18978 | Sequence 18978, A | c 321 | 13 | 41.9 | 1342 | 10 | US-09-934-455-419    | Sequence 419, App |
| c 249 | 13 | 41.9 | 779  | 17 | US-10-424-599-117976 | Sequence 117976,  | c 322 | 13 | 41.9 | 1342 | 14 | US-10-278-173-17     | Sequence 17, Appl |
| c 250 | 13 | 41.9 | 782  | 18 | US-10-425-115-134229 | Sequence 134229,  | c 323 | 13 | 41.9 | 1342 | 17 | US-10-225-066A-257   | Sequence 257, App |
| c 251 | 13 | 41.9 | 783  | 18 | US-10-437-963-7584   | Sequence 7584, Ap | c 324 | 13 | 41.9 | 1342 | 17 | US-10-374-780A-2079  | Sequence 2079, Ap |
| c 252 | 13 | 41.9 | 788  | 13 | US-10-027-632-169544 | Sequence 169544,  | c 325 | 13 | 41.9 | 1342 | 17 | US-10-412-699B-727   | Sequence 727, App |
| c 253 | 13 | 41.9 | 788  | 17 | US-10-027-632-169544 | Sequence 169544,  | c 326 | 13 | 41.9 | 1342 | 17 | US-10-412-699B-727   | Sequence 727, App |
| c 254 | 13 | 41.9 | 800  | 19 | US-10-660-811A-126   | Sequence 126, App | c 327 | 13 | 41.9 | 1342 | 18 | US-10-665-824-53     | Sequence 53, Appl |
| c 255 | 13 | 41.9 | 803  | 10 | US-09-397-945-39     | Sequence 39, Appl | c 328 | 13 | 41.9 | 1353 | 17 | US-10-332-859-202    | Sequence 202, App |
| c 256 | 13 | 41.9 | 803  | 17 | US-10-653-595-39     | Sequence 39, Appl | c 329 | 13 | 41.9 | 1353 | 16 | US-10-241-596-71     | Sequence 71, Appl |
| c 257 | 13 | 41.9 | 814  | 18 | US-10-653-047-1057   | Sequence 1057, Ap | c 330 | 13 | 41.9 | 1376 | 16 | US-10-241-596-73     | Sequence 73, Appl |
| c 258 | 13 | 41.9 | 825  | 17 | US-10-282-122A-39569 | Sequence 39569, A | c 331 | 13 | 41.9 | 1376 | 16 | US-10-241-596-75     | Sequence 75, Appl |
| c 259 | 13 | 41.9 | 828  | 18 | US-10-425-115-27098  | Sequence 27098, A | c 332 | 13 | 41.9 | 1376 | 16 | US-10-241-596-77     | Sequence 77, Appl |
| c 260 | 13 | 41.9 | 833  | 18 | US-10-425-115-177708 | Sequence 177708,  | c 333 | 13 | 41.9 | 1385 | 16 | US-10-241-596-69     | Sequence 69, Appl |
| c 261 | 13 | 41.9 | 837  | 13 | US-10-062-254-215    | Sequence 215, App | c 334 | 13 | 41.9 | 1410 | 18 | US-10-810-352-67     | Sequence 67, Appl |
| c 262 | 13 | 41.9 | 852  | 16 | US-10-029-386-20263  | Sequence 20263, A | c 335 | 13 | 41.9 | 1464 | 9  | US-09-815-242-7938   | Sequence 7938, Ap |
| c 263 | 13 | 41.9 | 862  | 17 | US-10-282-122A-36615 | Sequence 36615, A | c 336 | 13 | 41.9 | 1468 | 18 | US-10-767-701-125405 | Sequence 12405, A |
| c 264 | 13 | 41.9 | 865  | 13 | US-10-027-632-160405 | Sequence 160405,  | c 337 | 13 | 41.9 | 1479 | 18 | US-10-425-115-25229  | Sequence 25229, A |
| c 265 | 13 | 41.9 | 865  | 13 | US-10-027-632-160406 | Sequence 160406,  | c 338 | 13 | 41.9 | 1482 | 18 | US-10-437-963-81324  | Sequence 81324, A |
| c 266 | 13 | 41.9 | 865  | 13 | US-10-027-632-160407 | Sequence 160407,  | c 339 | 13 | 41.9 | 1558 | 18 | US-10-473-974-192    | Sequence 192, App |
| c 267 | 13 | 41.9 | 865  | 17 | US-10-027-632-160405 | Sequence 160405,  | c 340 | 13 | 41.9 | 1596 | 15 | US-10-230-026-11     | Sequence 11, Appl |
| c 268 | 13 | 41.9 | 865  | 17 | US-10-027-632-160406 | Sequence 160406,  | c 341 | 13 | 41.9 | 1596 | 18 | US-10-486-307-11     | Sequence 11, Appl |
| c 269 | 13 | 41.9 | 865  | 17 | US-10-027-632-160407 | Sequence 160407,  | c 342 | 13 | 41.9 | 1617 | 18 | US-10-437-963-9028   | Sequence 9028, Ap |
| c 270 | 13 | 41.9 | 909  | 17 | US-10-369-493-26442  | Sequence 26442, A | c 343 | 13 | 41.9 | 1652 | 17 | US-10-424-599-121328 | Sequence 121328,  |
| c 271 | 13 | 41.9 | 936  | 15 | US-10-146-772-67     | Sequence 67, Appl | c 344 | 13 | 41.9 | 1671 | 17 | US-10-627-476-219    | Sequence 219, App |
| c 272 | 13 | 41.9 | 936  | 17 | US-10-241-742-67     | Sequence 67, Appl | c 345 | 13 | 41.9 | 1695 | 18 | US-10-425-115-120823 | Sequence 120823,  |
| c 273 | 13 | 41.9 | 936  | 17 | US-10-440-523-67     | Sequence 67, Appl | c 346 | 13 | 41.9 | 1744 | 18 | US-10-739-930-5122   | Sequence 5122, Ap |
| c 274 | 13 | 41.9 | 936  | 17 | US-10-440-503-67     | Sequence 67, Appl | c 347 | 13 | 41.9 | 1779 | 17 | US-10-424-599-13432  | Sequence 13432, A |
| c 275 | 13 | 41.9 | 936  | 17 | US-10-461-925-67     | Sequence 67, Appl | c 348 | 13 | 41.9 | 1826 | 9  | US-09-883-720-1      | Sequence 1, Appl  |
| c 276 | 13 | 41.9 | 947  | 17 | US-10-264-237-265    | Sequence 265, App | c 349 | 13 | 41.9 | 1834 | 17 | US-10-369-493-37070  | Sequence 37070, A |
| c 277 | 13 | 41.9 | 982  | 17 | US-10-369-493-37026  | Sequence 37026, A | c 350 | 13 | 41.9 | 1836 | 18 | US-10-437-963-84532  | Sequence 84532, A |
| c 278 | 13 | 41.9 | 984  | 18 | US-10-437-963-65225  | Sequence 65225, A | c 351 | 13 | 41.9 | 1848 | 15 | US-10-156-761-5286   | Sequence 5286, Ap |
| c 279 | 13 | 41.9 | 1007 | 18 | US-10-739-930-138    | Sequence 138, App | c 352 | 13 | 41.9 | 1860 | 17 | US-10-282-122A-18347 | Sequence 18347, A |
| c 280 | 13 | 41.9 | 1008 | 17 | US-10-267-502-20     | Sequence 20, Appl | c 353 | 13 | 41.9 | 1870 | 18 | US-10-437-963-80473  | Sequence 80473, A |
| c 281 | 13 | 41.9 | 1014 | 18 | US-10-425-115-136018 | Sequence 136018,  | c 354 | 13 | 41.9 | 1945 | 18 | US-10-425-115-170233 | Sequence 170233,  |
| c 282 | 13 | 41.9 | 1024 | 18 | US-10-767-701-13784  | Sequence 13784, A | c 355 | 13 | 41.9 | 2001 | 18 | US-10-437-963-68116  | Sequence 68116, A |
| c 283 | 13 | 41.9 | 1045 | 9  | US-09-822-849A-368   | Sequence 368, App | c 356 | 13 | 41.9 | 2005 | 17 | US-10-425-114-32279  | Sequence 32279, A |
| c 284 | 13 | 41.9 | 1058 | 9  | US-09-925-301-108    | Sequence 108, App | c 357 | 13 | 41.9 | 2016 | 18 | US-10-437-963-33080  | Sequence 33080, A |
| c 285 | 13 | 41.9 | 1065 | 19 | US-10-873-593-1      | Sequence 1, Appl  | c 358 | 13 | 41.9 | 2037 | 9  | US-09-738-626-2495   | Sequence 2495, Ap |
| c 286 | 13 | 41.9 | 1077 | 17 | US-10-424-599-130988 | Sequence 130988,  | c 359 | 13 | 41.9 | 2043 | 9  | US-09-938-842A-1337  | Sequence 1337, Ap |
| c 287 | 13 | 41.9 | 1085 | 17 | US-10-276-774-1339   | Sequence 1339, Ap | c 360 | 13 | 41.9 | 2043 | 11 | US-10-495-918-153    | Sequence 153, App |
| c 288 | 13 | 41.9 | 1085 | 18 | US-10-425-115-41755  | Sequence 41755, A | c 361 | 13 | 41.9 | 2043 | 17 | US-10-369-493-35516  | Sequence 35516, A |
| c 289 | 13 | 41.9 | 1097 | 18 | US-10-437-963-76733  | Sequence 76733, A | c 362 | 13 | 41.9 | 2061 | 17 | US-10-369-493-35516  | Sequence 35516, A |
| c 290 | 13 | 41.9 | 1116 | 9  | US-09-974-300-3015   | Sequence 3015, Ap | c 363 | 13 | 41.9 | 2073 | 17 | US-10-369-493-35516  | Sequence 35516, A |
| c 291 | 13 | 41.9 | 1121 | 17 | US-10-425-114-2848   | Sequence 2848, Ap | c 364 | 13 | 41.9 | 2100 | 13 | US-10-027-632-97188  | Sequence 97188, A |
| c 292 | 13 | 41.9 | 1121 | 17 | US-10-425-114-20946  | Sequence 20946, A | c 365 | 13 | 41.9 | 2100 | 13 | US-10-027-632-97189  | Sequence 97189, A |
| c 293 | 13 | 41.9 | 1131 | 15 | US-10-156-761-2320   | Sequence 2320, Ap | c 366 | 13 | 41.9 | 2100 | 13 | US-10-027-632-97189  | Sequence 97189, A |
| c 294 | 13 | 41.9 | 1135 | 18 | US-10-739-930-5023   | Sequence 5023, Ap | c 367 | 13 | 41.9 | 2100 | 17 | US-10-027-632-97188  | Sequence 97188, A |
| c 295 | 13 | 41.9 | 1146 | 15 | US-10-126-279-3      | Sequence 3, Appl  | c 368 | 13 | 41.9 | 2100 | 17 | US-10-027-632-97189  | Sequence 97189, A |
| c 296 | 13 | 41.9 | 1146 | 16 | US-10-286-606-3      | Sequence 3, Appl  | c 369 | 13 | 41.9 | 2100 | 17 | US-10-027-632-97190  | Sequence 97190, A |
| c 297 | 13 | 41.9 | 1146 | 18 | US-10-891-383-3      | Sequence 3, Appl  | c 370 | 13 | 41.9 | 2106 | 13 | US-10-027-632-99059  | Sequence 99059, A |
| c 298 | 13 | 41.9 | 1196 | 17 | US-10-425-114-19357  | Sequence 19357, A | c 371 | 13 | 41.9 | 2106 | 13 | US-10-027-632-99060  | Sequence 99060, A |
| c 299 | 13 | 41.9 | 1209 | 9  | US-10-437-963-7581   | Sequence 7581, Ap | c 372 | 13 | 41.9 | 2106 | 17 | US-10-027-632-99059  | Sequence 99059, A |
| c 300 | 13 | 41.9 | 1212 | 9  | US-09-938-842A-1566  | Sequence 1566, Ap | c 373 | 13 | 41.9 | 2106 | 17 | US-10-027-632-99060  | Sequence 99060, A |
| c 301 | 13 | 41.9 | 1212 | 11 | US-09-938-842A-1566  | Sequence 1566, Ap | c 374 | 13 | 41.9 | 2116 | 18 | US-10-695-089-2      | Sequence 2, Appl  |
| c 302 | 13 | 41.9 | 1225 | 18 | US-10-425-115-127953 | Sequence 127953,  | c 375 | 13 | 41.9 | 2160 | 18 | US-10-695-089-4      | Sequence 4, Appl  |
| c 303 | 13 | 41.9 | 1235 | 18 | US-10-437-963-59964  | Sequence 59964, A | c 376 | 13 | 41.9 | 2160 | 18 | US-10-695-546-6      | Sequence 6, Appl  |

|     |    |      |      |    |                      |                    |    |      |      |    |                     |                   |
|-----|----|------|------|----|----------------------|--------------------|----|------|------|----|---------------------|-------------------|
| 377 | 13 | 41.9 | 2201 | 18 | US-10-767-795-1468   | Sequence 1468, Ap  | 13 | 41.9 | 4287 | 17 | US-10-149-310-171   | Sequence 171, App |
| 378 | 13 | 41.9 | 2253 | 18 | US-10-437-963-17537  | Sequence 17537, A  | 13 | 41.9 | 4410 | 18 | US-10-810-352-61    | Sequence 61, Appl |
| 379 | 13 | 41.9 | 2297 | 18 | US-10-723-860-6300   | Sequence 6300, Ap  | 13 | 41.9 | 4436 | 15 | US-10-128-714-26    | Sequence 26, Appl |
| 380 | 13 | 41.9 | 2319 | 18 | US-10-437-963-19771  | Sequence 19771, A  | 13 | 41.9 | 4449 | 18 | US-10-723-860-7936  | Sequence 7936, Ap |
| 381 | 13 | 41.9 | 2330 | 18 | US-10-437-963-85431  | Sequence 85431, A  | 13 | 41.9 | 4467 | 18 | US-10-437-963-23127 | Sequence 23127, A |
| 382 | 13 | 41.9 | 2345 | 17 | US-10-425-114-29589  | Sequence 29589, A  | 13 | 41.9 | 4481 | 15 | US-10-128-714-5026  | Sequence 5026, Ap |
| 383 | 13 | 41.9 | 2348 | 17 | US-10-424-599-64768  | Sequence 64768, A  | 13 | 41.9 | 4527 | 15 | US-10-240-485-170   | Sequence 170, App |
| 384 | 13 | 41.9 | 2359 | 18 | US-10-695-546-20     | Sequence 20, Appl  | 13 | 41.9 | 4537 | 18 | US-10-433-793-138   | Sequence 138, App |
| 385 | 13 | 41.9 | 2361 | 17 | US-10-433-794-24     | Sequence 24, Appl  | 13 | 41.9 | 4549 | 18 | US-10-433-793-2     | Sequence 2, Appl  |
| 386 | 13 | 41.9 | 2373 | 15 | US-10-156-761-1026   | Sequence 1026, Ap  | 13 | 41.9 | 4581 | 17 | US-10-257-166-94    | Sequence 94, Appl |
| 387 | 13 | 41.9 | 2385 | 17 | US-10-225-066A-335   | Sequence 335, App  | 13 | 41.9 | 4587 | 18 | US-10-755-889-547   | Sequence 547, App |
| 388 | 13 | 41.9 | 2381 | 17 | US-10-374-780A-2671  | Sequence 2671, Ap  | 13 | 41.9 | 4617 | 15 | US-10-311-455-998   | Sequence 998, App |
| 389 | 13 | 41.9 | 2485 | 18 | US-10-437-963-9937   | Sequence 9937, Ap  | 13 | 41.9 | 4623 | 17 | US-10-398-221-3868  | Sequence 3868, Ap |
| 390 | 13 | 41.9 | 2485 | 18 | US-10-437-963-35215  | Sequence 35215, A  | 13 | 41.9 | 4623 | 17 | US-10-257-166-72    | Sequence 72, Appl |
| 391 | 13 | 41.9 | 2540 | 15 | US-10-106-698-358    | Sequence 358, App  | 13 | 41.9 | 4658 | 18 | US-10-437-963-51423 | Sequence 51423, A |
| 392 | 13 | 41.9 | 2547 | 17 | US-10-424-599-121066 | Sequence 121066, A | 13 | 41.9 | 4659 | 17 | US-10-221-613-273   | Sequence 273, App |
| 393 | 13 | 41.9 | 2590 | 16 | US-10-041-018-412    | Sequence 412, App  | 13 | 41.9 | 4694 | 17 | US-09-764-877-3815  | Sequence 3815, Ap |
| 394 | 13 | 41.9 | 2600 | 16 | US-10-241-596-33     | Sequence 33, Appl  | 13 | 41.9 | 7105 | 9  | US-10-242-515-3815  | Sequence 3815, Ap |
| 395 | 13 | 41.9 | 2600 | 16 | US-10-241-596-35     | Sequence 35, Appl  | 13 | 41.9 | 7105 | 9  | US-10-394-339C-90   | Sequence 90, Appl |
| 396 | 13 | 41.9 | 2600 | 16 | US-10-241-596-37     | Sequence 37, Appl  | 13 | 41.9 | 7476 | 18 | US-10-265-689-29    | Sequence 29, Appl |
| 397 | 13 | 41.9 | 2609 | 16 | US-10-241-596-31     | Sequence 31, Appl  | 13 | 41.9 | 7578 | 15 | US-10-131-803-37    | Sequence 37, Appl |
| 398 | 13 | 41.9 | 2619 | 16 | US-10-241-596-152    | Sequence 152, App  | 13 | 41.9 | 8810 | 17 | US-10-152-319A-1535 | Sequence 1535, Ap |
| 399 | 13 | 41.9 | 2625 | 16 | US-10-241-596-150    | Sequence 150, App  | 13 | 41.9 | 8810 | 17 | US-10-437-963-18559 | Sequence 18559, A |
| 400 | 13 | 41.9 | 2625 | 16 | US-10-241-596-164    | Sequence 164, App  | 13 | 41.9 | 8937 | 18 | US-10-000-789-1     | Sequence 1, Appl  |
| 401 | 13 | 41.9 | 2625 | 16 | US-10-241-596-166    | Sequence 166, App  | 13 | 41.9 | 9090 | 15 | US-10-171-581-305   | Sequence 305, App |
| 402 | 13 | 41.9 | 2625 | 16 | US-10-241-596-168    | Sequence 168, App  | 13 | 41.9 | 9090 | 15 | US-10-482-029-65    | Sequence 65, Appl |
| 403 | 13 | 41.9 | 2637 | 16 | US-10-241-596-156    | Sequence 156, App  | 13 | 41.9 | 9091 | 19 | US-10-741-600-395   | Sequence 395, App |
| 404 | 13 | 41.9 | 2640 | 16 | US-10-241-596-29     | Sequence 29, Appl  | 13 | 41.9 | 9142 | 9  | US-09-764-877-3562  | Sequence 3562, Ap |
| 405 | 13 | 41.9 | 2642 | 17 | US-10-094-749-1164   | Sequence 1164, Ap  | 13 | 41.9 | 9142 | 10 | US-09-764-891-8122  | Sequence 8122, Ap |
| 406 | 13 | 41.9 | 2643 | 16 | US-10-241-596-61     | Sequence 61, Appl  | 13 | 41.9 | 9142 | 17 | US-10-242-515-3562  | Sequence 3562, Ap |
| 407 | 13 | 41.9 | 2643 | 16 | US-10-241-596-158    | Sequence 158, App  | 13 | 41.9 | 9186 | 18 | US-10-357-930-23237 | Sequence 23237, A |
| 408 | 13 | 41.9 | 2667 | 16 | US-10-241-596-160    | Sequence 160, App  | 13 | 41.9 | 9186 | 18 | US-10-357-930-29110 | Sequence 29110, A |
| 409 | 13 | 41.9 | 2718 | 18 | US-10-437-963-11978  | Sequence 11978, A  | 13 | 41.9 | 9186 | 18 | US-10-311-455-413   | Sequence 413, App |
| 410 | 13 | 41.9 | 2719 | 17 | US-10-425-115-31030  | Sequence 31030, A  | 13 | 41.9 | 9186 | 18 | US-10-394-517-5     | Sequence 5, Appl  |
| 411 | 13 | 41.9 | 2765 | 18 | US-09-815-242-5919   | Sequence 5919, Ap  | 13 | 41.9 | 9186 | 18 | US-10-311-455-2215  | Sequence 2215, Ap |
| 412 | 13 | 41.9 | 2817 | 9  | US-10-282-132A-7059  | Sequence 7059, Ap  | 13 | 41.9 | 9186 | 18 | US-10-311-455-1005  | Sequence 1005, Ap |
| 413 | 13 | 41.9 | 2817 | 17 | US-10-172-118-877    | Sequence 877, App  | 13 | 41.9 | 9186 | 18 | US-10-311-455-1691  | Sequence 1691, Ap |
| 414 | 13 | 41.9 | 2839 | 17 | US-10-342-887-877    | Sequence 877, App  | 13 | 41.9 | 9186 | 18 | US-10-087-192-1600  | Sequence 1600, Ap |
| 415 | 13 | 41.9 | 2839 | 17 | US-10-104-047-1963   | Sequence 1963, Ap  | 13 | 41.9 | 9186 | 18 | US-10-087-192-1600  | Sequence 100, App |
| 416 | 13 | 41.9 | 2858 | 17 | US-10-600-230-69     | Sequence 69, Appl  | 13 | 41.9 | 9186 | 18 | US-10-056-790-47    | Sequence 47, Appl |
| 417 | 13 | 41.9 | 2878 | 17 | US-10-094-749-265    | Sequence 265, App  | 13 | 41.9 | 9186 | 18 | US-10-087-192-91    | Sequence 91, Appl |
| 418 | 13 | 41.9 | 2888 | 17 | US-10-260-238-1049   | Sequence 1049, Ap  | 13 | 41.9 | 9186 | 18 | US-10-741-601-5633  | Sequence 5633, Ap |
| 419 | 13 | 41.9 | 3315 | 18 | US-10-437-963-76914  | Sequence 76914, A  | 13 | 41.9 | 9186 | 18 | US-10-741-601-5633  | Sequence 17622, A |
| 420 | 13 | 41.9 | 3382 | 16 | US-10-241-596-39     | Sequence 39, Appl  | 13 | 41.9 | 9186 | 18 | US-10-367-094-4     | Sequence 4, Appl  |
| 421 | 13 | 41.9 | 3382 | 16 | US-10-241-596-43     | Sequence 43, Appl  | 13 | 41.9 | 9186 | 18 | US-10-052-482-172   | Sequence 172, App |
| 422 | 13 | 41.9 | 3382 | 16 | US-10-241-596-49     | Sequence 49, Appl  | 13 | 41.9 | 9186 | 18 | US-10-741-601-5700  | Sequence 5700, Ap |
| 423 | 13 | 41.9 | 3382 | 16 | US-10-241-596-53     | Sequence 53, Appl  | 13 | 41.9 | 9186 | 18 | US-10-418-837-1     | Sequence 1, Appl  |
| 424 | 13 | 41.9 | 3382 | 16 | US-10-241-596-57     | Sequence 57, Appl  | 13 | 41.9 | 9186 | 18 | US-10-114-170-62    | Sequence 62, Appl |
| 425 | 13 | 41.9 | 3388 | 16 | US-10-241-596-41     | Sequence 41, Appl  | 13 | 41.9 | 9186 | 18 | US-09-880-107-3949  | Sequence 3949, Ap |
| 426 | 13 | 41.9 | 3388 | 16 | US-10-241-596-47     | Sequence 47, Appl  | 13 | 41.9 | 9186 | 18 | US-10-647-196-1     | Sequence 1, Appl  |
| 427 | 13 | 41.9 | 3388 | 16 | US-10-241-596-51     | Sequence 51, Appl  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 428 | 13 | 41.9 | 3388 | 16 | US-10-241-596-55     | Sequence 55, Appl  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 429 | 13 | 41.9 | 3391 | 16 | US-10-241-596-43     | Sequence 43, Appl  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 430 | 13 | 41.9 | 3397 | 16 | US-10-241-596-45     | Sequence 45, Appl  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 431 | 13 | 41.9 | 3447 | 18 | US-10-437-963-39433  | Sequence 39433, A  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 432 | 13 | 41.9 | 3483 | 18 | US-10-723-860-4050   | Sequence 4050, Ap  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 433 | 13 | 41.9 | 3486 | 18 | US-10-437-963-98912  | Sequence 98912, A  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 434 | 13 | 41.9 | 3487 | 14 | US-10-114-170-164    | Sequence 164, App  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 435 | 13 | 41.9 | 3487 | 18 | US-10-437-963-7808   | Sequence 7808, Ap  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 436 | 13 | 41.9 | 3612 | 9  | US-09-935-291A-10    | Sequence 10, Appl  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 437 | 13 | 41.9 | 3612 | 17 | US-10-377-072-72     | Sequence 72, Appl  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 438 | 13 | 41.9 | 3612 | 18 | US-10-377-072-72     | Sequence 72, Appl  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 439 | 13 | 41.9 | 3737 | 17 | US-10-398-221-2032   | Sequence 2032, Ap  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 440 | 13 | 41.9 | 3832 | 15 | US-10-102-524-1718   | Sequence 1718, Ap  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 441 | 13 | 41.9 | 3832 | 16 | US-10-376-564-86     | Sequence 86, Appl  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 442 | 13 | 41.9 | 3832 | 17 | US-10-159-563-291    | Sequence 291, App  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 443 | 13 | 41.9 | 3838 | 17 | US-10-094-749-903    | Sequence 903, App  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 444 | 13 | 41.9 | 3904 | 17 | US-10-085-198-41     | Sequence 41, Appl  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 445 | 13 | 41.9 | 3919 | 9  | US-09-935-291A-8     | Sequence 8, Appl   | 13 | 41.9 | 9186 | 18 |                     |                   |
| 446 | 13 | 41.9 | 3919 | 17 | US-10-377-072-70     | Sequence 70, Appl  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 447 | 13 | 41.9 | 3919 | 17 | US-10-377-072-70     | Sequence 70, Appl  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 448 | 13 | 41.9 | 3946 | 18 | US-10-437-963-50326  | Sequence 50326, A  | 13 | 41.9 | 9186 | 18 |                     |                   |
| 449 | 13 | 41.9 | 3950 | 17 | US-10-297-022-44     | Sequence 44, Appl  | 13 | 41.9 | 9186 | 18 |                     |                   |

## ALIGNMENTS

## RESULT 1

US-10-688-489-59  
; Sequence 59, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Darby, Paul M.  
; APPLICANT: Dennis, Geoffrey G.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: West Nile Virus  
; FILE REFERENCE: GPI40-04.UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,991  
; PRIOR FILING DATE: 2002-10-16

; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 59  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: West Nile Virus  
US-10-688-489-59

Query Match 100.0%; Score 31; DB 18; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31  
Db 1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31

RESULT 2  
US-10-361-002-5  
; Sequence 5, Application US/10361002  
; Publication No. US20040170954A1  
; GENERAL INFORMATION:  
; APPLICANT: Clearant, Inc.  
; APPLICANT: McKenney, Keith  
; APPLICANT: Gillmeister, Lidja  
; APPLICANT: Marlowe, Kristina  
; APPLICANT: Armistead, David  
; TITLE OF INVENTION: Pathogen Inactivation Assay  
; FILE REFERENCE: CI-0043  
; CURRENT APPLICATION NUMBER: US/10/361,002  
; CURRENT FILING DATE: 2003-02-10  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 10945  
; TYPE: DNA  
; ORGANISM: West Nile virus  
US-10-361-002-5

Query Match 96.8%; Score 30; DB 18; Length 10945;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31  
Db 10481 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10510

RESULT 3  
US-10-361-004-5  
; Sequence 5, Application US/10361004  
; Publication No. US20040170981A1  
; GENERAL INFORMATION:  
; APPLICANT: Clearant, Inc.  
; APPLICANT: McKenney, Keith  
; APPLICANT: Gillmeister, Lidja  
; APPLICANT: Marlowe, Kristina  
; APPLICANT: Armistead, David  
; TITLE OF INVENTION: Real-Time Polymerase Chain Reaction Using Large Target Amplicons  
; FILE REFERENCE: CI-0042  
; CURRENT APPLICATION NUMBER: US/10/361,004  
; CURRENT FILING DATE: 2003-02-10  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 10945  
; TYPE: DNA  
; ORGANISM: West Nile virus  
US-10-361-004-5

Query Match 96.8%; Score 30; DB 18; Length 10945;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31  
Db 10481 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10510

RESULT 4  
US-10-699-550-1  
; Sequence 1, Application US/10699550  
; Publication No. US20040197769A1  
; GENERAL INFORMATION:  
; APPLICANT: WONG, SUSAN J.  
; APPLICANT: SHI, PEI-YONG  
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS  
; FILE REFERENCE: 454311-2232.1  
; CURRENT APPLICATION NUMBER: US/10/699,550  
; CURRENT FILING DATE: 2003-10-31  
; PRIOR APPLICATION NUMBER: 60/476,513  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: 60/422,755  
; PRIOR FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: PCT/US02/09036  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: 60/402,860  
; PRIOR APPLICATION NUMBER: 60/281,947  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/275,025  
; PRIOR FILING DATE: 2001-03-12  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 10975  
; TYPE: DNA  
; ORGANISM: West Nile virus  
US-10-699-550-1

Query Match 96.8%; Score 30; DB 18; Length 10975;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31  
Db 10505 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10534

RESULT 5  
US-10-699-550-2  
; Sequence 2, Application US/10699550  
; Publication No. US20040197769A1  
; GENERAL INFORMATION:  
; APPLICANT: WONG, SUSAN J.  
; APPLICANT: SHI, PEI-YONG  
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS  
; FILE REFERENCE: 454311-2232.1  
; CURRENT APPLICATION NUMBER: US/10/699,550  
; CURRENT FILING DATE: 2003-10-31  
; PRIOR APPLICATION NUMBER: 60/476,513  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: 60/422,755  
; PRIOR FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: PCT/US02/09036  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: 60/402,860  
; PRIOR FILING DATE: 2002-08-08  
; PRIOR APPLICATION NUMBER: 60/281,947  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/275,025  
; PRIOR FILING DATE: 2001-03-12

; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 2  
; LENGTH: 11029  
; TYPE: DNA  
; ORGANISM: West Nile virus  
US-10-699-550-2

Query Match 96.8%; Score 30; DB 18; Length 11029;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31  
|||||  
Db 10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552

## RESULT 6

US-10-679-520A-66  
; Sequence 66, Application US/10679520A  
; Publication No. US20050031641A1  
; GENERAL INFORMATION:  
; APPLICANT: LOOSMORE, SHEENA MAY  
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE FRANCIS  
; APPLICANT: MINKE, JULES MAARTEN  
; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS  
; FILE REFERENCE: 574313-3161.4  
; CURRENT APPLICATION NUMBER: US/10/679,520A  
; PRIOR FILING DATE: 2003-10-06  
; PRIOR APPLICATION NUMBER: 10/374,953  
; PRIOR FILING DATE: 2003-02-26  
; PRIOR APPLICATION NUMBER: 10/116,298  
; PRIOR FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: 60/281,923  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: PCT/FR02/01200  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: FR 01/04737  
; PRIOR FILING DATE: 2001-04-06  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 66  
; LENGTH: 11029  
; TYPE: DNA  
; ORGANISM: West Nile virus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (97)..(10395)  
US-10-679-520A-66

Query Match 96.8%; Score 30; DB 19; Length 11029;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31  
|||||  
Db 10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552

## RESULT 7

US-10-706-892-1  
; Sequence 1, Application US/10706892  
; Publication No. US20050058987A1  
; GENERAL INFORMATION:  
; APPLICANT: SHI, PEI-YONG  
; TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY  
; FILE REFERENCE: 454311-2231.1  
; CURRENT APPLICATION NUMBER: US/10/706,892  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/427,117  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 1  
; LENGTH: 11029  
; TYPE: DNA  
; ORGANISM: West Nile virus  
US-10-706-892-1

Query Match 96.8%; Score 30; DB 19; Length 11029;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31  
|||||  
Db 10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552

## RESULT 8

US-10-706-892-2  
; Sequence 2, Application US/10706892  
; Publication No. US20050058987A1  
; GENERAL INFORMATION:  
; APPLICANT: SHI, PEI-YONG  
; TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY  
; FILE REFERENCE: 454311-2231.1  
; CURRENT APPLICATION NUMBER: US/10/706,892  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/427,117  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 2  
; LENGTH: 11029  
; TYPE: DNA  
; ORGANISM: West Nile virus  
US-10-706-892-2

Query Match 96.8%; Score 30; DB 19; Length 11029;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31  
|||||  
Db 10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552

## RESULT 9

US-10-688-489-68  
; Sequence 68, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GPI40-04.UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 68  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: West Nile virus  
US-10-688-489-68



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Query Match      71.0%; Score 22; DB 18; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGTTGAGTAGACGGTGCTG 31
    |||||
Db 1 GGAAGTTGAGTAGACGGTGCTG 22

RESULT 10
US-10-688-489-63
; Sequence 63, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-63

Query Match      67.7%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTTGACTA 21
    |||||
Db 1 TCCGCCACCGGAAGTTGACTA 21

RESULT 11
US-10-688-489-67
; Sequence 67, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-63

Query Match      71.0%; Score 22; DB 18; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGTTGAGTAGACGGTGCTG 31
    |||||
Db 1 GGAAGTTGAGTAGACGGTGCTG 22

RESULT 10
US-10-688-489-63
; Sequence 63, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-63

Query Match      67.7%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTTGACTA 21
    |||||
Db 1 TCCGCCACCGGAAGTTGACTA 21

RESULT 11
US-10-688-489-67
; Sequence 67, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-67

Query Match      67.7%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGAAGTTGAGTAGACGGTGCTG 31
    |||||
Db 1 GGAAGTTGAGTAGACGGTGCTG 21

RESULT 13
US-10-688-489-62
; Sequence 62, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-62

Query Match      67.7%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGAAGTTGAGTAGACGGTGCTG 31
    |||||
Db 1 GGAAGTTGAGTAGACGGTGCTG 21

RESULT 13
US-10-688-489-62
; Sequence 62, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-62
```

```

; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-62

Query Match      64.5%; Score 20; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTTGAGT 20
    |||||
DB 1 TCCGCCACCGGAAGTTGAGT 20

RESULT 14
US-10-688-489-69
; Sequence 69, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-69

Query Match      64.5%; Score 20; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAAGTTGAGTAGACGGTGCT 30
    |||||
DB 1 GAAGTTGAGTAGACGGTGCT 20

RESULT 15
US-10-688-489-71
; Sequence 71, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 20
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-71

Query Match      61.3%; Score 19; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTTGAG 19
    |||||
DB 1 TCCGCCACCGGAAGTTGAG 19

RESULT 17
US-10-688-489-66
; Sequence 66, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 19
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-66

Query Match      61.3%; Score 19; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTTGAG 19
    |||||
DB 1 TCCGCCACCGGAAGTTGAG 19

```

; PRIOR APPLICATION NUMBER: 60/429,006  
 ; PRIOR FILING DATE: 2002-11-25  
 ; PRIOR APPLICATION NUMBER: 60/449,810  
 ; PRIOR FILING DATE: 2003-02-24  
 ; NUMBER OF SEQ ID NOS: 196  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 66  
 ; LENGTH: 19  
 ; TYPE: DNA  
 ; ORGANISM: West Nile Virus  
 US-10-688-489-66

Query Match 61.3%; Score 19; DB 18; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 0.2;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCCACCGGAGTTGAGTA 21  
 Db 1 CGCCACCGGAGTTGAGTA 19

RESULT 18  
 US-10-688-489-64  
 ; Sequence 64, Application US/10688489  
 ; Publication No. US20040259108A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Linnen, Jeffrey M.  
 ; APPLICANT: Wu, Wen  
 ; APPLICANT: Pollner, Reinhold B.  
 ; APPLICANT: Dennis, Geoffrey G.  
 ; APPLICANT: Darby, Paul M.  
 ; TITLE OF INVENTION: Compositions and Methods for Detecting  
 ; FILE REFERENCE: GP140-04.UT  
 ; CURRENT APPLICATION NUMBER: US/10/688,489  
 ; CURRENT FILING DATE: 2003-10-16  
 ; PRIOR APPLICATION NUMBER: 60/418,891  
 ; PRIOR FILING DATE: 2002-10-16  
 ; PRIOR APPLICATION NUMBER: 60/429,006  
 ; PRIOR FILING DATE: 2002-11-25  
 ; PRIOR APPLICATION NUMBER: 60/449,810  
 ; PRIOR FILING DATE: 2003-02-24  
 ; NUMBER OF SEQ ID NOS: 196  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 64  
 ; LENGTH: 18  
 ; TYPE: DNA  
 ; ORGANISM: West Nile Virus  
 US-10-688-489-64

Query Match 58.1%; Score 18; DB 18; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 0.8;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCCACCGGAGTTGAGT 20  
 Db 1 CGCCACCGGAGTTGAGT 18

RESULT 19  
 US-10-688-489-61  
 ; Sequence 61, Application US/10688489  
 ; Publication No. US20040259108A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Linnen, Jeffrey M.  
 ; APPLICANT: Wu, Wen  
 ; APPLICANT: Pollner, Reinhold B.  
 ; APPLICANT: Dennis, Geoffrey G.  
 ; APPLICANT: Darby, Paul M.  
 ; TITLE OF INVENTION: Compositions and Methods for Detecting  
 ; FILE REFERENCE: GP140-04.UT  
 ; CURRENT APPLICATION NUMBER: US/10/688,489

; CURRENT FILING DATE: 2003-10-16  
 ; PRIOR APPLICATION NUMBER: 60/418,891  
 ; PRIOR FILING DATE: 2002-10-16  
 ; PRIOR APPLICATION NUMBER: 60/429,006  
 ; PRIOR FILING DATE: 2002-11-25  
 ; PRIOR APPLICATION NUMBER: 60/449,810  
 ; PRIOR FILING DATE: 2003-02-24  
 ; NUMBER OF SEQ ID NOS: 196  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 61  
 ; LENGTH: 19  
 ; TYPE: DNA  
 ; ORGANISM: West Nile Virus  
 ; FEATURE:  
 ; NAME/KEY: modified base  
 ; LOCATION: (1)...(1)  
 ; OTHER INFORMATION: I  
 US-10-688-489-61

Query Match 58.1%; Score 18; DB 18; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 0.8;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGCCACCGGAGTTGAG 19  
 Db 2 CGCCACCGGAGTTGAG 19

RESULT 20  
 US-10-688-489-147/c  
 ; Sequence 147, Application US/10688489  
 ; Publication No. US20040259108A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Linnen, Jeffrey M.  
 ; APPLICANT: Pollner, Reinhold B.  
 ; APPLICANT: Wu, Wen  
 ; APPLICANT: Dennis, Geoffrey G.  
 ; APPLICANT: Darby, Paul M.  
 ; TITLE OF INVENTION: Compositions and Methods for Detecting  
 ; FILE REFERENCE: GP140-04.UT  
 ; CURRENT APPLICATION NUMBER: US/10/688,489  
 ; CURRENT FILING DATE: 2003-10-16  
 ; PRIOR APPLICATION NUMBER: 60/418,891  
 ; PRIOR FILING DATE: 2002-10-16  
 ; PRIOR APPLICATION NUMBER: 60/429,006  
 ; PRIOR FILING DATE: 2002-11-25  
 ; PRIOR APPLICATION NUMBER: 60/449,810  
 ; PRIOR FILING DATE: 2003-02-24  
 ; NUMBER OF SEQ ID NOS: 196  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 147  
 ; LENGTH: 26  
 ; TYPE: RNA  
 ; ORGANISM: West Nile Virus  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)...(26)  
 ; OTHER INFORMATION: 2'-OME nucleotide analogs  
 US-10-688-489-147

Query Match 58.1%; Score 18; DB 18; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 0.79;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTGAGTAGACGGTGCTG 31  
 Db 26 GTTGAGTAGACGGTGCTG 9

RESULT 21  
 US-10-688-489-65  
 ; Sequence 65, Application US/10688489

Publication No. US20040259108A1  
GENERAL INFORMATION:  
APPLICANT: Linnen, Jeffrey M.  
APPLICANT: Pollner, Reinhold B.  
APPLICANT: Wu, Wen  
APPLICANT: Dennis, Geoffrey G.  
APPLICANT: Darby, Paul M.  
TITLE OF INVENTION: Compositions and Methods for Detecting  
TITLE OF INVENTION: West Nile Virus  
FILE REFERENCE: GP140-04.UT  
CURRENT APPLICATION NUMBER: US/10/688,489  
CURRENT FILING DATE: 2003-10-16  
PRIOR APPLICATION NUMBER: 60/418,891  
PRIOR FILING DATE: 2002-10-16  
PRIOR APPLICATION NUMBER: 60/429,006  
PRIOR FILING DATE: 2002-11-25  
PRIOR APPLICATION NUMBER: 60/449,810  
PRIOR FILING DATE: 2003-02-24  
NUMBER OF SEQ ID NOS: 196  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 65  
LENGTH: 18  
TYPE: DNA  
ORGANISM: West Nile Virus  
FEATURE:  
NAME/KEY: modified base  
LOCATION: (1)...(1)  
OTHER INFORMATION: I  
US-10-688-489-65

Query Match 54.8%; Score 17; DB 18; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACCGGAAGTTGAGT 20  
DB 2 GCCACCGGAAGTTGAGT 18

RESULT 22  
US-10-653-047-918/c  
Sequence 918, Application US/10653047  
Publication No. US20040229367A1  
GENERAL INFORMATION:  
APPLICANT: Randy M. Berka  
APPLICANT: Michael W. Key  
APPLICANT: Jeffrey R. Shuster  
APPLICANT: Sakari Kauppinen  
APPLICANT: Ib Groth Clausen  
APPLICANT: Peter Blarke Olsen  
TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
TITLE OF INVENTION: Expression  
FILE REFERENCE: 5849.200-US  
CURRENT APPLICATION NUMBER: US/10/653,047  
CURRENT FILING DATE: 2003-08-29  
PRIOR APPLICATION NUMBER: US/09/533,559  
PRIOR FILING DATE: 2003-03-22  
PRIOR APPLICATION NUMBER: 09/273,623  
PRIOR FILING DATE: 1999-03-22  
NUMBER OF SEQ ID NOS: 7860  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 918  
LENGTH: 628  
TYPE: DNA  
ORGANISM: Fusarium venenatum  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)...(628)  
OTHER INFORMATION: n = A,T,C or G  
US-10-653-047-918

Query Match 51.6%; Score 16; DB 18; Length 628;  
Best Local Similarity 100.0%; Pred. No. 9.9;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 14 GTTGAGTAGACGGTGC 29  
DB 205 GTTGAGTAGACGGTGC 190

RESULT 23  
US-10-027-632-274317/c  
Sequence 274317, Application US/10027632  
Publication No. US20020198371A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
TITLE OF INVENTION: Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 274317  
LENGTH: 632  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-274317

Query Match 51.6%; Score 16; DB 13; Length 632;  
Best Local Similarity 100.0%; Pred. No. 9.8;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGTTGAGTAGACG 25  
DB 547 GGAAGTTGAGTAGACG 532

RESULT 24  
US-10-027-632-274317/c  
Sequence 274317, Application US/10027632  
Publication No. US20030204075A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
TITLE OF INVENTION: Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 274317  
; LENGTH: 632  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-274317

Query Match 51.6%; Score 16; DB 17; Length 632;  
Best Local Similarity 100.0%; Pred. No. 9.8;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGTTGAGTAGACG 25  
|||  
DB 547 GGAAGTTGAGTAGACG 532

## RESULT 25

US-10-481-265-136/c  
; Sequence 136, Application US/10481265  
; Publication No. US20040254349A1  
; GENERAL INFORMATION:  
; APPLICANT: James, Brian William  
; APPLICANT: Bacon, Joanna  
; APPLICANT: Marsh, Philip  
; TITLE OF INVENTION: Mycobacterial Antigens Expressed Under Low Oxygen Tension  
; FILE REFERENCE: 1581.1020000  
; CURRENT APPLICATION NUMBER: US/10/481,265  
; CURRENT FILING DATE: 2003-12-19  
; PRIOR APPLICATION NUMBER: GB 0115365.9  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: GB 0121780.1  
; PRIOR FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: PCT/GB02/02845  
; PRIOR FILING DATE: 2002-06-21  
; NUMBER OF SEQ ID NOS: 138  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 136  
; LENGTH: 1323  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
US-10-481-265-136

Query Match 51.6%; Score 16; DB 18; Length 1323;  
Best Local Similarity 100.0%; Pred. No. 9.4;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACCGGAAGTTGAG 19  
|||  
DB 1037 GCCACCGGAAGTTGAG 1022

## RESULT 26

US-09-712-363-49/c  
; Sequence 49, Application US/09712363  
; Patent No. US20020164588A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, David  
; APPLICANT: Rotstein, Sergio H.  
; APPLICANT: Marcotte, Edward M.  
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND  
; INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS  
; FILE REFERENCE: 07419-032001  
; CURRENT APPLICATION NUMBER: US/09/712,363  
; CURRENT FILING DATE: 2000-11-13  
; PRIOR APPLICATION NUMBER: PCT/US00/02246  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/179,531  
; PRIOR FILING DATE: 2000-02-01  
; PRIOR APPLICATION NUMBER: 60/117,844  
; PRIOR FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: 60/118,206,

; PRIOR FILING DATE: 1999-02-01  
; PRIOR APPLICATION NUMBER: 60/126,593  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/134,093  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 60/134,092  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 60/165,124  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/165,086  
; PRIOR FILING DATE: 1999-11-12  
; NUMBER OF SEQ ID NOS: 292  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 49  
; LENGTH: 1326  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
US-09-712-363-49

Query Match 51.6%; Score 16; DB 9; Length 1326;  
Best Local Similarity 100.0%; Pred. No. 9.4;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACCGGAAGTTGAG 19  
|||  
DB 1037 GCCACCGGAAGTTGAG 1022

## RESULT 27

US-10-688-489-104  
; Sequence 104, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen  
; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; TITLE OF INVENTION: West Nile Virus  
; FILE REFERENCE: GP140-04.UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 104  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: West Nile Virus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(21)  
; OTHER INFORMATION: 2'-OME nucleotide analogs  
US-10-688-489-104

Query Match 48.4%; Score 15; DB 18; Length 21;  
Best Local Similarity 100.0%; Pred. No. 49;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GAGTAGACGGTCTG 31  
|||  
DB 1 GAGTAGACGGTCTG 15

## RESULT 28

US-10-688-489-185  
; Sequence 185, Application US/10688489

```

; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 185
; LENGTH: 22
; TYPE: RNA
; ORGANISM: West Nile Virus
; NAME/KEY: misc feature
; LOCATION: (1)..(22)
; OTHER INFORMATION: 2'-OME nucleotide analogs
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(5)
; OTHER INFORMATION: Molecular beacon arm sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18)..(22)
; OTHER INFORMATION: Molecular beacon arm sequence
US-10-688-489-185

Query Match      48.4%; Score 15; DB 18; Length 22;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      17 GAGTAGACGGTGCTG 31
        |||:|||||:|:|
Db       3 GAGUAGACGGUGUG 17

RESULT 29
US-10-098-263B-27587
; Sequence 27587, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 27587
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-27587

Query Match      48.4%; Score 15; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 CACCGAAGTTGAGT 20
        |||:|||||:|:|

```

```

Db       2 CACCGAAGTTGAGT 16

RESULT 30
US-10-688-489-186
; Sequence 186, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 186
; LENGTH: 28
; TYPE: RNA
; ORGANISM: West Nile Virus
; NAME/KEY: misc feature
; LOCATION: (1)..(28)
; OTHER INFORMATION: 2'-OME nucleotide analogs
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(5)
; OTHER INFORMATION: Molecular beacon arm sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (24)..(28)
; OTHER INFORMATION: Molecular beacon arm sequence
US-10-688-489-186

Query Match      48.4%; Score 15; DB 18; Length 28;
Best Local Similarity 80.0%; Pred. No. 48;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      17 GAGTAGACGGTGCTG 31
        |||:|||||:|:|
Db       3 GAGUAGACGGUGUG 17

RESULT 31
US-10-688-489-102
; Sequence 102, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810

```



```
; SEQ ID NO 156396
; LENGTH: 795
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-156396

Query Match      48.4%; Score 15; DB 13; Length 795;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10  GGAAGTTGAGTAGAC 24
      |||||
Db      659  GGAAGTTGAGTAGAC 673

RESULT 36
US-10-027-632-156396
; Sequence 156396, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156396
; LENGTH: 795
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-156396

Query Match      48.4%; Score 15; DB 17; Length 795;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10  GGAAGTTGAGTAGAC 24
      |||||
Db      659  GGAAGTTGAGTAGAC 673

RESULT 37
US-10-027-632-120761/c
; Sequence 120761, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120761
; LENGTH: 910
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-120761

Query Match      48.4%; Score 15; DB 13; Length 910;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15  TTGAGTAGACGGTGC 29
      |||||
Db      333  TTGAGTAGACGGTGC 319

RESULT 38
US-10-027-632-120762/c
; Sequence 120762, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120762
; LENGTH: 910
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-120762

Query Match      48.4%; Score 15; DB 13; Length 910;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15  TTGAGTAGACGGTGC 29
      |||||
Db      333  TTGAGTAGACGGTGC 319

RESULT 39
US-10-027-632-120761/c
; Sequence 120761, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
```



APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 120761  
LENGTH: 910  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-120761

Query Match 48.4%; Score 15; DB 17; Length 910;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTGAGTAGACGGTGC 29  
|||||  
Db 333 TTGAGTAGACGGTGC 319

RESULT 40  
US-10-027-632-120762/c  
Sequence 120762, Application US/10027632  
Publication No. US20030204075A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 120762  
LENGTH: 910  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-120762

Query Match 48.4%; Score 15; DB 17; Length 910;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTGAGTAGACGGTGC 29  
|||||  
Db 333 TTGAGTAGACGGTGC 319

RESULT 41  
US-10-363-345A-29275  
Sequence 29275, Application US/10363345A  
Publication No. US20040234960A1  
GENERAL INFORMATION:  
APPLICANT: Alexander Olek  
APPLICANT: Christian Piepenbrock  
APPLICANT: Kurt Berlin  
TITLE OF INVENTION: Method for determining the degree of methylation of defined  
cytosines in genomic DNA in the sequence context of 5'-CpG-3  
FILE REFERENCE: E01/1227  
CURRENT APPLICATION NUMBER: US/10/363,345A  
CURRENT FILING DATE: 2003-03-03  
NUMBER OF SEQ ID NOS: 40712  
SEQ ID NO 29275  
LENGTH: 1795  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)  
OTHER INFORMATION: CpG-island No: 29275  
US-10-363-345A-29275

Query Match 48.4%; Score 15; DB 18; Length 1795;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AGTTGAGTAGACGGT 27  
|||||  
Db 1002 AGTTGAGTAGACGGT 1016

RESULT 42  
US-10-363-345A-29276/c  
Sequence 29276, Application US/10363345A  
Publication No. US20040234960A1  
GENERAL INFORMATION:  
APPLICANT: Alexander Olek  
APPLICANT: Christian Piepenbrock  
APPLICANT: Kurt Berlin  
TITLE OF INVENTION: Method for determining the degree of methylation of defined  
cytosines in genomic DNA in the sequence context of 5'-CpG-3  
FILE REFERENCE: E01/1227  
CURRENT APPLICATION NUMBER: US/10/363,345A  
CURRENT FILING DATE: 2003-03-03  
NUMBER OF SEQ ID NOS: 40712  
SEQ ID NO 29276  
LENGTH: 1795  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)  
OTHER INFORMATION: CpG-island No: 29276  
US-10-363-345A-29276

Query Match 48.4%; Score 15; DB 18; Length 1795;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AGTTGAGTAGACGGT 27  
|||||  
Db 794 AGTTGAGTAGACGGT 780

RESULT 43  
US-09-738-626-437/c  
Sequence 437, Application US/09738626

Publication No. US20020197605A1  
GENERAL INFORMATION:  
APPLICANT: NAKAGAWA, SATOSHI  
APPLICANT: MIZOGUCHI, HIROSHI  
APPLICANT: ANDO, SEIKO  
APPLICANT: HAYASHI, MIKIRO  
APPLICANT: OCHIAI, KEIKO  
APPLICANT: YOKOI, HARUHIKO  
APPLICANT: TATEISHI, NAKAO  
APPLICANT: SENOH, AKIHIRO  
APPLICANT: IKEDA, MASATO  
APPLICANT: OZAKI, AKIO  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-125  
CURRENT APPLICATION NUMBER: US/09/738,626  
CURRENT FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: JP 99/377484  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: JP 00/159162  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: JP 00/280388  
PRIOR FILING DATE: 2000-08-03  
NUMBER OF SEQ ID NOS: 7059  
SOFTWARE: PatentIn ver. 3.0  
SEQ ID NO 437  
LENGTH: 1863  
TYPE: DNA  
ORGANISM: Corynebacterium glutamicum  
US-09-738-626-437

Query Match 48.4%; Score 15; DB 9; Length 1863;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAAGTTGAG 19  
|||||  
DB 734 CCACCGGAAGTTGAG 720

## RESULT 44

US-10-425-115-16225/c  
Sequence 16225, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 16225  
LENGTH: 1891  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(1891)  
OTHER INFORMATION: unsure at all n locations  
FEATURE:  
OTHER INFORMATION: Clone ID: MPT4577\_114797C.1  
US-10-425-115-16225

Query Match 48.4%; Score 15; DB 18; Length 1891;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCCACCGGAAGT 15  
|||||  
DB 884 TCGCCACCGGAAGT 870

## RESULT 45

US-10-494-672-341/c  
Sequence 341, Application US/10494672  
Publication No. US2005003494A1  
GENERAL INFORMATION:  
APPLICANT: Zelder, Oskar  
APPLICANT: Pompejus, Markus  
APPLICANT: Schroder, Hartwig  
APPLICANT: Kroger, Burkhard  
APPLICANT: Klopffrogge, Corinna  
APPLICANT: Haberhauser, Gregor  
TITLE OF INVENTION: Genes coding for novel proteins  
FILE REFERENCE: BGI-169US  
CURRENT APPLICATION NUMBER: US/10/494,672  
CURRENT FILING DATE: 2004-05-04  
PRIOR APPLICATION NUMBER: PCT/EP02/12134  
PRIOR FILING DATE: 2002-10-31  
PRIOR APPLICATION NUMBER: DE 10154177  
PRIOR FILING DATE: 2001-11-05  
NUMBER OF SEQ ID NOS: 434  
SEQ ID NO 341  
LENGTH: 1969  
TYPE: DNA  
ORGANISM: Corynebacterium glutamicum  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (101)..(1939)  
OTHER INFORMATION: RXA02825  
US-10-494-672-341

Query Match 48.4%; Score 15; DB 18; Length 1969;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAAGTTGAG 19  
|||||  
DB 810 CCACCGGAAGTTGAG 796

## RESULT 46

US-10-425-114-35701/c  
Sequence 35701, Application US/10425114  
Publication No. US20040034888A1  
GENERAL INFORMATION:  
APPLICANT: Liu, Jingdong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E  
APPLICANT: Tabaska, Jack E  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53313)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73128  
SEQ ID NO 35701  
LENGTH: 2066  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: UC-ZMROB73080G04\_FLI  
US-10-425-114-35701

Query Match 48.4%; Score 15; DB 17; Length 2066;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAAGTTGAG 19  
|||||  
DB 1689 CCACCGGAAGTTGAG 1675

RESULT 47  
US-10-280-576-23  
; Sequence 23, Application US/10280576  
; Publication No. US20040044405A1  
; GENERAL INFORMATION:  
; APPLICANT: Wolff, Matthew R.  
; TITLE OF INVENTION: VASCULAR STENT OR GRAFT COATED OR IMPREGNATED WITH PROTEIN  
; FILE REFERENCE: 09820.189  
; CURRENT APPLICATION NUMBER: US/10/280,576  
; CURRENT FILING DATE: 2002-10-22  
; PRIOR APPLICATION NUMBER: 60/343,732  
; PRIOR FILING DATE: 2001-10-25  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 3246  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-280-576-23

Query Match 48.4%; Score 15; DB 17; Length 3246;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GAGTAGACGGTGCTG 31  
|||||  
DB 1370 GAGTAGACGGTGCTG 1384

RESULT 48  
US-09-738-626-1/c  
; Sequence 1, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIO  
; APPLICANT: OCHIAI, KEIKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAKO  
; APPLICANT: SENOH, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738,626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/280988  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 7059  
; SOFTWARE: PatentIn ver. 3.0  
; SEQ ID NO 1  
; LENGTH: 3309400  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
US-09-738-626-1

Query Match 48.4%; Score 15; DB 9; Length 3309400;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAAGTTGAG 19  
|||||  
DB 411416 CCACCGGAAGTTGAG 411402

RESULT 49  
US-09-803-719-272/c  
; Sequence 272, Application US/09803719  
; Publication No. US20030044783A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Lewis T.  
; APPLICANT: Escobedo, Jaime  
; APPLICANT: Innis, Michael A.  
; APPLICANT: Garcia, Pablo Dominiguez  
; APPLICANT: Sudduth-Klinger, Julie  
; APPLICANT: Reinhard, Christoph  
; APPLICANT: Giese, Klaus  
; APPLICANT: Randazzo, Filippo  
; APPLICANT: Kennedy, Giulia C.  
; APPLICANT: Pot, David  
; APPLICANT: Kassam, Altaf  
; APPLICANT: Lamsam, George  
; APPLICANT: Drmanac, Radoje  
; APPLICANT: Crkvenjakov, Radomir  
; APPLICANT: Dickson, Mark  
; APPLICANT: Drmanac, Snezana  
; APPLICANT: Labat, Ivan  
; APPLICANT: Leshkowitz, Dena  
; APPLICANT: Kita, David  
; APPLICANT: Garcia, Veronica  
; APPLICANT: Jones, Lee William  
; APPLICANT: Stache-Crain, Birgit  
; TITLE OF INVENTION: Human Genes and Gene Products  
; FILE REFERENCE: 1624.002  
; CURRENT APPLICATION NUMBER: US/09/803,719  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,609  
; PRIOR FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 2396  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 272  
; LENGTH: 151  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-803-719-272

Query Match 45.2%; Score 14; DB 10; Length 151;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAG 14  
|||||  
DB 28 TCCGCCACCGGAAG 15

RESULT 50  
US-10-719-993-27926  
; Sequence 27926, Application US/10719993  
; Publication No. US20040265849A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001496  
; CURRENT APPLICATION NUMBER: US/10/719,993  
; CURRENT FILING DATE: 2003-11-24  
; NUMBER OF SEQ ID NOS: 55342  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27926  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-719-993-27926

Query Match 45.2%; Score 14; DB 18; Length 201;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGTTGAGTAGA 23  
Db 128 GGAAGTTGAGTAGA 141

Search completed: March 25, 2005, 11:07:28  
Job time : 226.709 secs